

;; FILING DATE: 22-JAN-1993
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 07/826935
;; FILING DATE: 22-JAN-1992
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Lee, Wendy M.
;; REGISTRATION NUMBER:
;; REFERENCE/DOCKET NUMBER: 821P2
;; TELEPHONE: 415/225-1994
;; TELEFAX: 415/952-9881
;; TELEX: 910/371-7168
;; INFORMATION FOR SEQ ID NO: 5:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 160 bases
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
PCT-US95-04228-5

Query Match 1.8%; Score 76; DB 1; Length 160;
Best Local Similarity 100.0%; Pred. No. 3.3e-25;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3141 ggaacattctgctgcgaaagcgcgtgtgaaagatctgtgaccttggccttgcccggg 3200
Db 30 GGACATCTCTGCTGCGAAAGCGACGTGTGAAGATCTGTGACTTTGGCCTTGCCCGGG 89
QY 3201 acatctacaaagacc 3216
Db 90 ACATCTACAAAGACCC 105

RESULT 13
PCT-US95-04228-5
;; Sequence 5, Application PC/TUS9504228
;; GENERAL INFORMATION:
;; APPLICANT: Genentech, Inc.
;; APPLICANT: Bennett, Brian D.
;; APPLICANT: Goeddel, David
;; APPLICANT: Lee, James M.
;; APPLICANT: Matthews, William
;; APPLICANT: Tsai, Siao ping
;; APPLICANT: Wood, William I.
;; TITLE OF INVENTION: PROTEIN TYROSINE KINASE AGONIST ANTIBODIES
;; NUMBER OF SEQUENCES: 45
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Genentech, Inc.
;; STREET: 460 Point San Bruno Blvd
;; CITY: South San Francisco
;; STATE: California
;; COUNTRY: USA
;; ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04228
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/222616
FILING DATE: 04-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Wendy M. Lee
REGISTRATION NUMBER: 00,000
REFERENCE/DOCKET NUMBER: 821P3PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881

;; TELEX: 910/371-7168
;; INFORMATION FOR SEQ ID NO: 5:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 160 bases
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
PCT-US95-04228-5

Query Match 1.8%; Score 76; DB 5; Length 160;
Best Local Similarity 100.0%; Pred. No. 3.3e-25;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3141 ggaacattctgctgcgaaagcgcgtgtgaaagatctgtgaccttggccttgcccggg 3200
Db 30 GGACATCTCTGCTGCGAAAGCGACGTGTGAAGATCTGTGACTTTGGCCTTGCCCGGG 89
QY 3201 acatctacaaagacc 3216
Db 90 ACATCTACAAAGACCC 105

RESULT 14
US-08-340-011-7
;; Sequence 7, Application US/08340011
;; Patent No. 5776755
;; GENERAL INFORMATION:
;; APPLICANT: Alitalo, et al.
;; TITLE OF INVENTION: FLT4, A NOVEL RECEPTOR TYROSIN KINASE
;; NUMBER OF SEQUENCES: 20
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
;; STREET: 6300 Sears Tower, 233 South Wacker Drive
;; CITY: Chicago
;; STATE: Illinois
;; COUNTRY: United States of America
;; ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/08/340,011
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/959,951
FILING DATE: 09-OCT-1992
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Thomas C.
REGISTRATION NUMBER: 36,989
REFERENCE/DOCKET NUMBER: 32267
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 70 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cdna
US-08-340-011-7

Query Match 1.4%; Score 56; DB 1; Length 70;
Best Local Similarity 100.0%; Pred. No. 4.4e-16;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 20 atgcagcggggcgccgctgctgcctgcgactgtgctctgcctgcgactcctgga 75


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Db 15 ATGCAGCGGGCGCGCGCTGTGCCTGCGACTGTGCTCTGCCTGGGACTCTCTCGGA 70
|||||
RESULT 15
US-08-901-710-7
: Sequence 7, Application US/08901710
: Patent No. 6107046
: GENERAL INFORMATION:
: APPLICANT: Alitalo, Kari
: APPLICANT: Joukov, Vladimir
: APPLICANT: Aprelikova, Olga
: APPLICANT: Pajusola, Katri
: APPLICANT: Korhonen, Eelina
: APPLICANT: Korhonen, Jaana
: APPLICANT: Kaipainen, Arja
: APPLICANT: Matikainen, Marja-Terttu
: TITLE OF INVENTION: FLT4, A RECEPTOR TYROSINE KINASE, AND USES
: TITLE OF INVENTION: THEREOF
: NUMBER OF SEQUENCES: 20
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
: STREET: 6300 Sears Tower, 233 South Wacker Drive
: CITY: Chicago
: STATE: Illinois
: COUNTRY: United States of America
: ZIP: 60606-6402
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/901,710
: FILING DATE:
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/340,011
: FILING DATE: 14-NOV-1994
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/257,754
: FILING DATE: 09-JUL-1994
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 07/959,951
: FILING DATE: 09-OCT-1992
: ATTORNEY/AGENT INFORMATION:
: NAME: Gass, David A.
: REGISTRATION NUMBER: 38,153
: REFERENCE/DOCKET NUMBER: 28113/33824
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 312/474-6300
: TELEFAX: 312/474-0448
: TELEX: 25-3856
: INFORMATION FOR SEQ ID NO: 7:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 70 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
US-08-901-710-7

Query Match 1.4% Score 56: DB 3: Length 70;
Best Local Similarity 100.0%; Pred. No. 4.4e-16;
Matches 56: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

Qy 20 atgcagcgggcgcgctgtgcctgcgactgtgctctgcctgggactctctgga 75
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Db 15 ATGCAGCGGGCGCGCGCTGTGCCTGCGACTGTGCTCTGCCTGGGACTCTCTCGGA 70
|||||

RESULT 16
US-08-510-133A-2
: Sequence 2, Application US/08510133A
: Patent No. 6221839
: GENERAL INFORMATION:
: APPLICANT: Alitalo, Kari
: APPLICANT: Joukov, Vladimir
: TITLE OF INVENTION: Receptor Ligand
: NUMBER OF SEQUENCES: 35
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
: STREET: 6300 Sears Tower, 233 South Wacker Drive
: CITY: Chicago
: STATE: Illinois
: COUNTRY: United States of America
: ZIP: 60606-6402
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/510,133A
: FILING DATE: 01-Aug-1995
: CLASSIFICATION: <Unknown>
: ATTORNEY/AGENT INFORMATION:
: NAME: Gass, David A.
: REGISTRATION NUMBER: 38,153
: REFERENCE/DOCKET NUMBER: 28113/32863
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 312/474-6300
: TELEFAX: 312/474-0448
: TELEX: 25-3856
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 70 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-08-510-133A-2

Query Match 1.4% Score 56: DB 4: Length 70;
Best Local Similarity 100.0%; Pred. No. 4.4e-16;
Matches 56: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

Qy 20 atgcagcgggcgcgctgtgcctgcgactgtgctctgcctgggactctctgga 75
|||||
Db 15 ATGCAGCGGGCGCGCGCTGTGCCTGCGACTGTGCTCTGCCTGGGACTCTCTCGGA 70
|||||

RESULT 17
US-08-585-895-2
: Sequence 2, Application US/08585895
: Patent No. 6245530
: GENERAL INFORMATION:
: APPLICANT: Alitalo, Kari
: APPLICANT: Joukov, Vladimir
: TITLE OF INVENTION: Receptor Ligand
: NUMBER OF SEQUENCES: 35
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
: STREET: 6300 Sears Tower, 233 South Wacker Drive
: CITY: Chicago
: STATE: Illinois
: COUNTRY: United States of America
: ZIP: 60606-6402
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
```

APPLICATION NUMBER: US/08/585,895
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Gass, David A.
REGISTRATION NUMBER: 38,153
REFERENCE/DOCKET NUMBER: 28113/33072
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 70 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-585-895-2

Query Match 1.4%; Score 56; DB 4; Length 70;
Best Local Similarity 100.0%; Pred. No. 4.4e-16;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 20 atgcagcgggcgccgctgtgcctgcgactgtgctctgcctgggactcctaga 75
|||||
Db 15 ATGCAGCGGGCGCCGCTGTGCTGCCTGCGACTGTGCTCTGCTGGGACTCCTGGA 70

RESULT 18
US-08-176-620A-3
Sequence 3, Application US/08176620A
Patent No. 5595904
GENERAL INFORMATION:

APPLICANT: Boulton, Teri G.
APPLICANT: Cobb, Melanie H.
APPLICANT: Yancopoulos, George D.
APPLICANT: Nye, Steven
APPLICANT: Panayotatos, Nikos
TITLE OF INVENTION: A Family of Map2 Protein Kinases
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/176,620A
FILING DATE: 03-JAN-1994
CLASSIFICATION: 800

ATTORNEY/AGENT INFORMATION:
NAME: Mirock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 6526-123
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1467 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)

FEATURE:
NAME/KEY: CDS
LOCATION: 1..1245
US-08-176-620A-3

Query Match 0.6%; Score 26; DB 1; Length 1467;
Best Local Similarity 100.0%; Pred. No. 0.018;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3173 aagatctgtgactttggccttgcccg 3198
|||||
Db 655 AAGATCTGTGACTTTGGCCTTGCCCG 680

RESULT 19
US-08-463-862-3
Sequence 3, Application US/08463862
Patent No. 5776751
GENERAL INFORMATION:

APPLICANT: Boulton, Teri G. et al.
TITLE OF INVENTION: A FAMILY OF MAP2 PROTEIN KINASES
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,862
FILING DATE: 05-JUN-1995

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/701,544
FILING DATE: 16-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Mirock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 6526-049
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
TELEFAX: 212 869-8864/9741
TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1467 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1245
US-08-463-862-3

Query Match 0.6%; Score 26; DB 1; Length 1467;
Best Local Similarity 100.0%; Pred. No. 0.018;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3173 aagatctgtgactttggccttgcccg 3198
|||||
Db 655 AAGATCTGTGACTTTGGCCTTGCCCG 680

RESULT 20

US-08-461-985-3
; Sequence 3, Application US/08461985
; Patent No. 5872006
; GENERAL INFORMATION:
; APPLICANT: Boulton, Teri G.
; APPLICANT: Cobb, Melanie H.
; APPLICANT: Yancopoulos, George D.
; APPLICANT: Nye, Steven
; APPLICANT: Panayotatos, Nikos
; TITLE OF INVENTION: A Family of Map2 Protein Kinases
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/461.985
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/176,620
; FILING DATE: 03-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 6526-123
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1467 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1245
US-08-461-985-3

Query Match 0.6% Score 26; DB 2: Length 1467;
Best Local Similarity 100.0%; Pred. No. 0.018;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3173 aagatctgtgactttggccttgcccg 3198
|||||
Db 655 AAGATCTGTGACTTTGGCCTTGCCCG 680

RESULT 21
US-08-458-887-3
; Sequence 3, Application US/08458887
; Patent No. 5914261
; GENERAL INFORMATION:
; APPLICANT: Boulton, Teri G. et al.
; TITLE OF INVENTION: A FAMILY OF MAP2 PROTEIN KINASES
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York

COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/458.887
FILING DATE: 02-JUN-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/701,544
FILING DATE: 16-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 6526-049
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
TELEFAX: 212 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1467 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1245
US-08-458-887-3

Query Match 0.6% Score 26; DB 2: Length 1467;
Best Local Similarity 100.0%; Pred. No. 0.018;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3173 aagatctgtgactttggccttgcccg 3198
|||||
Db 655 AAGATCTGTGACTTTGGCCTTGCCCG 680

RESULT 22
US-08-932-787B-3
; Sequence 3, Application US/08932787B
; Patent No. 6277963
; GENERAL INFORMATION:
; APPLICANT: Boulton et al.
; TITLE OF INVENTION: ANTIBODIES DIRECTED TOWARD EXTRACELLULAR SIGNAL-RELATED
; FILE REFERENCE: REG 430-A-1
; CURRENT APPLICATION NUMBER: US/08/932.787B
; CURRENT FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 08/469,547
; PRIOR FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: 08/178,488
; PRIOR FILING DATE: 1994-01-07
; PRIOR APPLICATION NUMBER: 07/701,544
; PRIOR FILING DATE: 1991-05-16
; PRIOR APPLICATION NUMBER: 07/532,004
; PRIOR FILING DATE: 1990-06-01
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 1467
; TYPE: DNA
; ORGANISM: RAT
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1245)
; OTHER INFORMATION: ERK2 CDNA

US-08-932-787B-3

Query Match 0.6%; Score 26; DB 4; Length 1467;
Best Local Similarity 100.0%; Pred. No. 0.018;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3173 aagatctgtgactttggccttgcccg 3198
|||||
Db 655 aagatctgtgactttggccttgcccg 680

RESULT 23

US-08-932-012C-3
; Sequence 3, Application US/08932012C
; Patent No. 6257035
; GENERAL INFORMATION:
; APPLICANT: Boulton et al.
; TITLE OF INVENTION: A FAMILY OF MAP2 PROTEIN KINASES
; FILE REFERENCE: REG 430-Y-1
; CURRENT APPLICATION NUMBER: US/08/932,012C
; CURRENT FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 08/462,874
; PRIOR FILING DATE: 1995-06-05
; PRIOR APPLICATION NUMBER: 08/178,488
; PRIOR FILING DATE: 1994-01-07
; PRIOR APPLICATION NUMBER: 07/701,544
; PRIOR FILING DATE: 1991-05-16
; PRIOR APPLICATION NUMBER: 07/532,004
; PRIOR FILING DATE: 1990-06-01
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 1467
; TYPE: DNA
; ORGANISM: RAT
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1245)
; OTHER INFORMATION: ERK2 CDNA
US-08-932-012C-3

Query Match 0.6%; Score 26; DB 4; Length 1467;
Best Local Similarity 100.0%; Pred. No. 0.018;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3173 aagatctgtgactttggccttgcccg 3198
|||||
Db 655 aagatctgtgactttggccttgcccg 680

RESULT 24

US-08-888-818C-3
; Sequence 3, Application US/08888818C
; Patent No. 6303358
; GENERAL INFORMATION:
; APPLICANT: Boulton et al.
; TITLE OF INVENTION: A FAMILY OF MAP2 PROTEIN KINASES
; FILE REFERENCE: REG 430-Y-1
; CURRENT APPLICATION NUMBER: US/08/888,818C
; CURRENT FILING DATE: 1997-07-07
; PRIOR APPLICATION NUMBER: 08/478,985
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: 08/178,488
; PRIOR FILING DATE: 1994-01-07
; PRIOR APPLICATION NUMBER: 07/701,544
; PRIOR FILING DATE: 1991-05-16
; PRIOR APPLICATION NUMBER: 07/532,004
; PRIOR FILING DATE: 1990-06-01
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3

; LENGTH: 1467
; TYPE: DNA
; ORGANISM: RAT
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1245)
; OTHER INFORMATION: ERK2 CDNA
US-08-888-818C-3

Query Match 0.6%; Score 26; DB 4; Length 1467;
Best Local Similarity 100.0%; Pred. No. 0.018;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3173 aagatctgtgactttggccttgcccg 3198
|||||
Db 655 aagatctgtgactttggccttgcccg 680

RESULT 25

US-08-469-537A-19
; Sequence 19, Application US/08469537A
; Patent No. 5843749
; GENERAL INFORMATION:
; APPLICANT: Maisonnier, et al.
; TITLE OF INVENTION: EHK AND KOR TYROSINE
; TITLE OF INVENTION: KINASES
; NUMBER OF SEQUENCES: 107
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Regeneron Pharmaceuticals, Inc.
; STREET: 777 Old Saw Mill River Road
; CITY: Tarrytown
; STATE: NY
; COUNTRY: U.S.A.
; ZIP: 10591
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,537A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/406,247
; FILING DATE: 17-MAR-1995
; APPLICATION NUMBER: USSN 08/144,992
; FILING DATE: 28-OCT-1993
; APPLICATION NUMBER: USSN 07/736,559
; FILING DATE: 26-JUL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Kempler, Ph.D., Gail M
; REGISTRATION NUMBER: 32,143
; REFERENCE/DOCKET NUMBER: REG 070C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 914-345-7400
; TELEFAX: 914-345-7721
; TELEX:
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 159 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: unknown
; MOLECULE TYPE: CDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..159
US-08-469-537A-19

Query Match 0.6%; Score 23; DB 2; Length 159;

Best Local Similarity 100.0%; Pred. No. 0.46; Indels 0; Gaps 0;
Matches 23; Conservative 0; Mismatches 0;

Qy 3167 gtggtgaagatctgtgactttgg 3189
|||||
Db 22 GTGGTGAAGATCTGTGACTTTGG 44

RESULT 26

US-07-912-122-3
; Sequence 3, Application US/07912122
; Patent No. 6228609
; GENERAL INFORMATION:
; APPLICANT: YANG, Zhi
; TITLE OF INVENTION: NOVEL FLK-2 AND ANALOGS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bertram I. Rowland
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/912,122
; FILING DATE: 19920709
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Rowland, Bertram I.
; REGISTRATION NUMBER: 20,015
; REFERENCE/DOCKET NUMBER: A-55931/BIR
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 789-1989
; TELEFAX: (415) 398-3249
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1894 base pairs
; TYPE: Nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 31..1473

US-07-912-122-3

Query Match 0.6%; Score 23; DB 4; Length 1894;
Best Local Similarity 100.0%; Pred. No. 0.42; Indels 0; Gaps 0;
Matches 23; Conservative 0; Mismatches 0;

Qy 3167 gtggtgaagatctgtgactttgg 3189
|||||
Db 976 GTGGTGAAGATCTGTGACTTTGG 998

RESULT 27

PCT-US93-06404-3
; Sequence 3, Application PC/TUS9306404
; GENERAL INFORMATION:
; APPLICANT: YANG, Zhi
; TITLE OF INVENTION: NOVEL FLK-2 AND ANALOGS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bertram I. Rowland
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California

; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/06404
; FILING DATE: 19930707
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Rowland, Bertram I.
; REGISTRATION NUMBER: 20,015
; REFERENCE/DOCKET NUMBER: FP-55931/BIR
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 789-1989
; TELEFAX: (415) 398-3249
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1894 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 31..1473
; PCT-US93-06404-3

Query Match 0.6%; Score 23; DB 5; Length 1894;
Best Local Similarity 100.0%; Pred. No. 0.42; Indels 0; Gaps 0;
Matches 23; Conservative 0; Mismatches 0;

Qy 3167 gtggtgaagatctgtgactttgg 3189
|||||
Db 976 GTGGTGAAGATCTGTGACTTTGG 998

RESULT 28

US-07-813-593-1
; Sequence 1, Application US/07813593
; Patent No. 5185438
; GENERAL INFORMATION:
; APPLICANT: Lemischka, Ihor R.
; TITLE OF INVENTION: TOTIPOTENT HEMATOPOIETIC STEM CELL
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: IMCLONE SYSTEMS INCORPORATED
; STREET: 180 VARICK STREET
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 10014

Query Match 0.6%; Score 23; DB 4; Length 1894;
Best Local Similarity 100.0%; Pred. No. 0.42; Indels 0; Gaps 0;
Matches 23; Conservative 0; Mismatches 0;

Qy 3167 gtggtgaagatctgtgactttgg 3189
|||||
Db 976 GTGGTGAAGATCTGTGACTTTGG 998

RESULT 27

PCT-US93-06404-3
; Sequence 3, Application PC/TUS9306404
; GENERAL INFORMATION:
; APPLICANT: YANG, Zhi
; TITLE OF INVENTION: NOVEL FLK-2 AND ANALOGS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bertram I. Rowland
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California

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; FILING DATE: 02-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Feit, Irving N.
; REGISTRATION NUMBER: 28,601
; REFERENCE/DOCKET NUMBER: LEM-3-PPP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-645-1405
; TELEFAX: 212-645-2054
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3453 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 31..3009
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 31..3006
; US-07-813-593-1

Query Match 0.6%; Score 23; DB 1; Length 3453:
Best Local Similarity 100.0%; Pred. No. 0.41;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0:

Qy 3167 gtcgtgaagatctgtgactttgg 3189
|||||
Db 2509 gtcgtgaagatctgtgactttgg 2531

RESULT 29
US-07-977-451-1
; Sequence 1, Application US/07977451
; Patent No. 5270458
; GENERAL INFORMATION:
; APPLICANT: Lemischka, Ihor R.
; TITLE OF INVENTION: TOTIPOTENT HEMATOPOIETIC STEM CELL
; TITLE OF INVENTION: RECEPTORS AND THEIR LIGANDS
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ImClone Systems Incorporated
; STREET: 180 Varick Street
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10014
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/977,451
; FILING DATE: 19921119
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US UNASSIGNED
; FILING DATE: 12-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/906,397
; FILING DATE: 26-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US PCT/US92/05401
; FILING DATE: 26-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: TW 81102961
; FILING DATE: 15-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US PCT/US92/02750
; FILING DATE: 02-APR-1992
```

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/813,593
; FILING DATE: 24-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/793,065
; FILING DATE: 15-NOV-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/728,913
; FILING DATE: 28-JUN-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/679,666
; FILING DATE: 02-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Feit, Irving N.
; REGISTRATION NUMBER: 28,601
; REFERENCE/DOCKET NUMBER: LEM-3-7P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-645-1405
; TELEFAX: 212-645-2054
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3453 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-Terminal
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 112..3006
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 31..111
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 31..3009
; US-07-977-451-1

Query Match 0.6%; Score 23; DB 1; Length 3453:
Best Local Similarity 100.0%; Pred. No. 0.41;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0:

Qy 3167 gtcgtgaagatctgtgactttgg 3189
|||||
Db 2509 gtcgtgaagatctgtgactttgg 2531

RESULT 30
US-07-946-507-1
; Sequence 1, Application US/07946507
; Patent No. 5283354
; GENERAL INFORMATION:
; APPLICANT: Lemischka, Ihor R.
; TITLE OF INVENTION: TOTIPOTENT HEMATOPOIETIC STEM CELL
; TITLE OF INVENTION: RECEPTORS AND THEIR LIGANDS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: IMCLONE SYSTEMS INCORPORATED
; STREET: 180 VARICK STREET
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 10014
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; APPLICATION NUMBER: US/07/946,507
; FILING DATE: 19921119
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US UNASSIGNED
; FILING DATE: 12-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/906,397
; FILING DATE: 26-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US PCT/US92/05401
; FILING DATE: 26-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: TW 81102961
; FILING DATE: 15-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US PCT/US92/02750
; FILING DATE: 02-APR-1992
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; FILING DATE: 19920917
; CLASSIFICATION: 536
; PRIOR APPLICATION NUMBER: US/07/813,593
; FILING DATE: 24-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/793,065
; FILING DATE: 15-NOV-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/728,913
; FILING DATE: 28-JUN-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/679,666
; FILING DATE: 02-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Feit, Irving N.
; REGISTRATION NUMBER: 28,601
; REFERENCE/DOCKET NUMBER: LEM-3-PPP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-645-1405
; TELEFAX: 212-645-2054
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3453 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 31..3009
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 31..3006
US-07-946-507-1

Query Match 0.6%; Score 23; DB 1; Length 3453;
Best Local Similarity 100.0%; Pred. No. 0.41;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3167 gtggtgaagatctgtgactttgg 3189
|||||
Db 2509 GTGGTGAAGATCTGTGACTTTGG 2531

RESULT 31
US-08-252-517-1
; Sequence 1, Application US/08252517
; Patent No. 5548065
; GENERAL INFORMATION:
; APPLICANT: Lemischka, Ihor R.
; TITLE OF INVENTION: TOTIPOTENT HEMATOPOIETIC STEM CELL
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ImClone Systems Incorporated
; STREET: 180 Varick Street
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10014
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/252,517
; FILING DATE: 31-OCT-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/977,451

; FILING DATE: 19-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/906,397
; FILING DATE: 26-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US PCT/US92/05401
; FILING DATE: 26-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: TW 81102961
; FILING DATE: 15-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US PCT/US92/02750
; FILING DATE: 02-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/813,593
; FILING DATE: 24-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/793,065
; FILING DATE: 15-NOV-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/728,913
; FILING DATE: 28-JUN-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/679,666
; FILING DATE: 02-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Feit, Irving N.
; REGISTRATION NUMBER: 28,601
; REFERENCE/DOCKET NUMBER: LEM-3-7P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-645-1405
; TELEFAX: 212-645-2054
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3453 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 112..3006
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 31..111
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 31..3009
US-08-252-517-1

Query Match 0.6%; Score 23; DB 1; Length 3453;
Best Local Similarity 100.0%; Pred. No. 0.41;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3167 gtggtgaagatctgtgactttgg 3189
|||||
Db 2509 GTGGTGAAGATCTGTGACTTTGG 2531

RESULT 32
US-07-906-397A-1
; Sequence 1, Application US/07906397A
; Patent No. 5621090
; GENERAL INFORMATION:
; APPLICANT: Lemischka, Ihor R.
; TITLE OF INVENTION: TOTIPOTENT HEMATOPOIETIC STEM CELL
; TITLE OF INVENTION: RECEPTORS AND THEIR LIGANDS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:

ADDRESSEE: IMCLONE SYSTEMS INCORPORATED
STREET: 180 VARICK STREET
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: U.S.A.
ZIP: 10014
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/906.397A
FILING DATE: 19920626
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/813,593
FILING DATE: 24-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/793,065
FILING DATE: 15-NOV-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/728,913
FILING DATE: 28-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/679,666
FILING DATE: 02-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Felt, Irving N.
REGISTRATION NUMBER: 28,601
REFERENCE/DOCKET NUMBER: LEM-3-PPPPPP
TELEPHONE: 212-645-1405
TELEFAX: 212-645-2054
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3453 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cdna
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
FEATURE:
NAME/KEY: CDS
LOCATION: 31..3009
NAME/KEY: mat_peptide
LOCATION: 31..3006
US-07-906-397A-1

Query Match 0.6%; Score 23; DB 1; Length 3453;
Best Local Similarity 100.0%; Pred. No. 0.41;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3167 gtggtgaagatctgtgactttgg 3189
|||||
DB 2509 GTGGTGAAGATCTGTGACTTTGG 2531

RESULT 33
US-08-601-891-1
Sequence 1, Application US/08601891
Patent No. 5747651
GENERAL INFORMATION:
APPLICANT: Lemischka, Ihor R.
TITLE OF INVENTION: TOTIPOTENT HEMATOPOIETIC STEM CELL
TITLE OF INVENTION: RECEPTORS AND THEIR LIGANDS
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: InClone Systems Incorporated

STREET: 180 Varick Street
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10014
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/601,891
FILING DATE: 15-FEB-1996
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/977,451
FILING DATE: 19-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/906,397
FILING DATE: 26-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US PCT/US92/05401
FILING DATE: 26-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: TW 81102961
FILING DATE: 15-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US PCT/US92/02750
FILING DATE: 02-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/813,593
FILING DATE: 24-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/793,065
FILING DATE: 15-NOV-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/728,913
FILING DATE: 28-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/679,666
FILING DATE: 02-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Felt, Irving N.
REGISTRATION NUMBER: 28,601
REFERENCE/DOCKET NUMBER: LEM-3-7P
TELEPHONE: 212-645-1405
TELEFAX: 212-645-2054
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3453 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cdna
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 112..3006
NAME/KEY: sig_peptide
LOCATION: 31..111
NAME/KEY: CDS
LOCATION: 31..3009
US-08-601-891-1

Query Match 0.6%; Score 23; DB 1; Length 3453;
Best Local Similarity 100.0%; Pred. No. 0.41;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 3167 gtggtgaagatctgtgactttgg 3189
|||||
Db 2509 GTGGTGAAGATCTGTGACTTTGG 2531

RESULT 34
US-09-021-324-1
: Sequence 1, Application US/09021324
: Patent No. 5912133
: GENERAL INFORMATION:
: APPLICANT: Lemischka, Ihor R.
: TITLE OF INVENTION: TOTIPOTENT HEMATOPOIETIC STEM CELL
: TITLE OF INVENTION: RECEPTORS AND THEIR LIGANDS
: NUMBER OF SEQUENCES: 10
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: InClone Systems Incorporated
: STREET: 180 Varlick Street
: CITY: New York
: STATE: New York
: COUNTRY: U.S.A.
: ZIP: 10014
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/021,324
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US/07/977,451
: FILING DATE: 1992-11-19
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/906,397
: FILING DATE: 26-JUN-1992
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US PCT/US92/05401
: FILING DATE: 26-JUN-1992
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: TW 81102961
: FILING DATE: 15-APR-1992
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US PCT/US92/02750
: FILING DATE: 02-APR-1992
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/813,593
: FILING DATE: 24-DEC-1991
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/793,065
: FILING DATE: 15-NOV-1991
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/728,913
: FILING DATE: 28-JUN-1991
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/679,666
: FILING DATE: 02-APR-1991
: ATTORNEY/AGENT INFORMATION:
: NAME: Feit, Irving N.
: REGISTRATION NUMBER: 28,601
: REFERENCE/DOCKET NUMBER: LEM-3-7P
: TELEPHONE: 212-645-1405
: TELEFAX: 212-645-2054
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 3453 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: HYPOTHETICAL: NO

: ANTI-SENSE: NO
: FRAGMENT TYPE: N-terminal
: FEATURE:
: NAME/KEY: mat_peptide
: LOCATION: 112..3006
: FEATURE:
: NAME/KEY: sig_peptide
: LOCATION: 31..111
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 31..3009
: US-09-021-324-1

Query Match 0.6%; Score 23; DB 2; Length 3453;
Best Local Similarity 100.0%; Pred. No. 0.41;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 3167 gtggtgaagatctgtgactttgg 3189
|||||
Db 2509 GTGGTGAAGATCTGTGACTTTGG 2531

RESULT 35
PCT-US92-02750-1
: Sequence 1, Application PC/TUS9202750
: GENERAL INFORMATION:
: APPLICANT: LEMISCHKA, IHOR R.
: TITLE OF INVENTION: Totipotent Hematopoietic Stem Cell
: TITLE OF INVENTION: Receptors And Their Ligands
: NUMBER OF SEQUENCES: 8
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: INCLONE SYSTEMS INCORPORATED
: STREET: 180 VARICK STREET
: CITY: NEW YORK
: STATE: NEW YORK
: COUNTRY: US
: ZIP: 10014
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: PCT/US92/02750
: FILING DATE: 19920402
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: FEIT, IRVING N.
: REGISTRATION NUMBER: 28,601
: REFERENCE/DOCKET NUMBER: LEM-3-PPPPT
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 212-645-1405
: TELEFAX: 212-645-2054
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 3453 base pairs
: TYPE: NUCLEIC ACID
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 31..3009
: FEATURE:
: NAME/KEY: mat_peptide
: LOCATION: 31..3006
: PCT-US92-02750-1

Query Match 0.6%; Score 23; DB 5; Length 3453;
Best Local Similarity 100.0%; Pred. No. 0.41;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3167 gtcgtgaagatctgtgactttgg 3189
|||||
Db 2509 GTGGTGAAGATCTGTGACTTTGG 2531

RESULT 36

PCT-US92-05401-1
; Sequence 1, Application PC/TUS9205401
; GENERAL INFORMATION:
; APPLICANT: Lemischka, Ihor R.
; TITLE OF INVENTION: TOTIPOTENT HEMATOPOIETIC STEM CELL
; TITLE OF INVENTION: RECEPTORS AND THEIR LIGANDS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: IMCLONE SYSTEMS INCORPORATED
; STREET: 180 VARICK STREET
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 10014
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/05401
; FILING DATE: 19920626
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Feit, Irving N.
; REGISTRATION NUMBER: 28,601
; REFERENCE/DOCKET NUMBER: LEM-3-PPPPPT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-645-1405
; TELEFAX: 212-645-2054
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3453 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 31..3009
; NAME/KEY: mat_peptide
; LOCATION: 31..3006
PCT-US92-05401-1

Query Match 0.6%; Score 23; DB 5; Length 3453;
Best Local Similarity 100.0%; Pred. No. 0.41;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3167 gtcgtgaagatctgtgactttgg 3189
|||||
Db 2509 GTGGTGAAGATCTGTGACTTTGG 2531

RESULT 37

PCT-US92-09893-1
; Sequence 1, Application PC/TUS9209893
; GENERAL INFORMATION:
; APPLICANT: Lemischka, Ihor R.
; TITLE OF INVENTION: TOTIPOTENT HEMATOPOIETIC STEM CELL
; TITLE OF INVENTION: RECEPTORS AND THEIR LIGANDS
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ImClone Systems Incorporated
; STREET: 180 Varick Street

; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10014
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/09893
; FILING DATE: 19921116
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Feit, Irving N.
; REGISTRATION NUMBER: 28,601
; REFERENCE/DOCKET NUMBER: LEM-3-7PT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-645-1405
; TELEFAX: 212-645-2054
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3453 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 112..3006
; NAME/KEY: sig_peptide
; LOCATION: 31..111
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 31..3009
PCT-US92-09893-1

Query Match 0.6%; Score 23; DB 5; Length 3453;
Best Local Similarity 100.0%; Pred. No. 0.41;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3167 gtcgtgaagatctgtgactttgg 3189
|||||
Db 2509 GTGGTGAAGATCTGTGACTTTGG 2531

RESULT 38

US-08-222-299-1
; Sequence 11, Application US/08122795B
; Patent No. 5635385
; GENERAL INFORMATION:
; APPLICANT: Lance H. Leopold
; APPLICANT: Scott K. Shore
; APPLICANT: Moolle V. R. Reddy
; APPLICANT: E. Premkumar Reddy
; TITLE OF INVENTION: MULTI-UNIT RIBOZYME
; TITLE OF INVENTION: INHIBITION OF ONCOGENE EXPRESSION
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seidel, Gonda, Lavorgna
; ADDRESSEE: & Monaco, P.C.
; STREET: Two Penn Center Plaza, Suite 1800
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: U.S.A.
; ZIP: 19102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 Inch, 720 Kb

COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/122,795B
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 122,795
FILING DATE: 15 September 1993
ATTORNEY/AGENT INFORMATION:
NAME: Monaco, Daniel A.
REGISTRATION NUMBER: 30,480
REFERENCE/DOCKET NUMBER: 6056-192
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-8383
TELEFAX: (215) 568-5549
TELEX: No. 563538E
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 Nucleotides
TYPE: nucleic acid
STRANDEDNESS: single stranded
Sequence 1, Application US/08222299
Patent No. 5635388
GENERAL INFORMATION:
APPLICANT: Bennett, Brian D.
APPLICANT: Broz, Susan D.
APPLICANT: Matthews, William
APPLICANT: Zeigler, Francis C.
TITLE OF INVENTION: AGONIST ANTIBODIES AGAINST THE FLK2/FLT3 RECEPTOR AND USES THEREOF
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/222,299
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Hasak, Janet E.
REGISTRATION NUMBER: 28,616
REFERENCE/DOCKET NUMBER: 879
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1896
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3521 bases
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-222-299-1

Query Match 0.68; Score 23; DB 1; Length 3521;
Best Local Similarity 100.0%; Pred. No. 0.4;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3167 gtggtgaagatctgtgactttgg 3189

Db 2560 GTGGTGAAGATCTGTGACTTTGG 2582
|||||
RESULT 39
US-08-434-878-1
Sequence 1, Application US/08434878
Patent No. 5957865
GENERAL INFORMATION:
APPLICANT: Bennett, Brian D.
APPLICANT: Broz, Susan D.
APPLICANT: Matthews, William
APPLICANT: Zeigler, Francis C.
TITLE OF INVENTION: AGONIST ANTIBODIES AGAINST THE FLK2/FLT3 RECEPTOR AND USES THEREOF
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/434,878
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Hasak, Janet E.
REGISTRATION NUMBER: 28,616
REFERENCE/DOCKET NUMBER: 879
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1896
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3521 bases
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-434-878-1

Query Match 0.6%; Score 23; DB 2; Length 3521;
Best Local Similarity 100.0%; Pred. No. 0.4;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3167 gtggtgaagatctgtgactttgg 3189
|||||
Db 2560 GTGGTGAAGATCTGTGACTTTGG 2582

RESULT 40
PCT-US95-03718-1
Sequence 1, Application PC/TUS9503718
GENERAL INFORMATION:
APPLICANT: GENENTECH, INC.
TITLE OF INVENTION: AGONIST ANTIBODIES AGAINST THE FLK2/FLT3 RECEPTOR AND USES THEREOF
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA

ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genetech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/03718
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Wendy M. Lee
REGISTRATION NUMBER: 00,000
REFERENCE/DOCKET NUMBER: 879PCT
TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3521 bases
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
PCT-US95-03718-1

Query Match 0.6%; Score 23; DB 5; Length 3521;
Best Local Similarity 100.0%; Pred. No. 0.4;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3167 gtggtgaagatctgtgactttgg 3189
|||||
Db 2560 GTGCTGAAGATCTGTGACTTTGG 2582

RESULT 41
US-08-180-195-35
Sequence 35, Application US/08180195
Patent No. 5567584
GENERAL INFORMATION:
APPLICANT: Sledziewski Ph.D., Andrzej Z
APPLICANT: Bell, Lillian A.
APPLICANT: Kindsvogel Ph.D., Wayne R.
TITLE OF INVENTION: METHODS OF PRODUCING SECRETED RECEPTOR ANALOGS
TITLE OF INVENTION: AND BIOLOGICALLY ACTIVE DIMERIZED POLYPEPTIDE
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry
STREET: 6300 Columbia Center
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/180,195
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/634,510
FILING DATE:
APPLICATION NUMBER: US 07/146,877
FILING DATE: 22-JAN-1988
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/347,291
FILING DATE: 02-MAY-1989
ATTORNEY/AGENT INFORMATION:
NAME: Maki J.D., David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 990008.446C3
TELEPHONE: 206-622-4900
TELEFAX: 206-682-6031
TELEX: 3723836
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 4054 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: N
ANTI-SENSE: N
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: p-alpha-17B
FEATURE:
NAME/KEY: CDS
LOCATION: 205..3471
OTHER INFORMATION:
US-08-180-195-35

Query Match 0.6%; Score 23; DB 1; Length 4054;
Best Local Similarity 100.0%; Pred. No. 0.4;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3170 gtgaagatctgtgactttggcct 3192
|||||
Db 2698 GTGAAGATCTGTGACTTTGGCCT 2720

RESULT 42
US-08-477-329-35
Sequence 35, Application US/08477329
Patent No. 5750375
GENERAL INFORMATION:
APPLICANT: Sledziewski Ph.D., Andrzej Z
APPLICANT: Bell, Lillian A.
APPLICANT: Kindsvogel Ph.D., Wayne R.
TITLE OF INVENTION: METHODS OF PRODUCING SECRETED RECEPTOR ANALOGS AND BIOLOGI
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,329
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 990008.446C6
TELEPHONE: 206-622-4900
TELEFAX: 206-682-6031
TELEX: 3723836

INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 4054 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: N
ANTI-SENSE: N
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: p-alpha-17B
FEATURE:
NAME/KEY: CDS
LOCATION: 205..3471
OTHER INFORMATION:
US-08-477-329-35

Query Match 0.6%; Score 23; DB 1; Length 4054;
Best Local Similarity 100.0%; Pred. No. 0.4;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3170 gtgaagatctgtgactttggcct 3192
|||||
Db 2698 GTGAAGATCTGTGACTTTGGCCT 2720

RESULT 43

US-08-475-458-35
Sequence 35, Application US/08475458
Patent No. 5843725
GENERAL INFORMATION:
APPLICANT: Sledziewski Ph.D., Andrzej Z
APPLICANT: Bell, Lillian A.
APPLICANT: Kindsvogel Ph.D., Wayne R.
TITLE OF INVENTION: METHODS OF PRODUCING SECRETED RECEPTOR ANALOGS AND BIOLOGICAL
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,458
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 990008.446D5
TELEPHONE: 206-622-4900
TELEFAX: 206-682-6031
TELEX: 3723836
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 4054 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: N
ANTI-SENSE: N
ORIGINAL SOURCE:

ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: p-alpha-17B
FEATURE:
NAME/KEY: CDS
LOCATION: 205..3471
OTHER INFORMATION:
US-08-475-458-35

Query Match 0.6%; Score 23; DB 2; Length 4054;
Best Local Similarity 100.0%; Pred. No. 0.4;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3170 gtgaagatctgtgactttggcct 3192
|||||
Db 2698 GTGAAGATCTGTGACTTTGGCCT 2720

RESULT 44

US-08-980-400-35
Sequence 35, Application US/08980400
Patent No. 6018026
GENERAL INFORMATION:
APPLICANT: Sledziewski Ph.D., Andrzej Z
APPLICANT: Bell, Lillian A.
APPLICANT: Kindsvogel Ph.D., Wayne R.
TITLE OF INVENTION: METHODS OF PRODUCING SECRETED RECEPTOR ANALOGS AND BIOLOGIC
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/980,400
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/477,329
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 990008.446C6
TELEPHONE: 206-622-4900
TELEFAX: 206-682-6031
TELEX: 3723836
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 4054 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: N
ANTI-SENSE: N
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: p-alpha-17B
FEATURE:
NAME/KEY: CDS
LOCATION: 205..3471
OTHER INFORMATION:

US-08-980-400-35

Query Match 0.6%; Score 23; DB 3; Length 4054;
Best Local Similarity 100.0%; Pred. No. 0.4;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3170 gtgaagatctgtgactttggcct 3192
|||||
Db 2698 GTGAAGATCTGTGACTTTGGCCT 2720

RESULT 45

US-09-583-459A-35
; Sequence 35, Application US/09583459A
; Patent No. 6291212
; GENERAL INFORMATION:
; APPLICANT: Sledziewski Ph.D., Andrzej Z
; APPLICANT: Bell, Lillian A.
; APPLICANT: Kindsvogel Ph.D., Wayne R.
; TITLE OF INVENTION: METHODS OF PRODUCING SECRETED RECEPTOR ANALOGS
; TITLE OF INVENTION: AND BIOLOGICALLY ACTIVE DIMERIZED POLYPEPTIDE
; TITLE OF INVENTION: FUSIONS
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry
; STREET: 6300 Columbia Center
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/583,459A
; FILING DATE: 30-MAY-2000
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/634,510
; FILING DATE: 27-DEC-1990
; APPLICATION NUMBER: US 07/146,877
; FILING DATE: 22-JAN-1988
; APPLICATION NUMBER: US 07/347,291
; FILING DATE: 02-MAY-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki J.D., David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 990008.446C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-622-4900
; TELEFAX: 206-682-6031
; TELEX: 3723836
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4054 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: N
; ANTI-SENSE: N
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; IMMEDIATE SOURCE:
; CLONE: p-alpha-17B
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 205..3471
; OTHER INFORMATION:
; IS-99-03-459A-35

Query Match 0.6%; Score 23; DB 4; Length 4054;
Best Local Similarity 100.0%; Pred. No. 0.4;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3170 gtgaagatctgtgactttggcct 3192
|||||
Db 2698 GTGAAGATCTGTGACTTTGGCCT 2720

Search completed: July 15, 2002, 22:53:39
Job time: 22152 sec

' . '

Db 1801 cctgtccacgctgcacgatgcycagcggaacccgccttctgtctcgacitgcagaacgltqca 1860
Qy 1861 tctgttcgcaaccctctctgcccgcagccttgagagaggtgacacctggggcgccacgc 1920
Db 1861 tctgttcgcaaccctctctgcccgcagccttgagagaggtgacacctggggcgccacgc 1920
Qy 1921 cactgtcagctgaglatccccccgcgtcgccgcagacacagagggccactatgtgtgcga 1980
Db 1921 cactgtcagctgaglatccccccgcgtcgccgcagacacagagggccactatgtgtgcga 1980
Qy 1981 agtgcagagacrrurcgcagccatgacaagcactgccacaagaagtacctgtcugtlycagc 2040
Db 1981 agtgcagagacrrurcgcagccatgacaagcactgccacaagaagtacctgtcugtlycagc 2040
Qy 2041 rrrtgaaacccctcgggtccagcagaaacttgacagacctctctgtgaacgttaucygcac 2100
Db 2041 ccttgaaacccctcgggtccagcagaaacttgacagacctctctgtgaacgttaucygcac 2100
Qy 2101 gcttqagatgcagtgtcttggctggccgagcgcacgcgcccaagcatcgtgtgtacaaga 2160
Db 2101 gcttqagatgcagtgtcttggctggccgagcgcacgcgcccaagcatcgtgtgtacaaga 2160
Qy 2161 cgagaggtcgtcgaggaagaaagtctggagtgcacttggcgactcccaaccagaagctgag 2220
Db 2161 cgagaggtcgtcgaggaagaaagtctggagtgcacttggcgactcccaaccagaagctgag 2220
Qy 2221 catcagcgcgtgcgcagagagagatgcgcagcgtactctgtgcagcgtgttcaacgcaca 2280
Db 2221 catcagcgcgtgcgcagagagagatgcgcagcgtactctgtgcagcgtgttcaacgcaca 2280
Qy 2281 gggcttgcttcaactcctccgcagcgtggccgttggaaggtccagagataaqqcagcat 2340
Db 2281 gggcttgcttcaactcctccgcagcgtggccgttggaaggtccagagataaqqcagcat 2340
Qy 2341 ggaagatcgatcctctgttcggtacacggcgtcatatgcgtgtcttcttctgtggtctctcct 2400
Db 2341 ggaagatcgatcctctgttcggtacacggcgtcatatgcgtgtcttcttctgtggtctctcct 2400
Qy 2401 cttcatctcttctaatacagaagagccgcgccacgcagacatcaagacggcctaccitctc 2460
Db 2401 cttcatctcttctaatacagaagagccgcgccacgcagacatcaagacggcctaccitctc 2460
Qy 2461 catcatcatgaccccgggagggtgcctctggagagcaatgcuaataacctatctctacya 2520
Db 2461 catcatcatgaccccgggagggtgcctctggagagcaatgcuaataacctatctctacya 2520
Qy 2521 tqcagcaggtgggaatccccccgagagcgcgtgcacctggggagagatgcctcgcctacgg 2580
Db 2521 tqcagcaggtgggaatccccccgagagcgcgtgcacctggggagagatgcctcgcctacgg 2580
Qy 2581 cgccttcgggaaagtgggtggagcctccgcttccggatccacaagggcagcagctgtga 2640
Db 2581 cgccttcgggaaagtgggtggagcctccgcttccggatccacaagggcagcagctgtga 2640
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RESULT 2
ID AAA37816 standard; cDNA; 4795 BP.
AC AAA37816;
XX 15-JAN-2001 (first entry)
DT Human Flt4 receptor tyrosine kinase long form coding sequence.
DE Human; Flt4 receptor tyrosine kinase; antibody; extracellular domain;
KW lymphatic vessel detection; lymphatic tissue; lymph node tissue;
KW endothelial venule; diagnosis; lymphoma; long form; ss.
XX Homo sapiens.
US
FI Key Location/Qualifiers
CD 20..4111
FT /*tag= a
FT /product= Flt4 receptor tyrosine kinase long form
XX US6107046-A.
XX 22-AUG-2000.
XX 28-JUL-1997; 97US-0901710.
XX 09-OCT-1992; 92US-0959951.
PR 09-JUN-1994; 94US-0257754.
PR 14-NOV-1994; 94US-0340011.
XX (ORIN) ORION CORP.
PA (LUDW-) LUDWIG INST CANCER RES.
XX Alitalo K, Aprelikova O, Armstrong E, Korhonen J, Kaipainen A;
P1 Matikainen M, Pajusola K;
XX WPI: 2000-571323/53.
DR P-PSDB: AAY90366.
XX Antibody to extracellular domain of or to an epitope unique to a
PT vertebrate Flt4 receptor tyrosine kinase protein useful for diagnosing
PT lymphoma and imaging lymphatic vessels or high endothelial venules in
PT tissue
XX Disclosure: Column 55-66; 66pp; English.
XX This sequence encodes the human Flt4 receptor tyrosine kinase long
CC form protein. The invention relates to an antibody (I) specific to the
CC extracellular domain of or to an epitope unique to a vertebrate Flt4
CC receptor tyrosine kinase protein (II). A composition comprising (I) is
CC useful for detecting lymphatic vessels, lymphatic tissue comprising lymph
CC node tissue or high endothelial venules in an organism preferably mammal
CC especially human. The method comprises administering the composition and
CC detecting (I) bound to lymphatic vessels, lymphatic tissue or high
CC endothelial venules. (I) is also useful for screening a biological sample
CC for the presence of (II) or diagnosing a disease state. The diagnosing
CC method of the disease state preferably lymphoma comprises obtaining a
CC tissue sample on a vertebrate organism suspected of being in a diseased
CC state characterised by in Flt4 expression in lymphatic cells or high
CC endothelial venules and screening the diseased state utilising (I).
CC (I) is also useful for imaging lymphatic vessels or high endothelial
CC venules in a tissue by contacting the tissue with (I) and imaging the
CC vessels by detecting (I) bound to the tissues.

XX SQ Sequence 4795 BP; 977 A; 1490 C; 1494 G; 834 T; 0 other;
Query Match 100.0%; Score 4111; DB 21; Length 4795;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 ccacgcgcagcggccggagatgcagcggggcgccgcgcgtgtgctcgcgactgtggtctctg 60
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Qy	181	gcaccctcgaatggcttggccraggagctcagagagcgccajccacccgagagacaaga	240
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RESULT 4

AAC68952

ID AAC68952 standard; cDNA; 4111 BP.

XX AAC68952;

XX AC

XX DT 27-FEB-2001 (first entry)

XX DE Human Flt4/VEGFR-3 coding sequence.

XX KW Human; gene therapy; lymphatic disorder; hereditary lymphoedema; Flt4; vascular endothelial growth factor receptor-3; VEGFR-3; VEGF-D; fms-like tyrosine kinase 4; ss.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX FT CDS 20..4111

XX FT /*tag= a

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XX PN CA283470-A1.

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Qy 1741 gctcctgagctgccaagcgacagctacaagtacagagatctgctgtgtatccgcgtcaa 1800
Db 1741 gctcctgagctgccaagcgacagctacaagtacagagatctgctgtgtatccgcgtcaa 1800
Qy 1801 cctgtccagcgtgacgatgcccagcgggaaccgctctctgctcgactgcaagaacgtgca 1860
Db 1801 cctgtccagcgtgacgatgcccagcgggaaccgctctctgctcgactgcaagaacgtgca 1860
Qy 1861 tctgttgcgaacccctctgcccgcagcctggaggaggtggcacctggggcgccacgc 1920
Db 1861 tctgttgcgaacccctctgcccgcagcctggaggaggtggcacctggggcgccacgc 1920
Qy 1921 caagctcaagcctgagtatcccccgctcgcccccagacagggccactatgtgtgca 1980
Db 1921 caagctcaagcctgagtatcccccgctcgcccccagacagggccactatgtgtgca 1980
Qy 1981 agtgcaagaccggcgacgcaatgacaagcaclgccaagaagatcctgtcggtgcagcg 2040
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Qy 2341 ggagatcgtgataccttgcgttaccggcgctatcgctgtcttctgtgggtcctcctct 2400
Db 2341 ggagatcgtgataccttgcgttaccggcgctatcgctgtcttctgtgggtcctcctct 2400
Qy 2401 cctcatctctgtatacatgagagggccggccacgcagacatacaagaggggtacctgtc 2460
Db 2401 cctcatctctgtatacatgagagggccggccacgcagacatacaagaggggtacctgtc 2460
Qy 2461 catcatcatggaccggggaggtgcctctggagagcaatgcgaaatcctgtctctaca 2520
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Qy 2521 tgcagccagtgaggaaatcccccgagagcggtgcacctggggagagtgctcggtacag 2580
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Db 2581 cgccttcgggaaggtggtggaagcctccgcttctgycatccacaagggcagcayctgta 2640

Qy 2641 caccgtggccgtgaaaaatgctgaaaagagggcgccacggcgagcaccgcgcgctgat 2700
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Qy 2701 gtcgagatcgaagtccatcattccatcggaacaacacctcaactggttcaacctcctcgg 2760
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QY 3841 cagtgggagtgctggcctcggaagagtttaagcagatagagacgagcagcatagacaaga 3900
|||||
Db 3841 cagtgggagtgctggcctcggaagagtttaagcagatagagacgagcagcatagacaaga 3900
QY 3901 aagcggcttcag 3912
|||||
Db 3901 aagcggcttcag 3912

RESULT 6
AAZ52333
ID AAZ52333 standard; cDNA; 4195 BP.
XX
AC AAZ52333;
XX
DT 17-AUG-2000 (first entry)
XX
Human tyrosine kinase receptor Flt4-short form cDNA.
XX
Human; receptor tyrosine kinase; RTK; Flt4; fms-like tyrosine kinase 4;
VEGFR-3; vascular endothelial growth factor receptor-3; chromosome 5q35;
cytostatic; tumour imaging; anti-tumour therapy; treatment; diagnosis;
neoplastic disease; lymphoma; carcinoma; breast; squamous cell; melanoma;
sarcoma; malignancy; ss.
XX
Homo sapiens.
OS
XX
Key Location/Qualifiers
FH CDS 20..3916
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FT /note= "The start codon is surrounded by typical
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FT sig_peptide
FT /*tag= b
FT /note= "Directs protein to endoplasmic reticulum"
FT 80..3913
FT mat_peptide
FT /*tag= c
FT /product= "Mature Flt4 receptor-short form"
XX
PN WO200021560-A1.
XX
XX 20-APR-2000.
PD
XX 08-OCT-1999; 99WO-US23525.
PF
XX 09-OCT-1998; 98US-0169079.
PR
XX (LUDW-) LUDWIG INST CANCER RES.
PA (UYHE-) UNIV HELSINKI LICENSING LTD OY.
PA
XX
PI Alitaio K, Kaipainen A, Valtola R, Jussila L;
XX
WPI: 2000-317850/27.
DR P-PSDB; RAY70746.
DR
XX
Treating neoplastic diseases such as lymphoma, carcinomas, melanomas
and sarcomas, involves administering a compound capable of inhibiting
binding of ligand proteins to fms-like tyrosine kinase-4 receptor .
XX
Example 14; Page 109-115; 148pp; English.
PS
XX
The patent discloses a method to treat neoplastic disease characterised
by expression of fms-like tyrosine kinase 4 (Flt4) receptor (also
referred as vascular endothelial growth factor receptor-3, VEGFR-3) in
endothelial cells of blood vessels adjacent to malignant neoplasm. The
method involves administering a compound that inhibits binding of a
ligand to Flt4 thereby inhibiting Flt4 mediated proliferation of vascular
endothelial cells. The compound is useful for treating neoplastic disease
such as breast carcinomas, squamous cell carcinomas, lymphomas, melanomas
and sarcomas. Flt4 receptor tyrosine kinase binding compounds can be used
for manufacturing medicament useful for diagnostic screening, imaging and
treatment of malignancies characterised by Flt4-expressing blood cells.
CC
The present sequence is a cDNA encoding the short form of Flt4 receptor
from an oligo-dr primed human erythroleukaemia cell line (HEL) cDNA
library in bacteriophage lambda g11. The Flt4 gene maps to chromosomal
region 5q35 and is expressed as 5.8 kb and 4.5 kb mRNAs which differ in
their 3' sequences and are differentially expressed in HEL and DAMI cell
lines. Flt4 belongs to a subfamily of class III receptor tyrosine kinases
(RTKs). It is used as a target for tumour imaging and anti-tumour
therapy.
CC

Db 2041 cctggaagccctcggtccacgcagaaacttgaccgacctctctggtgaacgtgagcagctc 2100
Qy 2101 gctggagatgcagtgcttggctggccggagcgacgcgcccagatcgttgtgtacaaga 2160
Db 2101 gctggagatgcagtgcttggctggccggagcgacgcgcccagatcgttgtgtacaaga 2160
Qy 2161 cgagagggctgctggaggaagcttggagtgagcttgccggaacttccaccagaagctgag 2220
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Db 2221 catccagcgcgtgcgcgaggagga tgcgggacgcgtatctgtgcagcgttgtgcaacgccaa 2280
Qy 2281 gggctgcgtcaactccctccgcagcgtgcgttggaagcgtccagagataaggcagcat 2340
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Qy 2941 gggagagcagcacagggttcctcttcgcgcggttctcgaagaccgagggcggagcgagcgg 3000
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Qy 3901 aagcggcttcag 3912
Db 3901 aagcggcttcag 3912

RESULT 7
AAT03090
ID AAT03090 standard; DNA; 4425 BP.
XX
AC AAT03090;
XX
DT 14-FEB-1996 (first entry)
XX
DE Protein tyrosine-kinase SAL-S1 gene.
XX
KW Protein tyrosine-kinase; pTK; SAL-S1; agonist; cell growth;
XX differentiation; ss.
XX Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 30..3927
FT /*tag= a
FT sig_peptide 30..102

PT		/*tag= b	
FT	mat_peptide	103...3924	
FT		/*tag= c	
PN	W09527061-A1.		
XX	12-OCT-1995.		
XX	04-APR-1995:	95WO-US04228.	
XX	04-APR-1994:	94US-0222616.	
XX	(GETH) GENENTECH INC.		
XX	Bennett BD, Goeddel D, Lee JM, Matthews W, Tsai SP;		
PI	Wood WI;		
XX	WPI: 1995-366160/47.		
DK	P-PSDB: AAR85937.		
XX			
PT	Agonist antibodies which activate specific protein tyrosine		
PT	kinase(s) - also activate chimeric proteins of kinase extracellular		
PT	domain and Iq constant domain, useful for studying, and therapeutic		
PT	modulation of, cell growth and differentiation		
XX			
PS	Disclosure: Fig 15A-F: 125pp: English.		
XX			
CC	DNA probes based on protein tyrosine-kinase (pTK) sequences were used		
CC	to screen cDNA libraries to identify novel pTK genes. The SAL-S1		
CC	gene (see also AAT03101) was isolated from several megakaryocytic cell		
CC	libraries. The gene can be used to produce recombinant SAL-S1 or its		
CC	fragments, to detect related genes, and to design drugs, peptides		
CC	or antisense nucleotides that modulate pTK activity.		
XX			
SO	Sequence 4425 bp; 939 A; 1348 C; 1361 G; 777 T; 0 other;		

[illegible][illegible]

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Db	2444		
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Qy 3901 aagcggttcag 3912
Db 4844 aagcggttcag 4855

RESULT 9
AAT12068
ID AAT12068 standard; DNA: 4195 BP.
AC AAT12068;
XX
XX
XX
XX 08-APR-1996 (first entry)
DE FLT4 receptor tyrosine kinase DNA.
XX
XX FLT4: receptor tyrosine kinase; probe: metastasis; lymphoma;
KW Lymphangioma; immunological disease; cancer; diagnosis; therapy; ss.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FT CDS 20..3976
FT /*tag= a
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XX W09533772-A1.
XX
XX 14-DEC-1995.
XX
XX 09-JUN-1995: 95WO-FI00337.
XX
XX 09-JUN-1994: 94US-0257754.
XX
XX (ALIT/) ALITALO K.
PA (KAIP/) KAIPAINEN A.
PA (KARN/) KARNANI P.
PA (KORH/) KORHONEN J.
PA (MATI/) MATIKAINEN M.
PA (MUST/) MUSTONEN T.
PA (PAJU/) PAJUSOLA K.

XX Alitalo K, Kaipainen A, Karnani P, Korhonen J, Matikainen M;
PI Mustonen T, Pajusola K;
XX
XX WPI: 1996-040189/04.
DR P-PSDB; AAR90528.
XX
XX Antibodies against FLT4 receptor tyrosine kinase, hybridomas and
PT nucleic acid probes - used to diagnose and treat e.g. metastatic
PT cancers, involving alterations to lymphatic vessels.
XX
XX Claim 9; Page 27-33; 54pp; English.
XX
XX A DNA sequence (AAT12068) coding for FLT4 receptor tyrosine kinase
CC (AAR90528) is used as a probe that specifically binds/hybridizes to
CC DNA encoding human FLT4. Such probes are used to detect FLT4, a
CC novel marker for lymphatic vessels and some high endothelial
CC venules, in biological tissue for use in diagnosis and therapy of
CC e.g. inflammatory, infectious and immunological diseases, metastatic
CC lymph nodes and lymphangiomas.
XX
XX Sequence 4195 BP: 889 A; 1278 C; 1305 G; 723 T; 0 other;
SQ

Query Match 93.9%; Score 3861; DB 17; Length 4195;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3911; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db	1741	gtctctgagctgccaaagccgaacagctacaaglacagagcatctgcgctggttaccgcgctctcaa	1801
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Qy	1861	ttctgttccgcaacctcttgccgcgcagcctggagagagtgccacttgggcgcgcgcacgc	1920
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50	Sequence 4450 BP: 968 A: 1352 C: 1349 G: 781 T: 0 other:									
	Query Match	69.3%	Score 2847:	DB 21:	Length 4450:					
	Best local Similarity	99.5%	Pred. No. 0:							
	Matches 3797:	Conservative	0:	Mismatches	19:	Indels	0:	Gaps		
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DB	99	catgaccccccgaccttgaaacatcacgagagagatccacacgctcatcgaacccagtgacag	158							
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QY	217	ggcgccagacacccggagacaagagacagcagagacacggggctgdtgcgagactatcragggg	276							
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Db 2259 tctgtcagcgctgtcagaccccaaggctgcgtccaactctccgcagcgctgacctgga 2318
|||||
QY 2317 agactccagagataaaggcagcatcgagatcgtgactccttctgtcgtaccagcgatcaatc 2376
|||||
Db 2319 ayyctccagagataaaggcagcatcgagatcgtgactccttctgtcgtaccagcgatcaatc 2378
|||||
QY 2377 tjtcttcttctgtgtctctctctctctctctctctctctctctctctctctctctctct 2436
|||||
Db 2379 tjtcttcttctgtgtctctctctctctctctctctctctctctctctctctctctctct 2438
|||||
QY 2437 agacatcaagacgggttaactctgccaatcatcgagaccccgagagtgacctcttgagaga 2496
|||||
Db 2439 agacatcaagacgggttaactctgccaatcatcgagaccccgagagtgacctcttgagaga 2498
|||||
QY 2497 gaaatgcgaataactctctctacgatgcccagcgctggaattcccccagagatgacttca 2556
|||||
Db 2499 gaaatgcgaataactctctctacgatgcccagcgctggaattcccccagagatgacttca 2558
|||||
QY 2557 cctgggagagatgctcggtctacggcgcttccgggaaggctggtggaagcctccgcttccgg 2616
|||||
Db 2559 cctgggagagatgctcggtctacggcgcttccgggaaggctggtggaagcctccgcttccgg 2618
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QY 2617 catccacaaggcagcagctgtgacacgctggccgtgaaatctgaaagagggcgccac 2676
|||||
Db 2619 catccacaaggcagcagctgtgacacgctggccgtgaaatctgaaagagggcgccac 2678
|||||
QY 2677 ggcagcgacacgcgcgcgtgatgtcgagctcaagatctcattccatctcggaacca 2736
|||||
Db 2679 ggcagcgacacgcgcgcgtgatgtcgagctcaagatctcattccatctcggaacca 2738
|||||
QY 2737 cctcaacggttcaactctctcggcgtgacacgctgacacgcgacggcgccctcatgtgat 2796
|||||
Db 2739 cctcaacggttcaactctctcggcgtgacacgctgacacgcgacggcgccctcatgtgat 2798
|||||
QY 2797 cgtgggaatctcgaagtacggcaacctctcctaacttctcgtcgccgcaagcgagacgctt 2856
|||||
Db 2799 cgtgggaatctcgaagtacggcaacctctcctaacttctcgtcgccgcaagcgagacgctt 2858
|||||
QY 2857 caacccctgcgcgagagaagctctccagcagcgacgcttccgcgcacatggtgagact 2916
|||||
Db 2859 caacccctgcgcgagagaagctctccagcagcgacgcttccgcgcacatggtgagact 2918
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Db 2919 cgcagcgctggatcgcgagcgccggcgcgcgagcagcagcgctctctcgcgcgcttctc 2978
|||||
QY 2977 gaagaccgagggcgagcgagggcgcttctccagaccgaagcctgaggaacctgtggt 3036
|||||
Db 2979 gaagaccgagggcgagcgagggcgcttctccagaccgaagcctgaggaacctgtggt 3038
|||||
QY 3037 gaccccgctgacccatggaagatcttctgtctacagcttccagctggccagagggatgga 3096
|||||
Db 3039 gaccccgctgacccatggaagatcttctgtctacagcttccagctggccagagggatgga 3098
|||||
QY 3097 gtctcggtctccgaaagtgcataccagagacgtggtgctcggaacattctgtgtc 3156
|||||
Db 3099 gtctcggtctccgaaagtgcataccagagacgtggtgctcggaacattctgtgtc 3158
|||||
QY 3157 ggaagcgacgtgtgaagatctgtactttggccttggccggagacatctataaagacc 3216
|||||
Db 3159 ggaagcgacgtgtgtgaagatctgtactttggccttggccggagacatctataaagacc 3218
|||||
QY 3217 tgactacgtccgaaggcagtgcccggtgcccctgaaagtggccttgaagatggccctgaaagcat 3276
|||||
Db 3219 cgactacgtccgaaggcagtgcccggtgcccctgaaagtggccttgaagatggccctgaaagcat 3278
|||||
```

```
QY 3277 cttcgacaagggtgtacaccacgcagagtgcagctgtggtctcttgggtgctctctcgga 3336
|||||
Db 3279 cttcgacaagggtgtacaccacgcagagtgcagctgtggtctcttgggtgctctctcgga 3338
|||||
QY 3337 gatcttctctcttgggggcttcccttacccttgggtgagatcaatgaggaattctcgca 3396
|||||
Db 3339 gatcttctctcttgggggcttcccttacccttgggtgagatcaatgaggaattctcgca 3398
|||||
QY 3397 ggcgctgagagacgcccacaaagatgagggcccgagctggccactcccgccatacgccg 3456
|||||
Db 3399 ggcgctgagagacgcccacaaagatgagggcccgagctggccactcccgccatacgca 3458
|||||
QY 3457 catcatgctgaactgctgttccggagaccccaaggcgagacctgcatctcggagctggt 3516
|||||
Db 3459 catcatgctgaactgctgttccggagaccccaaggcgagacctgcatctcggagctggt 3518
|||||
QY 3517 ggaagctctgggggacctgctccagggcagggcctgcaagagagagagaggtctgcat 3576
|||||
Db 3519 ggaagctctgggggacctgctccagggcagggccctgcaagagagagagaggtctgcat 3578
|||||
QY 3577 ggcctcgcgagctctctcagagctcagaagaggcgagcttctcgcaggtgtccaccatggc 3636
|||||
Db 3579 ggcctcgcgagctctctcagagatcagaagaggcgagcttctcgcaggtgtccaccatggc 3638
|||||
QY 3637 cctacaatctgcgcagggctgacgctgagagacagcccgccaagcctgcagcgccacgct 3696
|||||
Db 3639 cctacaatctgcgcagggctgacgctgagagacagcccgccaagcctgcagcgccacgct 3698
|||||
QY 3697 ggcgcgaggtattacaactgggtgctcttcccggtgctcggcagagggtcgagac 3756
|||||
Db 3699 ggcgcgaggtattacaactgggtgctcttcccggtgctcggcagagggtcgagac 3758
|||||
QY 3757 ccgtggttctccaggtgagagatcttgggaattcccatgaccccaacgacctacaa 3816
|||||
Db 3759 ccgtggttctccaggtgagagatcttgggaattcccatgaccccaacgacctacaa 3818
|||||
QY 3817 aggcctctggaacacacagacagctgggatgctgctggtgctcggagaggtttgagca 3876
|||||
Db 3819 aggcctctggaacacacagacagctgggatgctggtgctcggagaggtttgagca 3878
|||||
QY 3877 gatagagacgagcagatagacaagaaagcggtctcag 3912
|||||
Db 3879 gatagagacgagcagatagacaagaaagcggtctcag 3914
|||||
RESULT 11
AAQ49753/c
ID AAQ49753 standard; DNA: 6827 bp.
XX
AC AAQ49753;
XX
DT 10-MAR-1994 (first entry)
XX
DE pTK gene SAL-S1.
XX
KW pTK; protein tyrosine kinase; catalytic domain; c-kit; FLT/FLK;
fetal liver kinase; megakaryocyte; amplification; primer;
KW polymerase chain reaction; PCR; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
CDS complement (1877..2923)
FT /*tag= a
FT misc_difference 3026
FT /*tag= b
FT /*note= "base labelled as X in the specification"
FT misc_difference 5000
FT /*tag= c
FT /*note= "base illegible in the specification"
FT misc_difference 5699..5700
FT /*tag= d
FT /*note= "bases illegible in the specification"
```


PT Agonist antibodies which activate specific protein tyrosine
PT kinase(s) - also activate chimeric proteins of kinase extracellular
PT domain and Ig constant domain, useful for studying, and therapeutic
PT modulation of, cell growth and differentiation
XX
PS Disclosure; Page 39-46; 125pp; English.
XX
CC DNA probes based on protein tyrosine-kinase (pTK) sequences were used
CC to screen cDNA libraries to identify novel pTK genes. The SAL-S1
CC gene (see also A030309) was isolated from several megakaryocytic cell
CC libraries. The gene can be used to produce recombinant SAL-S1 or ILS
CC fragments, to detect related genes, and to design drugs, peptides
CC or antisense nucleotides that modulate pTK activity.
XX
SQ Sequence 6827 BP; 1558 A; 1870 C; 1738 G; 1660 T; 1 other;

Query Match		23.1%;	Score 950;	DB 16;	Length 6827;
Best Local Similarity		99.9%;	Pred. No. 0;		
Matches 1000;		Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;
Qy	2869	ggagaagtctcccgagcagcgagcgtctccgcgcgcattggtgagctcgcaggtcga	2928		
Db	2924	GGAGAACTCTCCGAGCAGCGCGACGCTTCCGCGCCATGCTGCAGCTCCGAGCTGA	2865		
Qy	2929	tcgagagcgccgggagcagcagcaggtctcttcgcgcggtcttcgaagaccgaagg	2988		
Db	2864	TCCGAGCGCGCGGGAGCAGCGAGGGTCTCTTCGCGCGGTCTCGAAGACCCGAGG	2805		
Qy	2989	cggagcagcgcggtctctccagaccgaagcgtgagcgtggtgagccgcgtgac	3048		
Db	2804	CGGAGCGAGCGGGCTTCTCCAGACCAAGAAGCTGAGGACCTGTGGCTGAGCCGCTGAC	2745		
Qy	3049	catgaagatcttctcgtacagcttccaggttcgagagggatgagttccttgcttc	3108		
Db	2744	CATGGAAGATCTTCTCTGTACAGCTTCCAGGTGCCAGAGCGGATGAGTTCCTGCTTC	2685		
Qy	3109	ccgaantgcatcacagagacctggctgctcgaacatctcgtcgtcgaagacacgt	3168		
Db	2684	CCGAAGTGCATCACAGACACCTGGCTGCTCGGAACATTTCTGCTGCGAAGACCGACGT	2625		
Qy	3169	qqiadaalatgtgactttggccttgcgcggagacatctacaaagacccctdaclacgtcgy	3228		
Db	2624	GCTGAAGATCTGTGACTTTGGCCTTGGCCGTGCCCGGACATCTACAAAGACCCGACTACGTCCG	2565		
Qy	3229	caagggcagtgcccggtgcccctgaagtggatggcgcctgaaagcattcttcgaaggt	3288		
Db	2564	CAAGGGCAGTGCCCGGCTGCCCTGAAAGTGATGGCGCCCTGAAAGCATCTTCCACAAGGT	2505		
Qy	3289	gtacaccacgcagagtgacgtgtgtctcttggggtgcttctcgtggaqalcitctctct	3348		
Db	2504	GTACACCACCGAGAGTCACGTGTGCTCTTTGGGGTCTCTCTGTGGGAGATCTTCTCTCT	2445		
Qy	3349	gggggctctcccgtaacctgggtgcaqatcaatgagaggttcttgcagcggtcgaaga	3408		
Db	2444	GCGGGCTCTCCCGTACCTTGGGTGCCAGATCAATGAGGAGTCTTGCCAGCGCTGAGAGA	2385		
Qy	3409	cggcaagagatgagggcccggaagctggcactlcccgccatcacgcgcacatctatgaa	3468		
Db	2384	CGGCACAAGGATGAGGGCCCGGAGCTGGCCACTTCCCGCCATACGCCGATCATGCTGAA	2325		
Qy	3469	ctgctgttccggagaccccaagcgagaccttgcatctcggagcttggatgagatccctggy	3528		
Db	2324	CTGCTGTGTCGGAGACCCCAAGGCGACACCTGCATTTCTCGGAGCTGTGGAGATCTTGGG	2265		
Qy	3529	ggacctgctcraggcgagggtctgcaagaggaagaggtcttgcagtcgcccccgag	3588		
Db	2264	GGACCTGCTCAGCGCAGGGGCTTCCAAAGAGGAAGAGAGGTCTGCATGCGCCCGCCAG	2205		
Qy	3589	ttctcagagctcgaagagggcagcttctcgcaggtgtccaccatggccctacacatcgc	3648		
Db	2204	CTCTCAGAGCTCAGAACAGGGCAGCTTCTCCAGGTGTCCACCATGCGCCCTAGACATCGC	2145		

Qy 3649 ccaggtgacgtgagcagcagccgccaagcctgcagcgcacagcctggccgccaagta 3708
|||||
Db 2144 CCAGGCTGACGCTGAGGACAGCGCCCAAGCCTGCAAGCCACAGCTTGGCCGACGTA 2085
|||||
Qy 3709 ttacaactgggtgtctcttcccggtgctgccaagagggctgagaccgtggttccle 3768
|||||
Db 2084 TTACAACCTGGGTGTCTTTCCCGGGTGCCTTGGCCAGAGGGGCTGAGACCCGTGTTCTTC 2025
|||||
Qy 3769 caggtgaaagacatttgagaaattccccatgaccccaacgacactacaaaggctctgtgga 3828
|||||
Db 2024 CAGGATGAAGACATTTGAGGAATTTCCCATGACCCCAACGACCTACAAAGGCTCTCTGGA 1965
|||||
Qy 3829 caaccagacagcagtgaggtgctgctgacctcgagagagt 3869
|||||
Db 1964 CAACCAGACAGACAGTGGGATGCTGCTGGCTCGGAGGAGT 1924
|||||

RESULT 13
AAH99658
ID AAH99658 standard; cDNA; 574 BP.
XX
AAH99658;
XX AC
XX DT
DT 16-OCT-2001 (first entry)
XX
DE Human protein encoding cDNA sequence SEQ ID NO:493.
XX
KW Human; cancer; ulcer; HIV infection; human immunodeficiency virus;
KW antiinflammatory; antirheumatic; antithratic; immunosuppressive;
KW antibacterial; endocrine; cardiant; central nervous system; virucide;
KW anti-HIV; fungicide; antimutagen; cardiovascular; antianaemic; anaemia;
KW antiaggregant; haemostatic; vulnary; antiulcer; osteopathic; eczema;
KW dermatological; antiallergic; antiasthmatic; antidiabetic; cytostatic;
KW neuroprotective; antidepressant; nootropic; antiparkinsonian; infection;
KW immunostimulant; gene therapy; antisense therapy; vaccine; inflammation;
KW antianaphylactic; rheumatoid arthritis; septic shock; pancreatitis;
KW cardiac dysfunction; neuropathology; cardiac anaphylaxis; autoimmunity;
KW genetic disease; haematopoietic disorder; platelet disorder; asthma;
KW thrombocytopaenia; osteoporosis; severe combined immunodeficiency;
KW allergic rhinitis; diabetes; multiple sclerosis; depression;
KW Alzheimer's disease; Parkinson's disease; neurodegenerative disorder;
KW neurological disorder; ss.
XX
OS Homo sapiens.
XX
PN WO200153455-A2.
XX
PD 26-JUL-2001.
XX
XX 22-DEC-2000; 2000WO-US35017.
XX
XX 23-DEC-1999; 99US-0471275.
PR 21-JAN-2000; 2000US-0488725.
PR 25-APR-2000; 2000US-0552317.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Tang YT, Liu C, Drmanac RT;
XX
XX WPI; 2001-457603/49.
DR P-PSDB; AAM25717.
XX
XX Isolated human polynucleotides encoding polypeptides, useful for the
PT treatment and diagnosis of e.g. cancer, ulcers and HIV infection -
PT
XX
PS Claim 1; Page 561; 1217pp; English.
XX
CC AAH99166 to AAH99904 encode the human proteins given in AAM25225 to
CC AAM25963. The proteins can have activities based on the tissues and
CC cells they are expressed in, such as: antiinflammatory; antirheumatic;
CC antithratic; immunosuppressive; antibacterial; endocrine; cardiant;
CC central nervous system; virucide; anti-HIV; fungicide; antimutagen;
CC cardiovascular; antianaemic; antiaggregant; haemostatic; vulnary;

CC antiulcer; osteopathic; dermatological; antiallergic; antiasthmatic;
CC antidiabetic; cytostatic; neuroprotective; antidepressant; nootropic;
CC antiparkinsonian; and immunostimulant. The proteins and polynucleotides
CC encoding them can be used in gene therapy, antitense therapy and vaccine
CC production. The proteins and polynucleotides are useful for screening for
CC agonists or antagonists of a protein and for the treatment and diagnosis
CC of disorders associated with the activity of a protein e.g. inflammation,
CC rheumatoid arthritis, septic shock, pancreatitis, cardiac dysfunction,
CC neuropathology, cardiac anaphylaxis, viral, bacterial, HIV and fungal
CC infections, autoimmunity, genetic diseases, haematopoietic disorders,
CC anaemia, platelet disorders, thrombocytopaenia, wounds, burns, ulcers,
CC osteoporosis, severe combined immunodeficiency, eczema, allergic
CC rhinitis, asthma, diabetes, cancer, multiple sclerosis, depression,
CC Alzheimer's disease, Parkinson's disease, neurodegenerative and
CC neurological disorders.

SQ Sequence 574 BP; 120 A; 168 C; 181 G; 105 T; 0 other;

Query Match 5.3%; Score 216; DB 22; Length 574;
Best Local Similarity 100.0%; Pred. No. 3.2e-86;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3896 caagaaacagcctcagcctgataagagcctgcccagaatctgcttgaccaggagcac 3955
Nb |||||
Nb 1 caagaaagcgcttcagctgataagagcctgcccagaatctgcttgaccaggagcac 60
QY 3956 cctgactcccaagagagcgccgctgacgagcgagggcccgagagagcgagttt 4015
Nb |||||
Nb 61 cttgactcccaagagagcgccgctgacgagcgagggcccgagagagcgagttt 120
QY 4016 tacaacagcagatgagggagcgtgagagcagagcagagagcagcagcagcagc 4075
Nb |||||
Nb 121 tacaacagcagatgagggagcgtgagagcagagcagagcagcagcagcagcagc 180
QY 4076 gccgcagcagcctctctcacagacacagcagcagcagcagcagcagcagcagc 4111
Nb |||||
Nb 181 gccgcagcagcctctctcacagacacagcagcagcagcagcagcagcagcagc 216

RESULT 14
AAA91075
ID AAA91075 standard; DNA; 1444 BP.
XX
AC AAA91075;
XX
UT 05-APR-2001 (first entry)
XX
DE Flt1 receptor fusion protein Flt1D2.VEGFR3D3.fcDeltaC1(a) DNA sequence.
XX
KW Flt1 receptor; fusion protein; chimeric protein; pharmacokinetic;
KW plasma leakage; vascular permeability; IgG Fc region; ss.
XX
OS Unidentified.
XX
PN WO200075319-A1.
XX
PD 14-DEC-2000.
XX
PF 23-MAY-2000; 2000WO-US14142.
XX
PR 08-JUN-1999; 99US-0138133.
XX
PA (REGE-) REGENERON PHARM INC.
XX
PI Papadopoulos NJ, Davis S, Yancopoulos GD;
XX
DR WPI: 2001-071076/08.
DR P-PSDB: AAY97595.
XX
PT Nucleic acid molecule encoding mammalian phospholipid transfer protein,
PT and its fragments, useful for diagnosis, evaluation, and treatment of
PT diseases associated with the gene expression and for producing model

PT systems -

XX Claim 9; Fig 22; 159pp; English.

XX This sequence encodes a fusion protein of the invention between
CC the Flt1 receptor and the Fc region of IgG. The specification relates
CC to modified chimeric polypeptides with improved pharmacokinetics. The
CC modified chimeric polypeptides are preferably Flt1 receptor polypeptides
CC that have been modified to improve their pharmacokinetic profile. The
CC polypeptides can be used to decrease or inhibit plasma leakage and/or
CC vascular permeability in a mammal.

SQ Sequence 1444 BP; 371 A; 426 C; 380 G; 267 T; 0 other;

Query Match 4.7%; Score 195; DB 22; Length 1444;
Best Local Similarity 99.3%; Pred. No. 7e-77;
Matches 295; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 713 atccagctgtgccaggagtcgctggagctgctgtagggagagagctggtcctgaac 772
Db |||||
Db 447 atccagctgtgccaggagtcgctggagctgctgtagggagagagctggtcctcaac 506
QY 773 tgaccgctggtgctgagtttaactcagctgctacactttgactggaactaccagggaag 832
Db |||||
Db 507 tgaccgctggtgctgagtttaactcagctgctacactttgactggaactaccagggaag 566
QY 833 caggcagagcggttaagtgggtgcccagcgagcgtcccgagcagacccacacagaaac 892
Db |||||
Db 567 caggcagagcggttaagtgggtgcccagcgagcgtcccgagcagacccacacagaaac 626
QY 893 tccagcagctcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 952
Db |||||
Db 627 tccagcagctcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 686
QY 953 gccacaacagcgatccagcgatttcgggagagcagcgagcagcagcagcagcagcagc 1009
Db |||||
Db 687 gccacaacagcgatccagcgatttcgggagagcagcgagcagcagcagcagcagcagc 743

RESULT 15
AAQ49747
ID AAQ49747 standard; DNA; 160 BP.
XX
AC AAQ49747;
XX
DT 10-MAR-1994 (first entry)
XX
DE pTK gene SAL-SI partial sequence.
XX
KW pTK; protein tyrosine kinase; catalytic domain; c-kit; FLT/FLK;
KW fetal liver kinase; megakaryocyte; amplification; primer;
KW polymerase chain reaction; PCR; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FH CDS 2..160
FT /*tag= a
FT misc_feature 1..21
FT /*tag= b
FT /*note= "pTK1/3 primers"
FT misc_feature 136..160
FT /*tag= c
FT /*note= "pTKKW primer"
XX
PN WO9315201-A.
XX
PD 05-AUG-1993.
XX
PF 22-JAN-1993; 93WO-US00586.
XX
PR 22-JAN-1992; 92US-0826935.

XX PA (NEW-) NEW ENGLAND DEACONESS HOSPITAL.
 XX PI Avraham H, Cowley S, Groopman J, Scadden D;
 XX PT WPI: 1993-320330/40.
 DR P-PSDB; AAR41894.
 XX
 XX New protein tyrosine kinase genes and proteins encoded by genes -
 PT are of human mega-karyocytic origin
 XX
 XX Claim 2: Fig 1: 60pp; English.
 XX
 CC pTK genes were identified using two sets of degenerative
 CC oligonucleotide primers: a first set which amplifies all pTK DNA
 CC segments (AAQ49743-44), and a second set which amplifies highly
 CC conserved sequences present in the catalytic domain of the c-kit
 CC subgroup of pTKs (AAQ49745-46). The pTK genes identified are described
 CC in AAQ49747-57 and AAR41897-02.
 CC SAL-S1 is expressed in several megakaryocytic cell lines, but not
 CC in erythroid cell lines. The SAL-S1 expression prod. exhibited
 CC significant sequence homology with known protein tyrosine kinases
 CC of the FLT/PLK family. The partial and full-length SAL-S1 gene
 CC sequences are given in AAQ49747 and AAQ49753 respectively.
 XX
 XX Sequence 160 BP; 35 A; 44 C; 47 G; 34 T; 0 other;
 SQ

Query Match 1.8%; Score 76; DB 14; Length 160;
 Best Local Similarity 100.0%; Pred. No. 1e-23;
 Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3141 ggaacattctgctgcggaagcgacgtggtgaagatctgtgactttggccttgcgcggg 3200
 ID | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 Db 30 ggaacattctgctgcggaagcgacgtggtgaagatctgtgactttggccttgcgcggg 89
 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 QY 3201 acatctacaaagacc 3216
 ID | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 Db 90 acatctacaaagacc 105
 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 16
 AAT03089
 ID AAT03089 standard; DNA; 160 BP.
 XX
 AC AAT03089;
 XX
 DT 14-FEB-1996 (first entry)
 XX
 DE Protein tyrosine-kinase SAL-S1 DNA fragment.
 XX
 DE Protein tyrosine-kinase; pTK; SAL-S1; agonist; cell growth;
 KW differentiation; ss.
 XX
 OS Homo sapiens.
 XX
 XX KEY Location/Qualifiers
 FH CDS 20..160
 FT /*lag= a
 FT
 XX
 XX WO9527061-A1.
 PN
 XX
 XX 12-OCT-1995.
 XX
 XX 04-APR-1995; 95WO-US04228.
 XX
 XX 04-APR-1994; 94US-0222616.
 XX
 XX (GETH) GENENTECH INC.
 XX
 XX Bennett BD, Goeddel D, Lee JM, Matthews W, Tsai SP;
 PI Wood WI;
 XX

DR WPI: 1995-366160/47.
 DR P-PSDB; AAR85922.
 XX
 XX Agonist antibodies which activate specific protein tyrosine
 PT kinase(s) - also activate chimeric proteins of kinase extracellular
 PT domain and Ig constant domain, useful for studying, and therapeutic
 PT modulation of, cell growth and differentiation
 XX
 XX Disclosure; Page 35; 125pp; English.
 XX
 XX DNA probes based on protein tyrosine-kinase (pTK) sequences were used
 CC to screen cDNA libraries to identify novel pTK genes. A SAL-S1 gene
 CC fragment (AAT03089) was isolated from several megakaryocytic cell lines
 CC (see AAT03090 for the full-length sequence).
 XX
 XX Sequence 160 BP; 35 A; 44 C; 47 G; 34 T; 0 other;
 SQ

Query Match 1.8%; Score 76; DB 16; Length 160;
 Best Local Similarity 100.0%; Pred. No. 1e-23;
 Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3141 ggaacattctgctgcggaagcgacgtggtgaagatctgtgactttggccttgcgcggg 3200
 ID | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 Db 30 ggaacattctgctgcggaagcgacgtggtgaagatctgtgactttggccttgcgcggg 89
 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 QY 3201 acatctacaaagacc 3216
 ID | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 Db 90 acatctacaaagacc 105
 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 17
 AAT84280
 ID AAT84280 standard; DNA; 70 BP.
 XX
 AC AAT84280;
 XX
 DT 10-NOV-1997 (first entry)
 XX
 DE Flt4 gene 5' end forward primer.
 XX
 XX VEGF-C; Flt4; receptor tyrosine kinase; VEGFR-3; human;
 KW vascular endothelial growth factor receptor-3; ligand;
 KW angiogenesis; polymerase chain reaction; PCR; primer; ss.
 XX
 OS Synthetic.
 XX
 XX WO9705250-A2.
 XX
 XX 13-FEB-1997.
 XX
 XX 01-AUG-1996; 96WO-FI00427.
 XX
 XX 28-JUN-1996; 96US-0671573.
 PR 01-AUG-1995; 95US-0510133.
 PR 12-JAN-1996; 96US-0585895.
 PR 14-FEB-1996; 96US-0601132.
 XX
 XX (UYHE-) UNIV HELSINKI LICENSING LTD OY.
 XX
 XX Alitalo K, Joukov V;
 PI
 XX
 XX WPI; 1997-145688/13.
 DR
 XX
 XX Flt4 receptor tyrosine kinase ligand and related nucleic acid - used
 PT to modulate growth of endothelial cells and for diagnosis of
 PT endothelial cell diseases
 XX
 XX Example 1; Page 33; 183pp; English.
 PS
 XX This primer sequence is based on the 5' end of S2.5, a clone
 CC containing bp 56-2534 of the short form of Flt4 receptor tyrosine
 CC kinase cDNA, and includes a SphI site and the translational
 CC

XX WO200075319-A1.
PN 14-DEC-2000.
XX 23-MAY-2000; 2000WO-US14142.
XX 08-JUN-1999; 99US-0138133.
XX (KEGE-) REGENERON PHARM INC.
XX Papadopoulos NJ, Davis S, Yancopoulos GD;
PI WPI: 2001-071076/08.
XX Nucleic acid molecule encoding mammalian phospholipid transfer protein,
PT and its fragments, useful for diagnosis, evaluation, and treatment of
PT diseases associated with the gene expression and for producing model
PT systems -
XX Example 17; Page 63; 159pp; English.
XX This sequence represents a PCR primer used to construct DNA
CC sequences encoding the fusion proteins of the invention between
CC the Flt1 receptor and the Fc region of IgG. The specification relates
CC to modified chimeric polypeptides with improved pharmacokinetics. The
CC modified chimeric polypeptides are preferably Flt1 receptor polypeptides
CC that have been modified to improve their pharmacokinetic profile. The
CC polypeptides can be used to decrease or inhibit plasma leakage and/or
CC vascular permeability in a mammal.
XX Sequence 38 BP; 9 A; 9 C; 11 G; 9 T; 0 other;
SQ

Query Match 0.7%; Score 30; DB 22; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.0039;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 713 atccagctgtgcccggaagtcgctggag 742
Db 9 atccagctgtgcccggaagtcgctggag 38

RESULT 23
ARA96501
ID ABA96501 standard; cDNA; 1047 BP.
XX
AC AHA96501;
XX
DT 12-MAR-2002 (first entry)
XX
DE Human extracellular signal-regulated protein kinase-2 (erk-2) cDNA.
XX
KW Human: extracellular signal-regulated protein kinase-2; erk-2;
KW recombinant production; Escherichia coli; HeLa cell; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..1047
FT /tag= a
FT /product= "Human erk-2"
FT
XX
PN KR98022142-A.
XX
PD 25-JUN-1998.
XX
PF 20-SEP-1996; 96KR-0041219.
XX
PR 20-SEP-1996; 96KR-0041219.
XX
PA (GLDS) LG CHEM LTD.
XX

Kim CH, Cho JM, Chung HH, Lee JH;
WPI: 1999-300710/25.
P-PSDB; AAW52700.
Process for preparing extracellular signal-regulated protein kinase-2
from E. coli -
Example 2; Fig 1a-c; 9pp; Korean.
The invention relates to a process for the recombinant production
of human extracellular signal-regulated protein kinase-2 (erk-2) in
Escherichia coli. The present sequence represents cDNA encoding human
erk-2 initially isolated from HeLa cells.
Sequence 1047 BP; 303 A; 255 C; 225 G; 264 T; 0 other;
SQ

Query Match 0.6%; Score 26; DB 20; Length 1047;
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3173 aagatctgtgacttggccttgcccg 3198
Db 45; aagatctgtgacttggccttgcccg 479

RESULT 24
AAQ20261
ID AAQ20261 standard; DNA; 1467 BP.
XX
AC AAQ20261;
XX
DT 31-MAR-1992 (first entry)
XX
DE ERK2.
XX
KW Microtubule-associated protein 2; central nervous system;
KW extracellular signal-regulated kinase; ERK; CNS; MAP2; ss
XX
OS Rat rattus.
XX
FH Key Location/Qualifiers
FT CDS 1..1248
FT /tag= a
FT /label= ERK2
FT misc_signal 172..174
FT /tag= b
FT /label= initiation_codon
FT misc_signal 202..204
FT /tag= c
FT /label= initiation_codon
FT terminator 1246..1248
FT /tag= d
XX
PN WO9119008-A.
XX
PD 12-DEC-1991.
XX
PF 03-JUN-1991; 91WO-US03894.
XX
PR 16-MAY-1991; 91US-0701544.
PR 01-JUN-1990; 90US-0532004.
XX
PA (KEGE-) REGENERON PHARM INC.
PA (TEXA) UNIV OF TEXAS SYSTEM.
XX
PI Boulton TG, Cobb MH, Yancopoulos GD, Nye S, Panayotatos N;
XX
DR WPI: 1992-007489/01.
DR P-PSDB; AAR20104.
XX
PT DNA encoding MAP2 kinase enzyme and vectors or host cells - are

PI Kim CH, Cho JM, Chung HH, Lee JH;
XX WPI: 1999-300710/25.
DR P-PSDB; AAW52700.
XX
PT Process for preparing extracellular signal-regulated protein kinase-2
from E. coli -
XX
PS Example 2; Fig 1a-c; 9pp; Korean.
XX
CC The invention relates to a process for the recombinant production
of human extracellular signal-regulated protein kinase-2 (erk-2) in
Escherichia coli. The present sequence represents cDNA encoding human
erk-2 initially isolated from HeLa cells.
XX
SQ Sequence 1047 BP; 303 A; 255 C; 225 G; 264 T; 0 other;
SQ

Query Match 0.6%; Score 26; DB 20; Length 1047;
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3173 aagatctgtgacttggccttgcccg 3198
Db 45; aagatctgtgacttggccttgcccg 479

RESULT 24
AAQ20261
ID AAQ20261 standard; DNA; 1467 BP.
XX
AC AAQ20261;
XX
DT 31-MAR-1992 (first entry)
XX
DE ERK2.
XX
KW Microtubule-associated protein 2; central nervous system;
KW extracellular signal-regulated kinase; ERK; CNS; MAP2; ss
XX
OS Rat rattus.
XX
FH Key Location/Qualifiers
FT CDS 1..1248
FT /tag= a
FT /label= ERK2
FT misc_signal 172..174
FT /tag= b
FT /label= initiation_codon
FT misc_signal 202..204
FT /tag= c
FT /label= initiation_codon
FT terminator 1246..1248
FT /tag= d
XX
PN WO9119008-A.
XX
PD 12-DEC-1991.
XX
PF 03-JUN-1991; 91WO-US03894.
XX
PR 16-MAY-1991; 91US-0701544.
PR 01-JUN-1990; 90US-0532004.
XX
PA (KEGE-) REGENERON PHARM INC.
PA (TEXA) UNIV OF TEXAS SYSTEM.
XX
PI Boulton TG, Cobb MH, Yancopoulos GD, Nye S, Panayotatos N;
XX
DR WPI: 1992-007489/01.
DR P-PSDB; AAR20104.
XX
PT DNA encoding MAP2 kinase enzyme and vectors or host cells - are

PT for assaying cellular factor (e.g. NGF), and drug screening

XX Disclosure: Fig 3A; 9pp; English.

XX The identification of a family of protein serine/threonine kinases
CC which phosphorylate microtubule-associated protein 2 (MAP2) is
CC based, in part, on the cloning and characterisation of MAP2 kinases
CC designated extracellular signal-regulated kinase 1, 2 and 3 (ERK1,
CC ERK2 and ERK3) which are expressed in the central nervous system,
CC and on the identification of another ERK family member, ERK4, with
CC antisera.

CC ERK1-3 are represented in AAQ20260-62.

XX Sequence 1467 BP; 365 A; 382 C; 355 G; 365 T; 0 other;

Query Match 0.6%; Score 26; DB 13; Length 1467;

Best Local Similarity 100.0%; Pred. No. 0.18;

Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3173 aagatctgtgactttggccttgcccg 3198

Db 655 aagaletgtgactttggccttgcccg 680

RESULT 25

AAV71031
ID AAV71031 standard; cDNA; 1815 BP.

XX AC AAV71031;

DT 08-FEB-1999 (first entry)

DE Erk2-green fluorescent protein fusion product.

KW Rat; Erk2 gene; fusion protein; green fluorescent protein; GFP;

KW intracellular signalling; chimera; ss.

OS Chimeric - Aequorea victoria.

OS Chimeric - Rattus sp.

XX Key Location/Qualifiers

FT CDS 1..1815

FT /*tag= a

PN WO9845704-A2.

PD 15-OCT-1998.

PF 07-APR-1998; 98WO-DK00145.

PR 07-APR-1997; 97DK-0000392.

XX (NOVO) NOVO-NORDISK AS.

PI Kasper A, Petersen Bjorn S, Scudder K, Thastrup O;

XX Tullin S;

XX WPI: 1998-594491/50.

DR P-PSDB; AAW85016.

XX Determining effect on signalling pathways in live cells from
PT redistribution of luminophores - specifically fusions of green
PT fluorescent protein with a signalling component, and new apparatus,
PT particularly for identifying toxins and potential therapeutic agents

PS Claim 63; Pages 122-125; 326pp; English.

XX The present sequence encodes a rat Erk2-green fluorescent

CC protein fusion product. The fusion protein is used in an assay

CC that exemplifies the invention. The specification describes how

CC quantitative information about the influence of a molecule on a cellular

CC response is obtained by recording the variation, caused by the molecule,

CC on mechanically intact living cells, in the spatially distributed light
CC emitted from a luminophore present in the cells. The variation in light
CC emission is processed to provide information that correlates spatial
CC distribution to the degree of the molecule. The method is used to
CC identify agents that (in)directly affect intracellular signalling,
CC especially to screen for potential therapeutic agents or toxins, and
CC to identify new drug targets.

XX Sequence 1815 BP; 480 A; 506 C; 451 G; 378 T; 0 other;

Query Match 0.6%; Score 26; DB 19; Length 1815;

Best Local Similarity 100.0%; Pred. No. 0.18;

Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3173 aagatctgtgactttggccttgcccg 3198

Db 484 aagatctgtgactttggccttgcccg 509

RESULT 26

AAV71023

ID AAV71023 standard; cDNA; 1818 BP.

XX AC AAV71023;

DT 08-FEB-1999 (first entry)

DE Green fluorescent protein-Erk2 fusion product.

KW Rat; Erk2 gene; fusion protein; green fluorescent protein; GFP;

KW intracellular signalling; chimera; ss.

XX Chimeric - Aequorea victoria.

XX Chimeric - Rattus sp.

XX Key Location/Qualifiers

FT CDS 1..1818

FT /*tag= a

PN WO9845704-A2.

PD 15-OCT-1998.

PF 07-APR-1998; 98WO-DK00145.

PR 07-APR-1997; 97DK-0000392.

XX (NOVO) NOVO-NORDISK AS.

PI Kasper A, Petersen Bjorn S, Scudder K, Thastrup O;

XX Tullin S;

XX WPI: 1998-594491/50.

DR P-PSDB; AAW85007.

XX Determining effect on signalling pathways in live cells from
PT redistribution of luminophores - specifically fusions of green
PT fluorescent protein with a signalling component, and new apparatus,
PT particularly for identifying toxins and potential therapeutic agents

PS Claim 63; Pages 71-74; 326pp; English.

XX The present sequence encodes a green fluorescent protein (GFP)-rat

CC Erk2 fusion product. The fusion protein is used in an assay

CC that exemplifies the invention. The specification describes how

CC quantitative information about the influence of a molecule on a cellular

CC response is obtained by recording the variation, caused by the molecule,

CC on mechanically intact living cells, in the spatially distributed light

CC emitted from a luminophore present in the cells. The variation in light

CC emission is processed to provide information that correlates spatial

CC distribution to the degree of the molecule. The method is used to

CC identify agents that (in)directly affect intracellular signalling,

CC especially to screen for potential therapeutic agents or toxins, and
 CC to identify new drug targets.

SQ Sequence 1818 BP; 482 A; 505 C; 451 G; 380 T; 0 other;

Query Match 0.6%; Score 26; DB 19; Length 1818;

Best Local Similarity 100.0%; Pred. No. 0.18;

Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3173 aagatctgtgacttggccttgccg 3198

DB 1225 aagatctgtgacttggccttgccg 1250

RESULT 27

AAAT1330

ID AAT1330 standard; cDNA to mRNA; 4696 BP.

XX AC AAT1330;

XX U9-JUL-1996 (first entry)

DE Rat type I insulin-like growth factor receptor cDNA.

XX Insulin-like growth factor I receptor; IGF IR; somatomedin C;

KW smooth muscle; cell growth; cell proliferation; healing;

KW nerve regeneration; angiogenesis; antisense RNA; atherosclerosis;

KW tumour; restenosis; ds.

XX Rattus norvegicus strain Sprague-Dawley.

XX Key Location/Qualifiers

FT CDS 46..4158

FT /*tag= a

FT sig_peptide 46..135

FT /*tag= b

FT mat_peptide 136..4155

FT /*tag= c

XX W09610401-A1.

XX 11-APR-1996.

XX 27-SEP-1995; 95WO-US12563.

XX 04-OCT-1994; 94US-0317898.

XX (UYEM-) UNIV EMORY.

XX Delafontaine P;

XX WPI; 1996-209180/21.

XX P-PSDB; AAR91430.

XX Insulin-like growth factor I receptor anti:sense RNA and

PT ATG-directed sense oligonucleotide(s) - useful for regulating

PT growth factor receptor gene expression for e.g. wound healing and

PT atherosclerosis

XX

PS Claim 18; Page 36-42; 73pp; English.

XX A cDNA clone (AAT13330) codes for rat insulin-like growth factor

CC I receptor (IGF IR) (AAR91430). It was obt'd. from a rat brain cell

CC cDNA library by PCR amplification (see AAT13332-33). IGF IR plays

CC a crucial role in vascular smooth muscle cell (VSMC) proliferative

CC responses. The gene provides the basis for antisense methods

CC (see AAT13325 and AAT13328) to down-regulate IGF IR gene expression and

CC retard VSMC growth, e.g. to treat restenosis and atherosclerosis,

CC and also for ATP-directed sense oligonucleotide (see AAT13326)

XX methods to stimulate VSMC growth e.g. for healing wounds and burns.

XX Sequence 4696 BP; 1151 A; 1268 C; 1241 G; 1036 T; 0 other;

Query Match 0.6%; Score 26; DB 17; Length 4696;

Best Local Similarity 100.0%; Pred. No. 0.17;

Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3120 tcacagagacctggctgctcggaac 3145

DB 3443 tcacagagacctggctgctcggaac 3468

RESULT 28

AAA91087/C

ID AAA91087 standard; DNA; 39 BP.

XX AC AAA91087;

XX 05-APR-2001 (first entry)

DE PCR primer VEGFR303/SRF.AS for Flt1 receptor fusion protein DNA sequence.

XX Flt1 receptor; fusion protein; chimeric protein; pharmacokinetic;

KW plasma leakage; vascular permeability; IgG Fc region; PCR primer; ss.

XX Unidentified.

XX W0200075319-A1.

XX 14-DEC-2000.

XX 23-MAY-2000; 2000WO-US14142.

XX 08-JUN-1999; 99US-0138133.

XX (REGE-) REGENERON PHARM INC.

XX Papadopoulos NJ, Davis S, Yancopoulos GD;

XX WPI; 2001-071076/08.

XX Nucleic acid molecule encoding mammalian phospholipid transfer protein,

PT and its fragments, useful for diagnosis, evaluation, and treatment of

PT diseases associated with the gene expression and for producing model

PT systems -

XX Example 17; Page 63; 159pp; English.

XX This sequence represents a PCR primer used to construct DNA

CC sequences encoding the fusion proteins of the invention between

CC the Flt1 receptor and the Fc region of IgG. The specification relates

CC to modified chimeric polypeptides with improved pharmacokinetics. The

CC modified chimeric polypeptides are preferably Flt1 receptor polypeptides

CC that have been modified to improve their pharmacokinetic profile. The

CC polypeptides can be used to decrease or inhibit plasma leakage and/or

CC vascular permeability in a mammal.

XX Sequence 39 BP; 9 A; 11 C; 9 G; 10 T; 0 other;

SQ

Query Match 0.6%; Score 24; DB 22; Length 39;

Best Local Similarity 100.0%; Pred. No. 1.8;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 986 accgaggtcattgcatgaaat 1009

DB 39 ACCGAGGTCTATTGTCATGAAAT 16

RESULT 29

AAQ30721

ID AAQ30721 standard; DNA; 159 BP.

XX

AC AAQ30721;


```

XX 22-MAR-1993 (first entry)
XX Tyrosine kinase clone RTK-6.
XX Tyrosine kinase receptor; ss.
XX Rattus rattus.
XX
XX Key Location/Qualifiers
XX CDS 1..159
XX /*tag= a
XX
XX WO9218149-A.
XX 29-OCT-1992.
XX
XX 23-APR-1992; 92WO-US03376.
XX
XX 23-APR-1991; 91US-0690199.
XX 26-JUL-1991; 91US-0736559.
XX
XX (REGE-) REGENERON PHARM INC.
XX
XX Aldrich TH, DiStephano P, Furth ME, Glass D, Masiakowski P,
XX P, Maison-Pierre PC, Squinto SP, Stitt T, Yancopoulos GD;
XX
XX WPI: 1992-381778/46.
XX P-PSDB: AAR28603.
XX
XX Assaying neurotrophin activity using cells that express trkB - also
XX for identifying agonists and antagonists, and new recombinant cells
XX and nucleic acid producing trkB, for diagnosis and treatment of
XX neurological disease
XX
XX Disclosure: Fig 12C: 156pp; English.
XX
XX The sequence is that of tyrosine kinase clone RTK-6, isolated
XX from adult or embryonic (E13) rat brain cDNA, which shows
XX homology to the known tyrosine kinase molecules h kit, h rsf1R,
XX hGcFalpha and mcsf1R. It may be of use in the treatment of
XX neurodegenerative disease/neurotrauma including motor neuron
XX disorders such as amyotrophic lateral sclerosis, Werdnig-Hofman
XX disease, chronic proximal spinal muscular atrophy and Guillain-Barre
XX syndrome. It may also be of use in the treatment of neurological
XX disorders associated with diabetes, Parkinson's disease,
XX Alzheimer's disease and Huntington's chorea.
XX See also AAQ30715-Q30728.
XX
XX Sequence 159 BP; 38 A; 36 C; 50 G; 35 T; 0 other;

Query Match 0.68; Score 23; DB 13; Length 159;
Best Local Similarity 100.0%; Pred. No. 4.7;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 3167 gtggtgaagatctgtgactttgg 3189
Db 22 gtggtgaagatctgtgactttgg 44
|||||
|||||

RESULT 30
AAV70215
ID AAV70215 standard; DNA; 159 BP.
XX
XX AC AAV70215;
XX
XX 11-FEB-1999 (first entry)
XX
XX Rat orphan tyrosine kinase receptor peptide clone RTK-6 encoding DNA.
XX
XX Receptor tyrosine kinase; Ror-1; Ror-2; Ehk-1; Ehk-2; detection;
XX neurotrophin activity; trkB; proto-oncogene; tyrosine kinase receptor;

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KW binding protein; BDNF; NT-3; diagnosis; ss.
XX
XX Synthetic.
XX Rattus sp.
XX
XX US5843749-A.
XX
XX 01-DEC-1998.
XX
XX 06-JUN-1995; 95US-0469537.
XX
XX 17-MAR-1995; 95US-0406247.
XX 26-JUL-1991; 91US-0736559.
XX 28-OCT-1993; 93US-0144992.
XX 06-JUN-1995; 95US-0469537.
XX
XX (REGE-) REGENERON PHARM INC.
XX
XX Maisonnier PC, Masiakowski P, Yancopoulos GD;
XX
XX WPI: 1999-044584/04.
XX P-PSDB: AAW83155.
XX
XX DNA encoding receptor tyrosine kinase proteins - and corresponding
XX proteins
XX
XX Example; Fig 12C: 194pp; English.
XX
XX The present invention describes nucleic acid molecules for ror-1,
XX ror-2, ehk-1 and ehk-2. Also described are the corresponding proteins:
XX Ror-1; Ror-2; Ehk-1; and Ehk-2. The proteins are orphan receptor
XX tyrosine kinases. The present sequence encodes a rat orphan tyrosine
XX kinase receptors peptide clone from the present invention.
XX
XX Sequence 159 BP; 38 A; 36 C; 51 G; 34 T; 0 other;

Query Match 0.6%; Score 23; DB 20; Length 159;
Best Local Similarity 100.0%; Pred. No. 4.7;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 3167 gtggtgaagatctgtgactttgg 3189
Db 22 gtggtgaagatctgtgactttgg 44
|||||
|||||

RESULT 31
AAQ54036
ID AAQ54036 standard; cDNA; 1894 BP.
XX
XX AC AAQ54036;
XX
XX 12-JUL-1994 (first entry)
XX
XX Flk-2ws gene.
XX
XX Polymerase chain reaction; primer; amplify; PCR; fetal liver kinase-2;
XX Flk-2; nested; mouse; mFlk-2; PCLII; inhibition; binding;
XX ligand; receptor; modulation; growth; haematopoietic progenitor cell;
XX antibody; ss.
XX
XX Mus musculus.
XX
XX Key Location/Qualifiers
XX CDS 31..1476
XX /*tag= a
XX /product= Soluble Flk-2
XX
XX WO9401576-A.
XX
XX 20-JAN-1994.
XX
XX 07-JUL-1993; 93WO-US06404.

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XX 09-JUL-1992: 92US-0912122.
XX (SYST-) SYSTEMIX INC.
XX Yang Z;
XX WPI: 1994-035079/04.
XX P-PSDB: AAR47579.
XX New soluble and human foetal liver kinase-2 DNA sequences - used
XX for obtaining prods. for modulating the growth of haematopoietic
XX progenitor cells
XX Claim 1: Page 11-14; 2lpp: English.
XX This sequence encodes murine soluble foetal liver kinase-2 (Flk-2ws).
XX This sequence was isolated using the primer sequences given in AA054034-
XX 35. Primer PCLF1 corresponds to mFlk-2 nucleotide positions 1-24,
XX except that at position 2, C is changed to A, and primer PCLF
XX corresponds to mFlk-2 nucleotide positions 341-3428 (sic). This
XX sequence may be used in the production of Flk-2 protein. The
XX resulting proteins may be used in culture and in vivo for inhibiting
XX binding of the Flk-2 ligand to the Flk-2 receptor. Therefore they may
XX be used for modulating the growth of haematopoietic progenitor cells.
XX The proteins may also be used for producing antibodies for identifying
XX cells carrying Flk-2, removing soluble Flk-2 from culture fluids or
XX natural fluids, purifying Flk-2 or assaying for the presence of
XX Flk-2.
XX Sequence 1894 BP; 494 A; 459 C; 500 G; 441 T; 0 other;

Query Match 0.6%; Score 23; DB 15; Length 1894;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3167 qcggtgaagatctgtgactttgg 3189
Db 976 qcggtgaagatctgtgactttgg 998

RESULT 32
AA029954
ID AA029954 standard; cDNA: 3453 BP.
AC AA029954;
XX 15-MAR-1993 (first entry)
XX Murine flk-2 cDNA sequence.
XX Thymidine kinase; TK; haematopoietic; stem cells; proliferation;
XX differentiation; progenitor cells; foetal liver kinase; ss.
XX Mus musculus.
XX Key Location/Qualifiers
XX CDS 31..3009
XX sig_peptide 31..111
XX mat_peptide 112..3006
XX FT /*tag= a
XX W09217486-A.
XX 15-OCT-1992.
XX 02-APR-1992; 92WO-US02750.
XX 02-APR-1991; 91US-0679666.
XX 28-JUN-1991; 91US-0728913.
XX 15-NOV-1991; 91US-0793065.
XX 24-DEC-1991; 91US-0813593.
XX (UYP-) UNIV PRINCETON.

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XX Lemischka IR;
XX WPI: 1992-366185/44.
XX P-PSDB: AAR28038.
XX Stimulating proliferation and/or differentiation of primitive
XX mammalian haematopoietic stem cells - using ligand that binds
XX thymidine kinase and flk-1 and flk-2
XX Claim 6; Fig 1a; 94pp: English.
XX The murine foetal liver kinase (flk) -2 clone was isolated by
XX standard PCR techniques from stem-cell receptor-contg. tissue cDNA
XX libraries. Suitable tissues include foetal liver, spleen or thymus
XX cells or adult marrow or brain cells. The PCR primers used are based
XX on known sections of the flk-2 gene. The murine flk-2 clone may be
XX used in a vector to transform haematopoietic cells. The thymidine
XX kinase encoded by flk-2 is expressed in primitive but not mature
XX haematopoietic cells. Ligand binding to the TK may be prepd. which
XX can stimulate proliferation and/or differentiation of primitive
XX haematopoietic cells in vivo. The ligands can stimulate the
XX proliferation of additional primitive stem cells, differentiation into
XX more mature progenitor cells, or both.
XX See also AAQ29955-7.
XX Sequence 3453 BP; 945 A; 822 C; 876 G; 809 T; 0 other;

Query Match 0.6%; Score 23; DB 13; Length 3453;
Best Local Similarity 100.0%; Pred. No. 3.8;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3167 gtggtgaagatctgtgactttgg 3189
Db 2509 gtggtgaagatctgtgactttgg 2531

RESULT 33
AAQ53502
ID AAQ53502 standard; cDNA: 3453 BP.
AC AAQ53502;
XX 27-JUN-1994 (first entry)
XX Murine flk-2 cDNA.
XX Receptor protein tyrosine kinase; pTK family; foetal liver kinase;
XX mflk; primitive; totipotent; haematopoietic cell; stem cell;
XX proliferation; stromal cell; ds.
XX Mus musculus.
XX Key Location/Qualifiers
XX CDS 31..3009
XX sig_peptide 31..111
XX mat_peptide 112..3006
XX FT /*tag= a
XX FT /*tag= b
XX FT /*tag= c
XX US5270458-A.
XX 14-DEC-1993.
XX 02-APR-1991; 91US-0679666.
XX 02-APR-1991; 91US-0679666.
XX 28-JUN-1991; 91US-0728913.
XX 15-NOV-1991; 91US-0793065.
XX 24-DEC-1991; 91US-0813593.
XX 26-JUN-1992; 92US-0906397.

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PR 12-NOV-1992; 92US-0975049.
PR 19-NOV-1992; 92US-0977451.
XX
XX (UYPR-) UNIV PRINCETON.
XX
XX Lemischka IR;
XX
XX WPI; 1993-405021/50.
XX
XX P-PSDB; AAR44994.
XX
XX Isolated nucleic acid molecules of hematopoietic stem cell
XX receptor flk-2 - encoding mammalian receptor protein tyrosine
XX kinases expressed in primitive haematopoietic cells
XX
XX Claim 2; Fig 1a; 60pp; English.
XX
XX Nucleic acid sequences coding for murine flk-2 and specified
XX subfragments of it are claimed. The flk-2 polypeptide is a protein
XX tyrosine kinase expressed only in primitive haematopoietic cells.
XX The cDNA can be used to recombinantly produce flk-2 for stimulating
XX self-renewal of totipotent stem cells and development of all
XX haematopoietic cells.
XX
XX Sequence 3453 BP; 947 A; 821 C; 876 G; 809 T; 0 other;
SQ

```

Query Match 0.6%; Score 23; DB 14; Length 3453;
 Best Local Similarity 100.0%; Pred. No. 3.8;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Qy 3167 gtggtgaagatctgtgactttgg 3189
      |||||
Db 2509 gtggtgaagatctgtgactttgg 2531

RESULT 34
ID AAQ35249 standard; cDNA; 3453 BP.
XX
XX AAQ35249;
XX
XX 25-JUN-1993 (first entry)
XX
XX Murine flk-2 coding sequence.
XX
XX Murine; receptor; protein; tyrosine kinase; pTK; primitive; mammalian;
XX hematopoietic cell; pHC; mature; mHC; fetal; liver kinase 2; flk-2;
XX liver; spleen; thymus; adult; brain; marrow; thymocyte; subset;
XX multipotential; T-lymphoid; lineage; ss.
XX
XX Mus musculus.
XX
XX Key Location/Qualifiers
XX CDS 31..3009
XX
XX misc_RNA
XX 31..111
XX /*tag= b
XX /note= "Hydrophobic leader"
XX
XX WO9300349-A.
XX
XX 07-JAN-1993.
XX
XX 26-JUN-1992; 92WO-US05401.
XX
XX 28-JUN-1991; 91US-0728913.
XX 15-NOV-1991; 91US-0793065.
XX 24-DEC-1991; 91US-0813593.
XX 02-APR-1992; 92WO-US02750.
XX
XX (UYPR-) UNIV PRINCETON.
XX
XX Lemischka IR;
PI

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XX
XX WPI; 1993-036323/04.
XX
XX P-PSDB; AAR31375.
XX
XX Nucleic acid encoding receptor protein tyrosine kinase - allows
XX development of ligands to stimulate proliferation and/or
XX differentiation of mammalian haematopoietic stem cells
XX
XX Claim 5; Fig 1a; 78pp; English.
XX
XX This sequence encodes a murine receptor protein tyrosine kinase which
XX belongs to a new functional class of protein tyrosine kinases (pTKs).
XX pTKs in this class are expressed in primitive mammalian hematopoietic
XX (pHC) cells but not in mature hematopoietic cells (mHC). The protein
XX encoded by this sequence is an example of a receptor pTK and is called
XX fetal liver kinase 2 (flk-2). flk-2 is expressed in fetal liver,
XX spleen and thymus, and adult brain and marrow. Expression of flk-2
XX mRNA occurs in the most primitive thymocyte subset, which is believed
XX to be uncommitted. Therefore, thymocytes expressing flk-2 may be
XX multipotential. flk-2 is the first receptor tyrosine kinase known to
XX be expressed in the T-lymphoid lineage.
XX
XX Sequence 3453 BP; 947 A; 821 C; 876 G; 809 T; 0 other;
SQ

```

Query Match 0.6%; Score 23; DB 14; Length 3453;
 Best Local Similarity 100.0%; Pred. No. 3.8;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Qy 3167 gtggtgaagatctgtgactttgg 3189
      |||||
Db 2509 gtggtgaagatctgtgactttgg 2531

RESULT 35
ID AAQ40914 standard; cDNA; 3453 BP.
XX
XX AAQ40914;
XX
XX 19-OCT-1993 (first entry)
XX
XX Murine flk-2 cDNA.
XX
XX Murine; receptor; protein; tyrosine kinase; pTK; flk-2; primitive;
XX hematopoietic cell; mature; family; conserved; region;
XX catalytic domain; c-kit; fetal liver kinase; flk; fetal; spleen;
XX thymus; adult; brain; bone marrow; multipotential; CFU-Blast colony;
XX hierarchy; transduction; T-lymphoid; lineage; ss.
XX
XX Mus musculus.
XX
XX Key Location/Qualifiers
XX CDS 31..3009
XX
XX sig_peptide
XX 31..111
XX /*tag= b
XX /note= "Hydrophobic leader sequence"
XX
XX mat_peptide
XX 112..3006
XX /*tag= c
XX
XX WO9310136-A.
XX
XX 27-MAY-1993.
XX
XX 16-NOV-1992; 92WO-US09893.
XX 15-NOV-1991; 91US-0793065.
XX
XX (UYPR-) UNIV PRINCETON.
XX
XX Lemischka IR;
XX

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DR WPI: 1995-005894/01.
 XX P-PSDB: AAR67535.
 PT Murine flk-2 receptor protein tyrosine kinase - used to stimulate
 PT proliferation and/or stimulation of primitive mammalian
 PT haematopoietic stem cells in vitro or in vivo.
 XX
 XX Disclosure: Fig. 1A-1F; 69pp; English.
 XX
 CC cDNAs encoding receptor protein tyrosine-kinases, mouse foetal liver
 CC kinase-2 (flk-2), human flk-2 and mouse flk-1 are given in AAR67535-70,
 CC respectively, and the deduced amino acid sequences in AAR67535-37,
 CC respectively.
 XX
 XX Sequence 3453 BP; 946 A; 822 C; 876 G; 809 T; 0 other;
 SQ

Query Match 0.6%; Score 23; DB 16; Length 3453;
 Best Local Similarity 100.0%; Pred. No. 3.8;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3167 gtcgtgaagatctgtgactttgg 3189
 |||||
 Db 2509 gtcgtgaagatctgtgactttgg 2531

RESULT 38
 AAT38733
 ID AAT38733 standard; cDNA; 3453 BP.
 XX
 AC AAT38733;
 XX
 XX 11-DEC-1996 (first entry)
 XX
 DE Human foetal liver kinase 2 cDNA.
 XX
 KW Human: foetal liver kinase 2; flk-2; protein tyrosine kinase;
 KW monoclonal; antibody; extracellular domain; receptor assay;
 KW haematopoietic stem cell; ligand; stimulation; proliferation;
 KW differentiation; treatment; anaemia; bone marrow damage;
 KW cancer chemotherapy; radiation; ds.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 31..3009
 FT /*tag= a
 FT sig_peptide 31..111
 FT /*tag= b
 FT mat_peptide 112..3006
 FT /*tag= c
 XX
 XX US548065-A.
 XX
 XX 20-AUG-1996.
 XX
 XX 02-APR-1991; 91US-0679666.
 XX
 PR 19-NOV-1992; 92US-0977451.
 PR 02-APR-1991; 91US-0679666.
 PR 28-JUN-1991; 91US-0728913.
 PR 15-NOV-1991; 91US-0793065.
 PR 24-DEC-1991; 91US-0813593.
 PR 26-JUN-1992; 92US-0906397.
 PR 12-NOV-1992; 92US-0975049.
 PR 30-APR-1993; 93US-0055269.
 PR 31-OCT-1994; 94US-0252517.
 XX
 XX (UYPR-) UNIV PRINCETON.
 XX
 PA Lemischka IR;
 XX
 XX WPI: 1996-392678/39.
 DR

DR P-PSDB: AAR97418.
 XX
 XX Anti-foetal liver kinase 2 (flk-2) antibodies - useful in assays,
 PT for isolating haematopoietic stem cells expressing receptor and for
 PT obtaining ligands
 XX
 XX Disclosure: Columns 27-34; 50pp; English.
 XX
 CC The present sequence encodes human foetal liver kinase 2 (flk-2), a
 CC protein tyrosine kinase. Isolated antibodies, pref. monoclonal,
 CC raised against the extracellular portion of flk-2 can be used to
 CC assay for flk receptors on the surface of primitive haematopoietic
 CC stem cells, and to isolate positive cells. The antibodies can also
 CC be used as, or to obtain ligands, which stimulate the proliferation
 CC and/or differentiation of stem cells. The ligands can be used, e.g.
 CC for treating anaemia, or bone marrow damage resulting from cancer
 CC chemotherapy, or radiation.
 XX
 XX Sequence 3453 BP; 947 A; 822 C; 875 G; 809 T; 0 other;
 SQ

Query Match 0.6%; Score 23; DB 17; Length 3453;
 Best Local Similarity 100.0%; Pred. No. 3.8;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3167 gtcgtgaagatctgtgactttgg 3189
 |||||
 Db 2509 gtcgtgaagatctgtgactttgg 2531

RESULT 39
 AAT72118
 ID AAT72118 standard; cDNA; 3453 BP.
 XX
 AC AAT72118;
 XX
 XX 19-AUG-1997 (first entry)
 DT
 XX Murine flk-2 receptor coding sequence.
 DE
 XX Human; fetal liver kinase 2; flk2; receptor protein tyrosine kinase;
 KW pTK; liver; spleen; thymus; adult; brain; bone marrow; primitive portion;
 KW haematopoietic hierarchy; extracellular domain; soluble form; ligand;
 KW proliferation; differentiation; mammalian; haematopoietic stem cell;
 KW macrocytic anaemia; aplastic anaemia; cancer; radiation; mouse; ss.
 XX
 OS Mus musculus.
 XX
 FH Key Location/Qualifiers
 FT CDS 31..3009
 FT /*tag= a
 FT sig_peptide 31..111
 FT /*tag= b
 FT mat_peptide 112..3006
 FT /*tag= c
 XX
 XX US5621090-A.
 XX
 XX 15-APR-1997.
 PD
 XX 02-APR-1991; 91US-0679666.
 PF
 XX 26-JUN-1992; 92US-0906397.
 PR 02-APR-1991; 91US-0679666.
 PR 28-JUN-1991; 91US-0728913.
 PR 15-NOV-1991; 91US-0793065.
 PR 24-DEC-1991; 91US-0813593.
 XX
 XX (UYPR-) UNIV PRINCETON.
 PA
 XX Lemischka IR;
 XX
 XX WPI: 1996-392678/39.
 DR

XX DNA (AAT00801) coding for murine stem cell tyrosine kinase receptor flk2
 CC (also called flt3) (AAR01868) was obtd. by RT-PCR amplification of RNA
 CC isolated from mid-gestation mouse foetal livers using primers based
 CC on the murine flt3 sequence, and subcloning of the product into pRK5.1.
 CC An flk2/flt3 extracellular domain-IgG1 Fc fusion protein was
 CC constructed and used to raise agonist antibodies able to bind Lo, and
 CC activate, flk2/flt3.
 XX
 SQ Sequence 3521 BP; 943 A; 853 C; 908 G; 817 T; 0 other;

Query Match 0.6%; Score 23; DB 16; Length 3521;
 Best Local Similarity 100.0%; Pred. No. 3.8;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3167 gtggtgaagatctgtgactttgg 3189
 |||||
 DB 2560 gtggtgaagatctgtgactttgg 2582

RESULT 42
 AA006869
 1D AAQ06869 standard; DNA: 4054 BP.

XX AC AA006869;
 XX
 XX 07-MAR-1991 (first entry)
 XX
 XX Sequence encodes Platelet derived growth factor (PDGF) receptor
 DE protein.
 DE

XX Atherosclerosis; fibrotic diseases; ds.

XX Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FT CDS 205..3471
 FT /*tag= a

XX WO9014425-A.
 XX
 XX 29-NOV-1990.
 XX
 XX 21-MAY-1990; 90WO-US02849.
 XX
 XX 22-MAY-1989; 89US-0355018.
 XX
 XX (ZYMO-) ZYMOGENETICS INC.
 XX
 XX Kelly JD, Murray MJ;
 XX
 XX WPI; 1990-375992/50.
 DR P-PSDB; AAR08267.

XX DNA encoding platelet-derived growth factor - used to transform
 PT cells for culturing to detect PDG agonists and antagonists

XX Claim 1; Fig 1; 30pp; English.

XX Gene product may be expressed from a transformed cell. It has
 CC utility in decision of PDGF agonist and antagonist analogues, binding
 CC AA, AB and BB isoforms. PDGF agonists may be used to enhance wound
 CC healing, and antagonists may be used to block the effects of PDGF
 CC eg. in treatment of atherosclerosis or fibrotic diseases.

XX Sequence 4054 BP; 1127 A; 886 C; 1027 G; 1014 T; 0 other;

Query Match 0.6%; Score 23; DB 11; Length 4054;
 Best Local Similarity 100.0%; Pred. No. 3.7;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3170 gtgaagatctgtgactttggcct 3192
 |||||
 DB 2698 gtgaagatctgtgactttggcct 2720

RESULT 43
 AAQ05989

1D AAQ05989 standard; cDNA: 6412 BP.

XX AC AAQ05989;

XX 16-JAN-1991 (first entry)

XX TR4 cDNA clone related to T11 gene encoding alpha type PDGF receptor.

XX Platelet derived growth factor; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

FT CDS 139..3408

FT /*tag= a

FT sig_peptide 139..207

FT /*tag= b

FT mat_peptide 208..3405

FT /*tag= c

FT /*product=T11 receptor

FT exon 2701..2812

FT /*tag= d

FT /*label-exon a

FT exon 2813..2912

FT /*tag= e

FT /*label-exon b

FT exon 2913..3018

FT /*tag= f

FT /*label-exon c

FT polyA_signal 6353..6358

FT /*tag= g

FT polyA_site 6376..6412

FT /*tag= h

XX WO9010013-A.

XX 07-SEP-1990.

XX 08-FEB-1990; 90WO-US00617.

XX 09-FEB-1989; 89US-0308282.

XX (USDC) US SEC OF COMMERCE.

XX Matsui T, Aaronson SA, Pierce JH;

XX WPI; 1990-290306/38.

DR P-PSDB; AAR06910.

XX Type alpha platelet-derived growth factor receptor gene - useful

PT for transforming cells to express novel protein receptor and also

PT susceptible to genetic engineering.

XX Claim 3; Fig 3; 64pp; English.

XX The TR4 clone is the largest cDNA clone related to the T11 genomic

CC clone, isolated from a library prepd from human thymus DNA. The

CC T4 cDNA clone was isolated from a M426 human embryo fibroblast

CC cDNA library. The exons shown were determined from the T11

CC genomic clone. The gene has been mapped to chromosome 4 at

CC location q 11-12, which is within the same region as the c-kit

CC proto-oncogene. The coding region can be introduced into the pSV2

CC gpt vector with a simian sarcoma virus LTR as a promoter and

CC expressed in a host. The resulting protein is a novel PDGF

CC receptor designated type alpha (the known receptor is designated

CC type beta). The cDNA can be used also to investigate the

CC mechanisms of PDGF regulatory processes or in bioassays for detect-
CC ing related genes, particularly for identification of classes of
CC tumour cells or of genetic defects in connective tissue and/or
CC healing response.
XX
SQ Sequence 6412 BP; 1885 A; 1299 C; 1443 G; 1785 T; 0 other;

Query Match 0.6%; Score 23; DB 11; Length 6412;
Best Local Similarity 100.0%; Pred. No. 3.6; 0; Indels 0; Gaps 0;
Matches 23; Conservative 0; Mismatches 0;

OY 3170 gtaagaatctgtacattggcct 3192
|||||
Db 2632 gtaagaatctgtacattggcct 2654

RESULT 44
AAT03102

ID AAT03102 standard; DNA; 22 BP.

XX AC AAT03102;

XX DT 14-FEB-1996 (first entry)

XX DE SAL-S1 gene PCR primer otk1.41.1.

XX KW Protein tyrosine-kinase; pTK; SAL-S1; agonist; cell growth;
XX differentiation; polymerase chain reaction; PCR; primer;
XX tG; antibody; ss.
XX OS Synthetic.

XX PN W09527061-A1.

XX PD 12-OCT-1995.

XX PF 04-APR-1995; 95WO-US04228.

XX PR 04-APR-1994; 94US-0222616.

XX PA (GETH) GENENTECH INC.

XX PI Bennett BD, Goeddel D, Lee JM, Matthews W, Tsai SP;

XX PL Wood WI;

XX DR WPI; 1995-366160/47.

XX Aqonist antibodies which activate specific protein tyrosine
PT kinase(s) - also activate chimeric proteins of kinase extracellular
PT domain and Ig constant domain, useful for studying, and therapeutic
PT modulation of, cell growth and differentiation
XX Example 7; Page 101; 125pp; English.

XX PCR primers given in AAT03102-03 were used to amplify plasmid
CC PRK5.tkl-1.1 (AAT03104) incorporating SAL-S1 (see AAT03090) DNA.
CC The product was used to construct a fusion of the SAL-S1
CC extracellular domain and human IgG1 Fc domain, which was expressed
CC in 293 and COS7 cells and used to raise antibodies having
CC protein tyrosine-kinase agonist activity.

XX Sequence 22 BP; 6 A; 3 C; 9 G; 4 T; 0 other;

Query Match 0.5%; Score 22; DB 16; Length 22;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2165 aggcctgctgagagaaagtctg 2186
|||||
Db 1 aggcctgctgagagaaagtctg 22

RESULT 45
AAT03103/c

ID AAT03103 standard; DNA; 32 BP.

XX AC AAT03103;

XX DT 14-FEB-1996 (first entry)

XX DE SAL-S1 gene PCR primer otk1.41.2.

XX KW Protein tyrosine-kinase; pTK; SAL-S1; agonist; cell growth;
XX differentiation; polymerase chain reaction; PCR; primer;
XX tG; antibody; ss.

XX OS Synthetic.

XX PN W09527061-A1.

XX PD 12-OCT-1995.

XX PF 04-APR-1995; 95WO-US04228.

XX PR 04-APR-1994; 94US-0222616.

XX PA (GETH) GENENTECH INC.

XX PI Bennett BD, Goeddel D, Lee JM, Matthews W, Tsai SP;

XX PL Wood WI;

XX DR WPI; 1995-366160/47.

XX Agonist antibodies which activate specific protein tyrosine
PT kinase(s) - also activate chimeric proteins of kinase extracellular
PT domain and Ig constant domain, useful for studying, and therapeutic
PT modulation of, cell growth and differentiation
XX Example 7; Page 101; 125pp; English.

XX PCR primers given in AAT03102-03 were used to amplify plasmid
CC PRK5.tkl-1.1 (AAT03104) incorporating SAL-S1 (see AAT03090) DNA.
CC The product was used to construct a fusion of the SAL-S1
CC extracellular domain and human IgG1 Fc domain, which was expressed
CC in 293 and COS7 cells and used to raise antibodies having
CC protein tyrosine-kinase agonist activity.

XX SQ Sequence 32 BP; 4 A; 11 C; 9 G; 8 T; 0 other;

Query Match 0.5%; Score 22; DB 16; Length 32;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2323 cgaggataaggcgacgatggag 2344
|||||
Db 32 CGAGGATAAGGCACGATGGAG 11

Search completed: July 15, 2002, 23:09:35
Job time: 18393 sec

Result No.	Score	Query Match	Length	DB	ID	Description
8						

100.0%; Score 4111; DB 6; Length 4795;

QY 2161 cagaggctctgagagaaagtctgtgagtcgacttagcgactccaaccagaagctgag 2220
|||||
DB 2161 CGAGAGCTGCTGGAGCGAAAGTCTGGAGTCGAGTTGGCGGACTTCCAAACGAGAGCTGAG 2220
QY 2221 catccagcgcgtacccagagaaatccgagacactatctgtcagcgtatgcaucuccaa 2280
|||||
DB 2221 CATCCAGCGGTGGCGGAGGAGGATGCGGAGCGTATCTGTGACAGCGTGTGCAACGCCAA 2280
QY 2281 gggctgcctcaactcctccgcgaagcgtggcgtgagaggtctccgagagataagagcagcat 2340
|||||
DB 2281 GGGCTGCTCAACTCTCCGCCAGCGTGGCGTGGAGGCTCCGAGGATTAAGGCCAGCAT 2340
QY 2341 ggagatcgtatctctgtcgtgtaacggcgctcaatcgctgtctctctgtcgtctctctct 2400
|||||
DB 2341 GGAGATGCTGATCTCTTCTGGGTACCGCGCTCATCGCTGTCTTCTCTGGTTCCTCTCCCT 2400
QY 2401 cctcctctctgttaacatgagagagcgcccgagagacatcaagacgagctaccctgtc 2460
|||||
DB 2401 CTCTCATCTTCTTAACTATGAGAGCGCGCGCCAGCAGACATCAAGACGGGCTACCTGTC 2460
QY 2461 catcatcatgaccccgagggtgctcctctggagagcaalgcgaaatacctgtcctacga 2520
|||||
DB 2461 CATCATCATGACCCCGGAGGTGCTCTTGGAGGAGCAATGCCAATACCTGTCTCTACGA 2520
QY 2521 tgcagcagctggaatcccccgagagcgctacacctaggagagatgctcagctacgg 2580
|||||
DB 2521 TGCCAGGCGAGTGGGAATTTCCCGGAGAGCGGCTGCACCTGGGGAGAGTGTCTGGGCTACGG 2580
QY 2581 cgcctctcgggaaatggtggagcctcgcgtcttcgggcatccacaagagcgagctgtga 2640
|||||
DB 2581 CGCTTCTGGGAAGCTGTGTGGGAAGCTTCCGCTTCTGGGATTCACAAAGGCAAGCACTCTGA 2640
QY 2641 caccctgacgtgagaaatgctgaaagagggcgccagcgctcagagcagcagcagcagctgaa 2700
|||||
DB 2641 CACCTGTGCGCTGAAATGCTTAAAGAGGGTGGCACGCGCCAGCGAGCACCGCGGCTCAT 2700
QY 2701 gtcggaactcgaatcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcct 2760
|||||
DB 2701 GTGCGAGCTCAAGATCTTCATTTACATCGGCAATCACCTCAACCTGTGTCAACTCTCTCTCGG 2760
QY 2761 ggcgtgacacacgaggg 2820
|||||
DB 2761 GCGCTGACCAAGCGGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2820
QY 2821 cctctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcct 2880
|||||
DB 2821 CTTCTTCCAACTTCTTGGCGGCAAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2880
QY 2881 cagcagc 2940
|||||
DB 2881 CGAGCAGCGCGGAGCGCTTCCGCGGTCATGCTGGAGCTTCCGAGGCTTGGATTCGAGGCGGCG 2940
QY 2941 ggggagcagcagcaggg 3000
|||||
DB 2941 GGGGAGCAGCGCACAGGGTCTCTTGGCGGCTTCTCGAAGACCGAGGCGCGAGCGAGCGCG 3000
QY 3001 ggcctctcagacccaagaagctgaggaacctgtggtcgaagccgcgtgaccallgaaagatct 3060
|||||
DB 3001 GGTCTTCTCCAGACCAAGAAGCTGAGGAGCTGTGGCTGAGCGCGGCTGACCATTCGAAGATCT 3060
QY 3061 gctcgtctacagcttccagggtggcgagaggtgagttcctggtctcccgaaagtgcat 3120
|||||
DB 3061 TGCTCTCTACAGCTTCCAGGTGGCGAGAGGATGAGTCTCTGGCTTCCCGAAAGTGTGAT 3120
QY 3121 ccacagagacctggtcgtcgtcgaacatctcgtcgtggaagcagcagctggtgaaagatctg 3180
|||||
DB 3121 CCACAGACACCTGCGTCTCGGAACATTTCTGCTCGGAAAGCGAGCGTGGTGAAGATCTG 3180
QY 3181 gactcttgccttgcgggggacatctacaaagacccctgactacgtcccaagagcagctgac 3240
|||||
DB 3181 TGACTTTGGGCTTGGCGGAGCATCTACAAAGACCTGACTACGTTCGCGCAAGGCGAGTGC 3240

QY 3241 ccggctgccccctgaagtgaaggccctgaaagcatcttcgacaagtggtacacaccgca 3300
|||||
DB 3241 CCGGCTGCCCCCTCAAGTGGATGGCCCTTCAAAGCATCTTCGACAAGGTGTACACCACGCA 3300
QY 3301 gagtgcagctggtgctcttggggtgctctctgaggagatctctctctctctctctctctctct 3360
|||||
DB 3301 GACTGAGCTGTGCTCTCTTGGGTGCTTCTCTCGGAGATCTTCTCTCTCTGGGCGCTCCCG 3360
QY 3361 gtacctgggggtcagatcaatgagagttctctccagggctgagagagcagcacaaggat 3420
|||||
DB 3361 GTACCTTGGGTTCAGATCAATGAGGAGTTCTGCCAGCGCTGAGAGCGGCAACAAGGAT 3420
QY 3421 gagggcccgagagctgcccactcccccatacagccacatcatctgactgactgctggtccgg 3480
|||||
DB 3421 GAGGGCCCCGAGACTGCCACTCCCGCCATACCGCCGATCATGCTGAACCTGCTGTGTCGG 3480
QY 3481 agaccccaagcgagacacctgcatctctcgaggtggtggagatcctctggggagcctgctcca 3540
|||||
DB 3481 AGACCCCAAGCGGAGACTGCAATTTCTGGAGTGGTGGAGATCTCTGGGGACCTGTCTCA 3540
QY 3541 ggcagggggcctcagagagagagaggtctctcatggcccccgagcagctctcagagctc 3600
|||||
DB 3541 GGCAGGGGGCTTCAAGAGAGAGAGAGGTCTGCATGGCCCCCGGCGAGCTTCTCAGAGCTC 3600
QY 3601 agagagggcagctctctcgaggtgtccaccatggccctacacatcgccccagggctgacgc 3660
|||||
DB 3601 AGAAGAGGGCAGCTTCTCGCAGGTGTCCACCATGGCCCTACACATCGCCCGAGCTGACGC 3660
QY 3661 tgaggacagcccgccaaagcctgcagcgccacagcctggcgccaggttatataactgggt 3720
|||||
DB 3661 TGAGGACAGCCCGCCAAAGCCTGCAGCGCCACAGCCTGGCGCGCAGGTATTTACAACTGGGT 3720
QY 3721 gtcctttccgggtgcttgccagaggggctgagaccgtggtctccaggalgaaac 3780
|||||
DB 3721 GTCTTTTCCGGGTGCTTGGCCAGAGGGGTGAGACCGGTGGTTCCTTCCAGGATGAAGAC 3780
QY 3781 atttgagaaattcccatgaccccaacagcctacaaaggctctgtgacacacagacaga 3840
|||||
DB 3781 ATTTGAGAAATTTCCCATGACCCCAACGACCTACAAAGGCTCTCTGGACAACCCAGACA 3840
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|||||
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RESULT 2

LOCUS AR106406 4795 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 3 from patent US 6107046.
ACCESSION AR106406
VERSION AR106406.1 GI:12820936
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 4795)
AUTHORS Alitalo,K., Aprelikova,O., Pajusola,K., Armstrong,E., Korhonen,J.,

Kaipainen, A. and Matikainen, M.
Antibodies to Fil4, a receptor tyrosine kinase and uses thereof
Patent: US 6107046-A 3 22-AUG-2000;
Location/Qualifiers
1. .4795
source

HASE COUNT	977 a	1490 c	1494 g	834 t
ORIGIN				

Query Match	100.0%	Score 4111	DB 6	Length 4795
Best Local Similarity	100.0%	Pred. No. 0		
Matches 4111	Conservative	Mismatches 0	Indels 0	Gaps 0

[illegible]

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RESULT 6

HSFLT4

LOCUS

DEFINITION

H.sapiens mRNA for FLT4, 4416 bp mRNA linear PRI 30-NOV-1993
HSLT4
class III receptor tyrosine kinase.

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AUTHORS	Lee, J., Gray, A., Yuan, J., Luoh, S.-M., Avraham, H. and Wood, W.I.		
TITLE	Vascular Endothelial Growth Factor Related Protein (VRP): A Ligand and Specific Activator of the Tyrosine Kinase Receptor Flt4		
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. (1996) In press		
REFERENCE	2 (bases 1 to 4425)		
AUTHORS	Wood, W.I.		
TITLE	Direct Submission		
JOURNAL	Submitted (12-DEC-1995) William I. Wood, Molecular Biology, Genentech, Inc., 460 Pt. San Bruno Blvd., S. San Francisco, CA 94080, USA		
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BASE COUNT 939 a 1348 c 1361 g 777 t

ORIGIN

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RESULT 10
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ORGANISM Unknown.
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AUTHORS Bennett,B.D., Goeddel,D. and Matthews,W.
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JOURNAL Patent: US 5635177-A 17 03-JUN-1997;
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VERSION AC022095.5 GI:13699618
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SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 127488)
AUTHORS DOE Joint Genome Institute.
TITLE Sequencing of Human Chromosome 5
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 127488)
AUTHORS DOE Joint Genome Institute.
TITLE Direct Submission
JOURNAL Submitted (26-JAN-2000) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
COMMENT On Apr 20, 2001 this sequence version replaced gi:7711676.
-----Genome Center
Center: Joint Genome Institute
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Center Code: JGI
Web site: http://www.jgi.doe.gov

Project Information
Center Project Name: 78060
Center clone name: CIT978SKB_36B8

Summary Statistics
Consensus quality: 110477 bases at least Q40
Consensus quality: 117221 bases at least Q30
Consensus quality: 120225 bases at least Q20
Estimated insert size: 131000; pulse field gel estimation
Estimated insert size: 126288; sum-of-contigs estimation
Quality coverage: 7.48 in Q20 bases; sum-of-contigs estimation
Quality coverage: 7.76 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 13 workings. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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* 1117 1216: gap of unknown length
* 1217 2254: contig of 1038 bp in length
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* 3513 5005: contig of 1493 bp in length
* 5006 5105: gap of unknown length
* 5106 7647: contig of 2542 bp in length
* 7648 7747: gap of unknown length
* 7748 10237: contig of 2490 bp in length
* 10238 10337: gap of unknown length
* 10338 12440: contig of 2103 bp in length
* 12441 12540: gap of unknown length
* 12541 15935: contig of 3395 bp in length
* 15936 16035: gap of unknown length
* 16036 24396: contig of 8361 bp in length
* 24397 24496: gap of unknown length
* 24497 39085: contig of 14589 bp in length
* 39086 39185: gap of unknown length
* 39186 60545: contig of 21360 bp in length
* 60546 60645: gap of unknown length
* 60646 79490: contig of 18845 bp in length
* 79491 79590: gap of unknown length
* 79591 127488: contig of 47898 bp in length.

Location/Qualifiers
1. .127488
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="5"
/clone_lib="CTB-36B8"
/clone="CTB-36B8"
/clone_lib="CalTech human BAC library B"
31643 a 32392 c 31616 g 30626 t 1211 others

Query Match 8.8%; Score 363; DB 2; Length 127488;
Best Local Similarity 100.0%; Pred. No. 4.e-168;
Matches 363; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1677 ccattcccgagcgttcaccatcgatccaagccatccaggagctactagagggccagc 1736
|||||
Db 114615 CCATCCCCGAGCGCTTACCATCGAATCCCAAGCCATCCGAGGAGCTACTAGAGGGCCAGC 114556
|||||
QY 1737 cgggtcctcctgagctccaaagccagctacaagtacgagcatctgcgctggtaccgcc 1796
|||||
Db 114555 CGGTGCTCTCTAGCTGCCAGCCGACAGCTACAAAGTACAGGACATCTGCCCTGGTACCGCC 114496
|||||
QY 1797 tcaactgtccagctgcagatgctgcacgggaaccgcgtctctgctcgtactgcaagaacg 1856
|||||

Center Code: JGI
Web site: http://www.jgi.doe.gov

Project Information
Center Project Name: 78060
Center clone name: CIT978SKB_36B8

Summary Statistics
Consensus quality: 110477 bases at least Q40
Consensus quality: 117221 bases at least Q30
Consensus quality: 120225 bases at least Q20
Estimated insert size: 131000; pulse field gel estimation
Estimated insert size: 126288; sum-of-contigs estimation
Quality coverage: 7.48 in Q20 bases; sum-of-contigs estimation
Quality coverage: 7.76 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 13 workings. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 1116: contig of 1116 bp in length
* 1117 1216: gap of unknown length
* 1217 2254: contig of 1038 bp in length
* 2255 2354: gap of unknown length
* 2355 3412: contig of 1058 bp in length
* 3412 3513: gap of unknown length
* 3513 5005: contig of 1493 bp in length
* 5006 5105: gap of unknown length
* 5106 7647: contig of 2542 bp in length
* 7648 7747: gap of unknown length
* 7748 10237: contig of 2490 bp in length
* 10238 10337: gap of unknown length
* 10338 12440: contig of 2103 bp in length
* 12441 12540: gap of unknown length
* 12541 15935: contig of 3395 bp in length
* 15936 16035: gap of unknown length
* 16036 24396: contig of 8361 bp in length
* 24397 24496: gap of unknown length
* 24497 39085: contig of 14589 bp in length
* 39086 39185: gap of unknown length
* 39186 60545: contig of 21360 bp in length
* 60546 60645: gap of unknown length
* 60646 79490: contig of 18845 bp in length
* 79491 79590: gap of unknown length
* 79591 127488: contig of 47898 bp in length.

Location/Qualifiers
1. .127488
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="5"
/clone_lib="CTB-36B8"
/clone="CTB-36B8"
/clone_lib="CalTech human BAC library B"
31643 a 32392 c 31616 g 30626 t 1211 others

QY 1857 tgcattgttccgacacccctctggccgagcagctgagaggtgagccttgggagcgcgc 1916
|||||
Db 114435 TGCACTGTTCGCCACCCCTCTGGCCGCCAGCCTGGAGGAGGTGGACCTGGGCGCGCC 114376
|||||
QY 1917 agccacgctcagcctgagtatcccccccgctgcgcgccccagcacagggccactatgtc 1976
|||||
Db 114375 AGCCACGCTCAGCCTGAGTATCCCCCGCTGCGCGCCAGCAGCAGGAGGCCACTATGTCT 114316
|||||
QY 1977 gcaagtcaagacccgagcagccatgacaagcactgcccacagaagtagtacctgctcgtgc 2036
|||||
Db 114315 GCGAAGTGAAGACCCGCGCAGCCATGACACCACTGCCCAAGAAGTACCTGCTCGGTGC 114256
|||||
QY 2037 agg 2039
|||
Db 114255 AGG 114253
|||

RESULT 12
AC108083
LOCUS
DEFINITION Homo sapiens chromosome 5 clone CTD-2013L15, WORKING DRAFT
AC108083
SEQUENCE, 4 unordered pieces.
ACCESSION AC108083.1 GI:18369929
VERSION AC108083.1
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 130129)
DOE Joint Genome Institute.
Sequencing of Human Chromosome 5
Unpublished
2 (bases 1 to 130129)
DOE Joint Genome Institute.
Direct Submission
Submitted (25-JAN-2002) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
-----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov

Project Information
Center Project Name: 632820
Center clone name: CITB-H1_2013L15

Summary Statistics
Consensus quality: 124488 bases at least Q40
Consensus quality: 128031 bases at least Q30
Consensus quality: 128842 bases at least Q20
Estimated insert size: 135000; agarose-fp estimation
Estimated insert size: 129829; sum-of-contigs estimation
Quality coverage: 7.66 in Q20 bases; agarose-fp estimation
Quality coverage: 7.97 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 4 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 4320: contig of 4320 bp in length
* 4321 4420: gap of unknown length
* 4421 23712: contig of 19292 bp in length
* 23713 23812: gap of unknown length
* 23813 48602: contig of 24790 bp in length
* 48603 48703: gap of unknown length
* 48703 130129: contig of 81427 bp in length.

Location/Qualifiers


```
source 1. .130129
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="5"
/clone="CTD-2013L15"
/clone_lib="CalTech human BAC library D"
BASE COUNT 35337 a 32337 c 30949 g 31146 t 300 others
ORIGIN
-----
Query Match 8.8%; Score 363; DB 2; Length 130129;
Best Local Similarity 100.0%; Pred. No. 4.4e-168;
Matches 363; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1677 ccattcccgacggcttcaccatcgcaatccaaagccatccgaggagctactagagggccagc 1736
|||||
Db 17322 CCATCCCGACGGCTTCACCATCGAATCCAAAGCCATCCGAGGAGCTACTAGAGGCCAGC 17381

Qy 1737 cggctactcttaagctgcaaacccagctacaagtacagcatctgcctgctatccgcc 1796
|||||
Db 17382 CGGTGCTCTCAGCTGGCAAGCCGACAGCTACAAGTAGGAGCATCTGCGCTGGTACC GCC 17441

Qy 1797 tcaacctgtccacgctgcacgatgcgacgggaacccgctctctgctgactgcgaagaacg 1856
|||||
Db 17442 TCACCTGTCCACGCTGCACCATCGCAGCGGAACCCGCTTCTGCTCGACTGCAGAAGC 17501

Qy 1857 tgcattctgtccgcaacccctctgcccgcagcctggaaggagtggaacctgagggcgcgc 1916
|||||
Db 17502 TGCATCTCTTCCGACCCCTCTGGCCGCGACGCTCGAGGAGGTGGACCTGGGCGCGCC 17561

Qy 1917 acgcacactcagctgagtagtccccgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 1976
|||||
Db 17562 ACGCCACGCTCAGCTGAGTATCCCGCCGCTGCGCGCCGACGACGAGCGGCACATATGTGT 17621

Qy 1977 gcaagtgcaagacggcgccgcatgacaaagcactgcacaaagatcacctgctgcgtgc 2036
|||||
Db 17622 CGGAAGTCCAAGACGGCGCGCAGCCATGCAAGCACTGCACAAGAAGTACCTGTGCGTGC 17681

Qy 2037 agg 2039
|||
Db 17682 AGG 17684

RESULT 13
AC106813
LOCUS AC106813 173341 bp DNA linear HTG 25-JAN-2002
DEFINITION Homo sapiens chromosome 5 clone RP11-586L9, WORKING DRAFT SEQUENCE,
7 unordered pieces.
ACCESSION AC106813
VERSION AC106813.2 GI:18369924
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 173341)
AUTHORS DOE Joint Genome Institute.
TITLE Sequencing of Human Chromosome 5
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 173341)
AUTHORS DOE Joint Genome Institute.
TITLE Direct Submission
JOURNAL Submitted (12-JAN-2002) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
COMMENT
-----
On Jan 25, 2002 this sequence version replaced gi:18139363.
Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov
-----
Project Information
Center Project Name: 1519801
Center clone name: RP11-586L9
```

```
-----
Summary Statistics
Consensus quality: 164442 bases at least Q40
Consensus quality: 167261 bases at least Q30
Consensus quality: 167771 bases at least Q20
Estimated insert size: 186250; agarose-fp estimation
Estimated insert size: 172741; sum-of-contigs estimation
Quality coverage: 10.29 in Q20 bases; agarose-fp estimation
Quality coverage: 11.1 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 7 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 1596: contig of 1596 bp in length
* 1597 1696: gap of unknown length
* 1697 3940: contig of 2244 bp in length
* 3940 4040: gap of unknown length
* 4040 5104: contig of 1064 bp in length
* 5104 5204: gap of unknown length
* 5204 6286: contig of 1082 bp in length
* 6286 6387: gap of unknown length
* 6387 20063: contig of 13677 bp in length
* 20063 20163: gap of unknown length
* 20163 82401: contig of 62238 bp in length
* 82401 82502: gap of unknown length
* 82502 173341: contig of 90840 bp in length.
FEATURES
Location/Qualifiers
source 1. .173341
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="5"
/clone="RP11-586L9"
/clone_lib="RP11 human BAC library 11"
BASE COUNT 45837 a 42564 c 41389 g 42871 t 680 others
ORIGIN
```

```
Query Match 8.8%; Score 363; DB 2; Length 173341;
Best Local Similarity 100.0%; Pred. No. 4.2e-168;
Matches 363; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1677 ccattcccgacggcttcaccatcgcaatccaaagccatccgaggagctactagagggccagc 1736
|||||
Db 95297 CCATCCCGACGGCTTCACCATCGAATCCAAAGCCATCCGAGGAGCTACTAGAGGCCAGC 95356

Qy 1737 cggctactctgagctgcaaacccgacagctlacaagtacagcatctgcgtggtaccgcc 1796
|||||
Db 95357 CGGTGCTCTCAGCTGGCAAGCCGACAGCTACAAGTAGGAGCATCTGCGCTGGTACC GCC 95416

Qy 1797 tcaacctgtccacgctgcacgatgcgacgggaacccgctctgctgcacgcaagaacg 1856
|||||
Db 95417 TCAACCTGTCCACGCTGCACGATCGGCACGGGAACCCGCTTCTGCTGCTGCAAGAAGC 95476

Qy 1857 tgcattctgtccgcaacccctctgcccgcagcctggaaggagtggaacctgagggcgcgc 1916
|||||
Db 95477 TGCATCTGTTCGCCACCCCTCTGGCCGCCACGCTTGGAGGAGTGCGACCTGGGCGCGCC 95536

Qy 1917 acgcacgctcagctgagtagtccccgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 1976
|||||
Db 95537 ACGCCACGCTCAGCTGAGTATCCCGCCGCTGCGCGCCGACGACGAGGCGGCACATATGTGT 95596

Qy 1977 gcaagtgcaagacggcgccagcagccatgcaagcactgccacaagaagtacgtgcgtgc 2036
|||||
Db 95597 CGGAAGTCCAAGACGGCGCGCAGCCATGCAAGCACTGCACAAGAAGTACCTGTGCGTGC 95656

Qy 2037 agg 2039
|||
Db 95657 AGG 95659
```


•	42303	42402:	gap of	100 bp
•	42403	47816:	contig of	5414 bp in length
•	47817	47916:	gap of	100 bp
•	47917	52586:	contig of	4670 bp in length
•	52587	52686:	gap of	100 bp
•	52687	56567:	contig of	3881 bp in length
•	56568	56667:	gap of	100 bp
•	56668	61557:	contig of	4890 bp in length
•	61558	61657:	gap of	100 bp
•	61658	66724:	contig of	5067 bp in length
•	66725	66824:	gap of	100 bp
•	66825	71568:	contig of	4744 bp in length
•	71569	71668:	gap of	100 bp
•	71669	76578:	contig of	4910 bp in length
•	76579	76678:	gap of	100 bp
•	76679	83112:	contig of	6634 bp in length
•	83113	83412:	gap of	100 bp
•	83413	90053:	contig of	6641 bp in length
•	90054	90153:	gap of	100 bp
•	90154	99426:	contig of	9273 bp in length
•	99427	99526:	gap of	100 bp
•	99527	108015:	contig of	8489 bp in length
•	108016	108115:	gap of	100 bp
•	108116	118144:	contig of	10029 bp in length
•	118145	118244:	gap of	100 bp
•	118245	130468:	contig of	12224 bp in length
•	130469	130568:	gap of	100 bp
•	130569	142339:	contig of	11671 bp in length
•	142340	142339:	gap of	100 bp
•	142340	157135:	contig of	14796 bp in length
•	157136	157235:	gap of	100 bp
•	157236	168347:	contig of	11112 bp in length.

Db 184 AGACCAGGACTTCTTTTCCAACCCCTTCTGCTGCACATCACAGG 228

RESULT 22
HSA336018 802 bp DNA linear PRI 01-OCT-2001
LOCUS Homo sapiens genomic sequence surrounding NotI site, clone
DEFINITION NL6-DJ118RS.
ACCESSION AJ336018
VERSION AJ336018.1 GI:15880436
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 802)
AUTHORS Kutsenko,A.S., Gizatullin,R.Z., Al-Amin,A.N., Wang,F.,
Podowski,R.M., Matushkin,Y.G., Kvasha,S.M., Gyanchandani,A.,
Muravenko,O.V., Protopopov,A.I., Kashuba,V.I., Kisselev,L.L.,
Wasserman,W., Wahlestedt,C. and Zabarovsky,E.R.
TITLE Analysis of NotI flanking sequences: a new tool for gene discovery
and verification of the human genome
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 802)
AUTHORS Zabarovsky,E.R.
TITLE Direct Submission
JOURNAL Submitted (16-MAY-2001) Microbiology and Tumorbiology Centre,
Karolinska Institute, Theorells vag, 3, Box 280, Stockholm 171 77,
Sweden
FEATURES
source Location/Qualifiers
1..802
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="NL6-DJ118RS"
BASE COUNT 155 a 186 c 260 g 200 t 1 others
ORIGIN

Query Match 4.0%; Score 165; DB 9; Length 802;
Best Local Similarity 100.0%; Pred. No. 7.3e-70;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 532 gcaaaagctcgtgtgctgtgcccagcggcaggagtggtgtggtgacccggggcat 591
|||||
Db 64 GCAAGCTCGTGTGTGGCCACAGCGGCGGAGGTGGTGTGGATGACCGCGGGCAT 123
|||||

QY 592 gctcgtgtccacgccactgctgcacgatgccctgtacctgtacctgcagtcgagaccacctgggg 651
|||||
Db 124 GCTCGTGTCCACGCCACTGCTGCACGATCCCTGTACCTGTACCTGCGAGACCACTGGGG 183
|||||

QY 652 agaccaggacttccttccaaccccttctcctggtgcacatcacagg 696
|||||

Db 184 AGACCAGGACTTCTTTTCCAACCCCTTCTGCTGCACATCACAGG 228

RESULT 23
AC106813 173341 bp DNA linear HTG 25-JAN-2002
LOCUS Homo sapiens chromosome 5 clone RP11-586L9, WORKING DRAFT SEQUENCE,
DEFINITION 7 unordered pieces.
ACCESSION AC106813
VERSION AC106813.2 GI:18369924
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 173341)
AUTHORS DOE Joint Genome Institute.
TITLE Sequencing of Human Chromosome 5
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 173341)
AUTHORS DOE Joint Genome Institute.

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="NRL-SPI8R"
BASE COUNT 126 a 222 c 278 g 149 t 5 others
ORIGIN

Query Match 4.0%; Score 165; DB 9; Length 780;
Best Local Similarity 100.0%; Pred. No. 7.3e-70;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 532 gcaaaagctcgtgtgctgtgcccagcggcaggagtggtgtggtgacccggggcat 591
|||||
Db 64 GCAAGCTCGTGTGTGGCCACAGCGGCGGAGGTGGTGTGGATGACCGCGGGCAT 123
|||||

QY 592 gctcgtgtccacgccactgctgcacgatgccctgtacctgtacctgcagtcgagaccacctgggg 651
|||||
Db 124 GCTCGTGTCCACGCCACTGCTGCACGATCCCTGTACCTGTACCTGCGAGACCACTGGGG 183
|||||

QY 652 agaccaggacttccttccaaccccttctcctggtgcacatcacagg 696
|||||

Db 184 AGACCAGGACTTCTTTTCCAACCCCTTCTGCTGCACATCACAGG 228

RESULT 21
HSA334721 785 bp DNA linear PRI 01-OCT-2001
LOCUS Homo sapiens genomic sequence surrounding NotI site, clone
DEFINITION NL6-BA13RS.
ACCESSION AJ334721
VERSION AJ334721.1 GI:15879139
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 785)
AUTHORS Kutsenko,A.S., Gizatullin,R.Z., Al-Amin,A.N., Wang,F.,
Podowski,R.M., Matushkin,Y.G., Kvasha,S.M., Gyanchandani,A.,
Muravenko,O.V., Protopopov,A.I., Kashuba,V.I., Kisselev,L.L.,
Wasserman,W., Wahlestedt,C. and Zabarovsky,E.R.
TITLE Analysis of NotI flanking sequences: a new tool for gene discovery
and verification of the human genome
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 785)
AUTHORS Zabarovsky,E.R.
TITLE Direct Submission
JOURNAL Submitted (16-MAY-2001) Microbiology and Tumorbiology Centre,
Karolinska Institute, Theorells vag, 3, Box 280, Stockholm 171 77,
Sweden
FEATURES
source Location/Qualifiers
1..785
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="NL6-BA13RS"
BASE COUNT 132 a 207 c 270 g 174 t 2 others
ORIGIN

Query Match 4.0%; Score 165; DB 9; Length 785;
Best Local Similarity 100.0%; Pred. No. 7.3e-70;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 532 gcaaaagctcgtgtgctgtgcccagcggcaggagtggtgtggtgacccggggcat 591
|||||
Db 64 GCAAGCTCGTGTGTGGCCACAGCGGCGGAGGTGGTGTGGATGACCGCGGGCAT 123
|||||

QY 592 gctcgtgtccacgccactgctgcacgatgccctgtacctgtacctgcagtcgagaccacctgggg 651
|||||
Db 124 GCTCGTGTCCACGCCACTGCTGCACGATCCCTGTACCTGTACCTGCGAGACCACTGGGG 183
|||||

QY 652 agaccaggacttccttccaaccccttctcctggtgcacatcacagg 696
|||||

TITLE
JOURNAL
COMMENT

Direct Submission
Submitted (12-JAN-2002) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
On Jan 25, 2002 this sequence version replaced gi:18139363.
-----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov

Project Information
Center Project Name: 1519801
Center clone name: RPC1-11_586L9

Summary Statistics
Consensus quality: 164442 bases at least Q40
Consensus quality: 167261 bases at least Q30
Consensus quality: 167771 bases at least Q20
Estimated insert size: 186250; agarose-fp estimation
Quality coverage: 10.29 in Q20 bases; agarose-fp estimation
Quality coverage: 11.1 in Q20 bases; sum-of-contigs estimation
* NOTE: This is a 'working draft' sequence. It currently
* consists of 7 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence.
* as soon as it is available and the accession number will
* be preserved.

1 1596: contig of 1596 bp in length
* 1597 1696: gap of unknown length
* 1697 3940: contig of 2244 bp in length
* 3941 4040: gap of unknown length
* 4041 5104: contig of 1064 bp in length
* 5105 5204: gap of unknown length
* 5205 6286: contig of 1082 bp in length
* 6287 6386: gap of unknown length
* 6387 20063: contig of 13677 bp in length
* 20064 20163: gap of unknown length
* 20164 82401: contig of 62238 bp in length
* 82402 82501: gap of unknown length
* 82502 173341: contig of 90840 bp in length.
Location/Qualifiers

FEATURES
source

1. .173341
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="5"
/clone_lib="RPC1 human BAC library 11"
45837 a 42564 c 41389 g 42871 t 680 others

Query Match 3.7%; Score 151; DB 2; Length 173341;
Best Local Similarity 100.0%; Pred. No. 2.8e-63;
Matches 151; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3557 gaggaagaggaggtctgctgagcccgccgagctctcagagctcagaagagggcagcttc 3616
|||||
Db 5613 GAGGAAGAGGAGGTCTGCATCGGCCCGCCGAGCTCTCAGAGCTCAGAAGAGGGCAGCTTC 5554
|||||
Qy 3617 tcgcaggtgtccaccatggccctacacatcgcccgagctgacgctgaggaagccgacca 3676
|||||
Db 5553 TCGCAGGTGTCCACCATGGCCCTACACATGCCACAGCTGACGCTGAGGACAGCCGCCCA 5494
|||||
Qy 3677 agcttcagagccacagcctggccgcaggt 3707
|||||
Db 5493 AGCCTGCAGGCCACAGCCTGGCCGCCAAGCT 5463
|||||

RESULT 24
144509
LOCUS 144509 160 bp DNA linear PAT 07-OCT-1997

DEFINITION Sequence 5 from patent US 5635177.
ACCESSION 144509
VERSION 144509.1 GI:2469222
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
UNCLASSIFIED.

REFERENCE 1 (bases 1 to 160)
AUTHORS Bennett,B.D., Goeddel,D. and Matthews,W.
TITLE Protein tyrosine kinase agonist antibodies
JOURNAL Patent: US 5635177-A 5 03-JUN-1997;
FEATURES Location/Qualifiers
1..160
source

BASE COUNT 35 a 44 c 47 g 34 t
ORIGIN

Query Match 1.8%; Score 76; DB 6; Length 160;
Best Local Similarity 100.0%; Pred. No. 9.3e-26;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3141 ggaacattctgctgcggaagcagcgtggtgaagatctgtgacttggccttgcccggg 3200
|||||
Db 30 GGAACATTCTGCTGCGGAAGCGACGTGCTGAAGATCTGTGACTTTGCCCTTGCCCGGG 89
|||||

Qy 3201 acatctacaaagacc 3216
|||||
Db 90 ACATCTACAAAGACCC 105
|||||

RESULT 25

LOCUS AR016570 70 bp DNA linear PAT 05-DEC-1998
DEFINITION Sequence 7 from patent US 5776755.
ACCESSION AR016570
VERSION AR016570.1 GI:3972847
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
UNCLASSIFIED.

REFERENCE 1 (bases 1 to 70)
AUTHORS Alitalo,K., Aprelikova,O., Pajusola,K., Armstrong,E., Korhonen,J.
and Kaipainen,A.
TITLE FLT4, a receptor tyrosine kinase
JOURNAL Patent: US 5776755-A 7 07-JUL-1998;
FEATURES Location/Qualifiers
1..70
source

BASE COUNT 9 a 24 c 24 g 13 t
ORIGIN

Query Match 1.4%; Score 56; DB 6; Length 70;
Best Local Similarity 100.0%; Pred. No. 8.1e-16;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 20 atgcagcggggcgccgctgtgcctgcgactgtgctctgctgaggaactcctgga 75
|||||
Db 15 ATGCAGCGGGCGCCGCTGTGCTGCGACTGTGCTGCGACTTGGGACTCCTTGA 70
|||||

RESULT 26

LOCUS AR106407 70 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 7 from patent US 6107046.
ACCESSION AR106407
VERSION AR106407.1 GI:12820937
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
UNCLASSIFIED.

REFERENCE 1 (bases 1 to 70)

AUTHORS Alitalo,K., Aprelikova,O., Pajusola,O., Armstrong,E., Korhonen,J.,
Kaipainen,A. and Matikainen,M.
TITLE Antibodies to Flc4, a receptor tyrosine kinase and uses thereof
JOURNAL Patent: US 6107046-A 7 22-AUG-2000;
FEATURES Location/Qualifiers

source 1. .70
BASE COUNT 9 a 24 c 24 g 13 t
ORIGIN

Query Match 1.4%; Score 56; DB 6; Length 70;
Best Local Similarity 100.0%; Pred. No. 8.1e-16;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 20 atgcagcggggcgccgctgtgcctgcgactgtgctgctggactcctctgga 75
|||||
Db 15 ATGCACGGGGCGCGCGCTGTGCCTGCGACTGTGCTGTGCTGGACTCCTGGA 70

RESULT 27
ARI57562
LOCUS ARI57562 70 bp DNA linear PAT 17-OCT-2001
DEFINITION Sequence 2 from patent US 6245530.
ACCESSION ARI57562
VERSION ARI57562.1 GI:16218511
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 70)
TITLE Alitalo,K. and Joukov,V.
JOURNAL Receptor ligand
Patent: US 6245530-A 2 12-JUN-2001;
FEATURES Location/Qualifiers

source 1. .70
BASE COUNT 9 a 24 c 24 g 13 t
ORIGIN

Query Match 1.4%; Score 56; DB 6; Length 70;
Best Local Similarity 100.0%; Pred. No. 8.1e-16;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 20 atgcagcggggcgccgctgtgcctgcgactgtgctgctggactcctctgga 75
|||||
Db 15 ATGCACGGGGCGCGCGCTGTGCCTGCGACTGTGCTGTGCTGGACTCCTGGA 70

RESULT 28
HSA329585/c
LOCUS HSA329585 688 bp DNA linear PRI 01-OCT-2001
DEFINITION Homo sapiens genomic sequence surrounding NotI site, clone
NRI-SPI8C.
ACCESSION ARI57562
VERSION ARI57562.1 GI:15874003
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS 1 (bases 1 to 688)
Kutsenko,A.S., Gizatullin,R.Z., Al-Amin,A.N., Wang,F.,
Podowski,R.M., Matushkin,Y.G., Kvasha,S.M., Gyanchandani,A.,
Muravenko,O.V., Protolopov,A.I., Kashuba,V.I., Kisselev,L.L.,
Wasserman,W., Wahlested,C. and Zabarovsky,E.R.
TITLE Analysis of NotI flanking sequences: a new tool for gene discovery
and verification of the human genome

JOURNAL Unpublished
AUTHORS 2 (bases 1 to 688)
Zabarovsky,E.R.
TITLE Direct Submission

JOURNAL Submitted (16-MAY-2001) Microbiology and Tumorbiology Centre,
Karolinska Institute, Theorells vag, 3, Box 280, Stockholm 171 77,
Sweden

FEATURES Location/Qualifiers
source 1. .688
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="NRI-SPI8C"

BASE COUNT 116 a 206 c 226 g 140 t
ORIGIN

Query Match 1.3%; Score 55; DB 9; Length 688;
Best Local Similarity 100.0%; Pred. No. 1.8e-15;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 418 agacttgagcagccattcatcaacagccctgacacgcctcttggtcaacaggaag 472
|||||
Db 178 AGACTTTCAGCAGCCATTTCATCAACAGCCTGCACACGCTCTTGGTCAACAGGAAG 124

RESULT 29
AF402786
LOCUS AF402786 4254 bp mRNA linear ROD 11-OCT-2001
DEFINITION Rattus norvegicus receptor tyrosine kinase VEGFR-3kt (Vegfr3) mRNA,
complete cds, alternatively spliced.
ACCESSION AF402786
VERSION AF402786.1 GI:16033529
KEYWORDS
SOURCE Norway rat.
ORGANISM Rattus norvegicus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
AUTHORS 1 (bases 1 to 4254)
Krishnan,J. and Sleeman,J.P.
TITLE Characterization of a novel alternatively spliced form of VEGFR-3
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 4254)
Krishnan,J. and Sleeman,J.P.
AUTHORS Direct Submission
TITLE
JOURNAL Submitted (25-JUL-2001) Institut fuer Toxikologie und Genetik,
Forschungszentrum Karlsruhe, Postfach 3640, Karlsruhe 76021,
Germany

FEATURES Location/Qualifiers
source 1. 4254
/organism="Rattus norvegicus"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
1. 4254
/gene="Vegfr3"
1. 3279
/gene="Vegfr3"
/note="kinase domain truncated form of VEGFR-3;
alternatively spliced"
/codon_start=1
/product="receptor tyrosine kinase VEGFR-3kt"
/protein_id="AAJ13270.1"
/db_xref="GI:16033530"

/translation="MQPCALNRRLWLCGLLQGLANGYNTPTTLNITDSYVIDTG
DSUSISCRGQPLEWTRGAEVLTTCGKDEDTQVVDCEGTPEAPYCKVLSLAOTV
ANNTGYCYKYIKARIEGTAASTYFVFRDEQFPINRPTLLVNRKDSMWVPCLV
SIPGLNLTSSQSVLHPDGEVLWDDRRGMVPTLLRLDALYLQCTETGDDDFLSN
PFLVHTGNELYDIOLYPKSLELLVGEKLVNCTVWAEFDSGVTGPDMDYPGQAERA
KWPERRSQOHTLSLILTHNVSHQDLGPYCEANNGLOQPRESTEVLVHEKPFIS
VELWKGPVLEATAGDEMVKLPVLAATPPPEFQYKORRKAATGRHNHALVLKEVTEA
SAGUYTLANSAAGLRQNLISLELVNVPPIHEKEASSPSIYSRHSRQTLCTCYGV
PQPLSVQWHRPMTPKCTFAQSLRRRQPGMPCQCRMKETVTQDAVNIIESLDWT
ESVGEKNTVSKLVIODANYKAMYKCVFNKQODERLIYFYVTTIPDGFSEISEPSE
DPLEGQSVRLSCRADNPTYEHLRWYRLNLTLDHDAQGNPLLLDCKNVHLFATPLEANL
EEAEPGARHTLSLNIPRAPEDEGDYVCEVQDRRSQDKHCKHLYSQVALEAPRLTQ
NLTDLLVNRVTSLEMRCPAGAHVPSIWTYKDKERLLEKESGIDLDASNRLSQRVRE
EDAGRYLCSVCNKAQCVNSASVAVEGSEDKGSMEIILITGTGVIATVFFWVLLLLIFC

NMKRAHADIKTGYSLIIMDPCEVPLEEOCEYLSYDVSWQEFPRERHLGRVLHGCAF
GKVEASAFGINKGSSCDTAVVVKMLKEGATSEHRAHMSSELKILIHGNHNVNLLG
ACTKPNGLMWIVFECKYGNLSNFRVARETFDPAEKSPQRRRFRAMVEGAKADRR
RUGSDRALFTFLMGKSARRAPFVQAEADLWLSPLTMEDLVCYSFOVARGMEFLAS
RKCIRHDLAARNILLESIDIVKICDFGLARDIYKDPDYVRKGSARLPLKWMAPESIED
KVTYQSDVSWFSGVLLMEIFSLGASYPGVQINEEFQORLKGDMRAPELATPAIRH
IMQSGDQPKARPAFSDLVEILAGLLQGGGWQEEBECMALHSSQSEEDGFMQAST
TALHITTEADAESSPPSMHCHSLAARYNCVSPGRLVRGTKAPGSSRMKTFPEELPMP
TTRYKASVDNQTDSGMVLASEFEQIESRHHROEGSFSRKDPQHMDISRGHPDLQGRRR
RPTOGAAGGKVFYNNVEYVQPCTEGDCFCPSAGSTTFADSNY*

BASE COUNT 989 a 1236 c 1224 g 805 t
ORIGIN

Query Match 1.3%; Score 54; DB 10; Length 4254;
Best Local Similarity 100.0%; Pred. No. 4.4e-15;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2435 gcagacatcaagcggctacctgtccatcatcatgagccggagagtgctt 2488
|||||
Db 2416 GCAGACATCAAGCGGCTACCTGTCCATCATCATGACCCGGGAGGTGCT 2469

RESULT 30
AF402785
LOCUS AF402785 4360 bp mRNA linear ROD 11-OCT-2001
DEFINITION Rattus norvegicus receptor tyrosine kinase VEGFR-3 (Vegfr3) mRNA,
complete cds, alternatively spliced.
ACCESSION AF402785
VERSION 2
KEYWORDS AF402785.1 GI:16033526
SOURCE Norway rat.
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

REFERENCE 1 (bases 1 to 4360)
AUTHORS Krishnan,J. and Sleeman,J.P.
TITLE Characterization of a novel alternatively spliced form of VEGFR-3
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 4360)
AUTHORS Krishnan,J. and Sleeman,J.P.
TITLE Direct Submission
JOURNAL Submitted (25-JUL-2001) Institut fuer Toxikologie und Genetik,
Forschungszentrum Karlsruhe, Postfach 3640, Karlsruhe 76021,
Germany

FEATURES
source Location/Qualifiers
1. .4360
/organism="Rattus norvegicus"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
1. .4360
/gene="Vegfr3"
1. .4092
/gene="Vegfr3"
/note="VEGFR-3 long form; activated by VEGF-C and VEGF-D;
alternatively spliced"
/codon_start=1
/product="receptor tyrosine kinase VEGFR-3"
/protein_id="AAL13269.1"
/db_xref="GI:16033527"

/translation="MQPAAALNRRLWLCGLGLOGLANGYSMTPTPLNITEDSVYIDTG
DLSISCRGHQPLEMTWGAQEVLTGKSEDQVQDCEGTAEARPYCKVLSLAQTH
ANNTGYSYCYIYKARIEGTTAASTYVVRDFEQFP INKPTDLLVNRKDSMMWPCLV
SIPGLNITLRSSSVLHPDQGVLDWDRGRMRVPTLLRLDALYLCQCTTWGDDQLSN
PFLVGTITNELYDIOLYPKLSLELLVGEKLVNCTVMAEFDGVTFDWDYPCQKQERA
KWPPRRSQQTHTESSILT INHVSQHDLPYVCEANNQIOQFRESTEIVHEKPFIS
VWMLKGPVLEATAGDEMVKLPVLAAYPPPEFYWKDRKATGRNHPHALVLEKVEFA
SAGVYTLALNWSAAGLRQNLISLELVNVPPIHKEASSPSIYSRHSQTLTCTTGV
POPLSVQHWHPWTCKTFAQSLRRQPRDGMQPCQDKMEKVTQDAVNPTESDLTWT
ESVEGKNTKYSVLQIDANVSAMKYCVNFKVGQDERLIYFVTT IPDGFISIESEP
DEAPECARHATLSLNI PRVAPEDGTYCEVQDRSDKHCHKYLVSQALEAPRLTO
NLTDLLNVNRTSLEMRCPVAGAHVPSIYVKDERLLEKESGIDLDSNORLSIORVE
ENAGRYLCSVNAKGVSNSSAVVEGSEDKGSMIEVILIGTVIAVFWVLLLIIFC
NMKRAHADIKTGYSLIIMDPCEVPLEEOCEYLSYDVSWQEFPRERHLGRVLHGCAF
GKVEASAFGINKGSSCDTAVVVKMLKEGATSEHRAHMSSELKILIHGNHNVNLLG

ACTKPNGLMWIVFECKYGNLSNFRVARETFDPAEKSPQRRRFRAMVEGAKADRR
RUGSDRALFTFLMGKSARRAPFVQAEADLWLSPLTMEDLVCYSFOVARGMEFLAS
RKCIRHDLAARNILLESIDIVKICDFGLARDIYKDPDYVRKGSARLPLKWMAPESIED
KVTYQSDVSWFSGVLLMEIFSLGASYPGVQINEEFQORLKGDMRAPELATPAIRH
IMQSGDQPKARPAFSDLVEILAGLLQGGGWQEEBECMALHSSQSEEDGFMQAST
TALHITTEADAESSPPSMHCHSLAARYNCVSPGRLVRGTKAPGSSRMKTFPEELPMP
TTRYKASVDNQTDSGMVLASEFEQIESRHHROEGSFSRKDPQHMDISRGHPDLQGRRR
RPTOGAAGGKVFYNNVEYVQPCTEGDCFCPSAGSTTFADSNY*

BASE COUNT 1008 a 1260 c 1259 g 833 t
ORIGIN

Query Match 1.3%; Score 54; DB 10; Length 4360;
Best Local Similarity 100.0%; Pred. No. 4.4e-15;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2435 gcagacatcaagcggctacctgtccatcatcatgagccggagagtgctt 2488
|||||
Db 2416 GCAGACATCAAGCGGCTACCTGTCCATCATCATGACCCGGGAGGTGCT 2469

RESULT 31
MUSRTKA
LOCUS MUSRTKA 5284 bp mRNA linear ROD 09-AUG-1993
DEFINITION Mus musculus receptor tyrosine kinase (PLT4) mRNA, complete cds.
ACCESSION L07296
VERSION L07296.1 GI:293780
KEYWORDS receptor protein tyrosine kinase.
SOURCE Mus musculus (strain C57BL/6J, sub_species domesticus) cDNA to
mRNA.

ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 5284)
AUTHORS Finnerty,H., Kelleher,K., Morris,G.E., Bean,K., Merberg,D.M.,
Kriz,R., Morris,J.C., Sookdeo,H., Turner,K.J. and Wood,C.R.
TITLE Molecular cloning of murine FLT and FLT4
JOURNAL Oncogene 8, 2293-2298 (1993)
MEDLINE 93330572
FEATURES Location/Qualifiers

1. .5284
/organism="Mus musculus"
/strain="C57BL/6J"
/sub_species="domesticus"
/db_xref="taxon:10090"
1. .5284
/gene="FLT4"
45. .4136
/gene="FLT4"
/note="putative"
/codon_start=1
/product="receptor tyrosine kinase"
/protein_id="AAA40077.1"
/db_xref="GI:293781"

/translation="MQPAAALNRRLWLCGLGLOGLANGYSMTPTPLNITEDSVYIDTG
DLSISCRGHQPLEMTWGAQEVLTGKSEDQVQDCEGTAEARPYCKVLSLAQTH
ANNTGYSYCYIYKARIEGTTAASTYVVRDFKHPT INKPTDLLVNRKDSMMWPCLV
SIPGLNITLRSSSVLHPDQGVLDWDRGRMRVPTLLRLDALYLCQCTTWGDDQLSN
PFLVGTITNELYDIOLYPKLSLELLVGEKLVNCTVMAEFDGVTFDWDYPCQKQERA
KWPPRRSQQTHTESSILT INHVSQHDLPYVCEANNQIOQFRESTEIVHEKPFIS
VWMLKGPVLEATAGDEMVKLPVLAAYPPPEFYWKDRKATGRNHPHALVLEKVEFA
SAGVYTLALNWSAAGLRQNLISLELVNVPPIHKEASSPSIYSRHSQTLTCTTGV
POPLSVQHWHPWTCKTFAQSLRRQPRDGMQPCQDKMEKVTQDAVNPTESDLTWT
ESVEGKNTKYSVLQIDANVSAMKYCVNFKVGQDERLIYFVTT IPDGFISIESEP
DEAPECARHATLSLNI PRVAPEDGTYCEVQDRSDKHCHKYLVSQALEAPRLTO
NLTDLLNVNRTSLEMRCPVAGAHVPSIYVKDERLLEKESGIDLDSNORLSIORVE
ENAGRYLCSVNAKGVSNSSAVVEGSEDKGSMIEVILIGTVIAVFWVLLLIIFC
NMKRAHADIKTGYSLIIMDPCEVPLEEOCEYLSYDVSWQEFPRERHLGRVLHGCAF
GKVEASAFGINKGSSCDTAVVVKMLKEGATSEHRAHMSSELKILIHGNHNVNLLG
ACTKPNGLMWIVFECKYGNLSNFRVARETFDPAEKSPQRRRFRAMVEGAKADRR
RUGSDRALFTFLMGKSARRAPFVQAEADLWLSPLTMEDLVCYSFOVARGMEFLAS
RKCIRHDLAARNILLESIDIVKICDFGLARDIYKDPDYVRKGSARLPLKWMAPESIED

KVYTTQSDVMSFGVLLWFISLGSASPVGQVINEEFQORLKDGTMRAPELATPATRH
IMQSCWSDPKARPAFSDLVILGLDGGGMOEERFERMALHSSOSSEEDGMOAST
TALHITADADDSPSMCHUSLAARYNCVFCRLARGCTKTCOSSRKKTFEELPWP
TTYKASNDSDSNVLAIEFEELSRHPEGSFCKGPGQHMDIPRGHPDPQGRRR
RPTQAGOGKVFYNNYGEVSPQCTGDCGCPGAGTFFADSSY"
BASE COUNT 1221 a 1533 c 1466 g 1064 t
ORIGIN

Query Match 1.3%; Score 54; DB 10; Length 5284;
Best Local Similarity 100.0%; Pred. No. 4.3e-15;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2435 gcagacatcaagcggctactctccatcatcgagcccgaggagtgctc 2488
|||||
DB 2460 GCAGACATCAAGCGGCTACCTGTCATCATCGAGCCCGGAGGCTGCT 2513

RESULT 32
AC098957/c
LOCUS
DEFINITION AC098957 161580 bp DNA linear HTG 20-DEC-2001
*** 75 unordered pieces.
AC098957 AC098957.2 Gi:17973745
HTG: HTGS_PHASE1.
SOURCE Norway rat.
ORGANISM Rattus norvegicus
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

REFERENCE 1 (bases 1 to 161580)
AUTHORS Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,
Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Banks,T., Barbarella,J.,
Benton,J., Bimage,K., Blankenburg,K., Bonnin,D., Bouck,J.,
Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P., Buhay,C.,
Burch,P., Burket,C., Burrell,K.L., Byrd,N.C., Carron,T.F.,
Carter,M., Cavazos,S.R., Chacko,J., Chavez,D., Chen,G., Chen,R.,
Chen,Z., Chowdhry,I., Christopoulos,C., Cleveland,C.D., Cox,C.,
Coyle,M.D., Dathorne,S.R., David,R., Davila,M.L., Davis,C.,
Davy-Carroll,L., Dederich,D.A., Delaney,K.R., Delgado,O.,
Denn,A.L., Ding,Y., Dinh,H.H., Douthwaite,K.J., Draper,H.,
Dugan-Rocha,S., Durbin,K.J., Earnhart,C., Edgar,D., Edwards,C.C.,
Elhaj,C., Escotto,M., Falls,T., Ferraguto,D., Flagg,N., Ford,J.,
Foster,P., Fontz,P., Gabisi,A., Gao,J., Garcia,A., Garner,T.,
Garza,N., Gill,R., Gorrell,J.H., Guevara,M., Gunaratne,P., Hale,S.,
Hamilton,K., Harris,C., Harris,K., Hart,M., Havlak,P., Hawes,A.,
Hernandez,J., Hernandez,O., Hodgson,A., Hoques,M., Holloway,C.,
Hollins,B., Homs,F., Howard,S., Huber,J., Hulyk,S., Hume,J.,
Jackson,L.E., Jacobson,B., Jia,Y., Johnson,R., Jolivet,S.,
Joudah,S., Karlsson,E., Kelly,S., Khan,U., King,L., Korvah,J.,
Kovar,C., Kratovic,J., Kureshi,A., Landry,N., Leal,B., Lewis,L.C.,
Lewis,L., Li,J., Li,Z., Lichtarge,O., Lieu,C., Liu,J., Liu,W.,
Louisged,H., Lozaro,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R.,
Ma,J., Maheshwari,M., Mapua,P., Martin,R., Martindale,A.,
Martinez,E., Massey,E., Mawhney,E., McLeod,M.P., Meador,M.,
Mel,G., Metzker,M., Miner,G., Miner,Z., Mitchell,T., Mohabbat,K.,
Morgan,M., Morris,S., Moser,M., Neal,D., Newton,J., Newton,N.,
Nguyen,A., Nguyen,N., Nguyen,M., Nickerson,E., Nwokkwo,S.,
Ogih,M., Okwuon,G., Oragunye,N., Oviedo,R., Pace,A., Payton,B.,
Peury,J., Perez,L., Peters,L., Pickens,R., Primus,E., Pu,L.L.,
Quiles,M., Ren,Y., Rives,M., Rojas,A., Rojibokan,I., Rolfe,M.,
Ruiz,S., Savary,G., Scherer,S., Scott,G., Shen,H., Shoohtari,N.,
Sisson,I., Sodergren,E., Sonaike,T., Sparks,A., Stanley,H.,
Stone,H., Sutton,A., Svatek,A., Tabor,P., Tamerisa,A., Tamerisa,K.,
Tang,H., Tansey,J., Taylor,C., Taylor,T., Telford,B., Thomas,N.,
Thomas,S., Usmani,K., Vasquez,L., Vera,V., Villalón,D., Vinson,R.,
Wall,R., Wang,S., Ward-Moore,S., Warren,R., Washington,C.,
Watlington,S., Williams,G., Williamson,A., Wleczyk,R., Wooden,S.,
Worley,K., Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D.,
Weinstock,G. and Gibbs,R.
Direct Submission
Unpublished

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

2 (bases 1 to 161580)
Worley,K.C.
Direct Submission
Submitted (07-NOV-2001) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Dec 20, 2001 this sequence version replaced gi:16756151.
----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: G1JR
Center clone name: CH230-193G14
----- Summary Statistics
Assembly program: Phrap; version 0.990329First call to
findPhrapList
Consensus quality: 121539 bases at least Q40
Consensus quality: 129496 bases at least Q30
Consensus quality: 136265 bases at least Q20
Estimated insert size: 111412; sum-of-contigs estimation
Quality coverage: 0x in Q20 bases; agarose-gel estimation
Quality coverage: 1.5x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 75 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 5831: contig of 5831 bp in length
* 5832: gap of unknown length
* 5932: contig of 5453 bp in length
* 11384: gap of unknown length
* 11485: contig of 5411 bp in length
* 16895: gap of unknown length
* 16896: contig of 4789 bp in length
* 16956: gap of unknown length
* 21785: contig of 3470 bp in length
* 21885: gap of unknown length
* 25355: gap of unknown length
* 25455: contig of 4006 bp in length
* 29461: gap of unknown length
* 29560: contig of 2747 bp in length
* 29581: gap of unknown length
* 32308: contig of 2936 bp in length
* 32407: gap of unknown length
* 32408: contig of 2773 bp in length
* 35344: gap of unknown length
* 38217: gap of unknown length
* 38317: contig of 2867 bp in length
* 41184: gap of unknown length
* 41284: contig of 2676 bp in length
* 43959: gap of unknown length
* 44059: contig of 3226 bp in length
* 47285: gap of unknown length
* 47385: contig of 3154 bp in length
* 50539: gap of unknown length
* 50639: contig of 3637 bp in length
* 50640: gap of unknown length
* 54277: contig of 3544 bp in length
* 54737: gap of unknown length
* 57920: contig of 2485 bp in length
* 58021: gap of unknown length
* 60505: contig of 2295 bp in length
* 60605: gap of unknown length
* 62900: contig of 1914 bp in length
* 63001: gap of unknown length
* 64915: contig of 2519 bp in length
* 65014: gap of unknown length
* 67633: contig of 5831 bp in length
* 67634: gap of unknown length

* 67634 70777: contig of 3144 bp in length
* 70778 70777: gap of unknown length
* 70878 73509: contig of 2632 bp in length
* 73510 73609: gap of unknown length
* 73610 76056: contig of 2447 bp in length
* 76057 76156: gap of unknown length
* 76157 78450: contig of 2294 bp in length
* 78451 78550: gap of unknown length
* 78551 80050: contig of 1500 bp in length
* 80051 80150: gap of unknown length
* 80151 82169: contig of 2019 bp in length
* 82170 82269: gap of unknown length
* 82270 83776: contig of 1507 bp in length
* 83777 83876: gap of unknown length
* 83877 85747: contig of 1871 bp in length
* 85748 85847: gap of unknown length
* 85848 87906: contig of 1959 bp in length
* 87907 87906: gap of unknown length
* 87907 89679: contig of 1773 bp in length
* 89680 89779: gap of unknown length
* 89780 91266: contig of 1487 bp in length
* 91267 91366: gap of unknown length
* 91367 93812: contig of 2446 bp in length
* 93813 93912: gap of unknown length
* 93913 95639: contig of 1727 bp in length
* 95640 95739: gap of unknown length
* 95740 97396: contig of 1657 bp in length
* 97397 97496: gap of unknown length
* 97497 99145: contig of 1649 bp in length
* 99146 99245: gap of unknown length
* 99246 100913: contig of 1668 bp in length
* 100914 101013: gap of unknown length
* 101014 102955: contig of 1942 bp in length
* 102956 103055: gap of unknown length
* 103056 104468: contig of 1413 bp in length
* 104469 104568: gap of unknown length
* 104569 106375: contig of 1807 bp in length
* 106376 106475: gap of unknown length
* 106476 108591: contig of 2216 bp in length
* 108592 108791: gap of unknown length
* 108792 110626: contig of 1835 bp in length
* 110627 110726: gap of unknown length
* 110727 111801: contig of 1075 bp in length
* 111802 111901: gap of unknown length
* 111902 113358: contig of 1457 bp in length
* 113359 113458: gap of unknown length
* 113459 114629: contig of 1171 bp in length
* 114630 114729: gap of unknown length
* 114730 116364: contig of 1635 bp in length
* 116365 116464: gap of unknown length
* 116465 118200: contig of 1736 bp in length
* 118201 118300: gap of unknown length
* 118301 119530: contig of 1230 bp in length
* 119531 119630: gap of unknown length
* 119631 121318: contig of 1688 bp in length
* 121319 121418: gap of unknown length
* 121419 122620: contig of 1202 bp in length
* 122621 122720: gap of unknown length
* 122721 124128: contig of 1408 bp in length
* 124129 124228: gap of unknown length
* 124229 126159: contig of 1931 bp in length
* 126160 126259: gap of unknown length
* 126260 128394: contig of 2135 bp in length
* 128395 128494: gap of unknown length
* 128495 130496: contig of 2002 bp in length
* 130497 130596: gap of unknown length
* 130597 132111: contig of 1515 bp in length
* 132112 132211: gap of unknown length
* 132212 133294: contig of 1083 bp in length
* 133295 133394: gap of unknown length
* 133395 134851: contig of 1457 bp in length
* 134852 134951: gap of unknown length
* 134952 136002: contig of 1051 bp in length

* 136003 136102: gap of unknown length

Query Match 1.3% Score 54: DB 2: Length 161580;
Best Local Similarity 100.0%; Pred. No. 2.6e-15;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2435 gcagacatcaagcggctacctgtccatcatcatcgaccgccggagggtgcct 2488
|||||
Db 28372 GCAGACATCAAGCGGCTACCTGTCCATCATCATGACCCCGGAGGTGCTT 28319
|||||

RESULT 33
AL646088
LOCUS 260266 bp DNA linear HTG 30-JAN-2002
DEFINITION Mus musculus chromosome 11 clone RP23-58E13, *** SEQUENCING IN
PROGRESS ***, in unordered pieces.
ACCESSION AL646088
VERSION AL646088.11 GI:18476932
KEYWORDS HTG; HTGS_PHASE1; HTGS_ACTIVEFIN; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (sites)
REFERENCE
AUTHORS Clark,S.
TITLE Direct Submission
JOURNAL Submitted (28-JAN-2002) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Feb 1, 2002 this sequence version replaced gi:18151535.
COMMENT
----- Genome Center
Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
----- Project Information
Center project name: BM58E13
----- Summary Statistics
Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid; L08752; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality: 258539 bases at least Q40
Consensus quality: 258926 bases at least Q30
Consensus quality: 259227 bases at least Q20
Insert size: 259766; sum-of-contigs
Insert size: 225486; 6.3% error; agarose-fp
Quality coverage: 9.68x in Q20 bases; sum-of-contigs Quality
coverage: 11.43x in Q20 bases; agarose-fp

* NOTE: This is a 'working draft' sequence.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

FEATURES
Location/Qualifiers
1. 260266
/organism="Mus musculus"
/db_xref="taxon:10090"
/chromosome="11"
/clone="RP23-58E13"
/clone_lib="RPC1-23"
1. 8902
/note="assembly_fragment:05530
fragment_chain:1"
9003. 87162
/note="assembly_fragment:05707
fragment_chain:1"
87263. 123670
/note="assembly_fragment:05852
fragment_chain:1"
123771. 188404
/note="assembly_fragment:00429"
188505. 214152
/note="assembly_fragment:05868"

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misc_feature 214253..260266
/note="assembly_fragment:05872"
BASE COUNT 80139 a 55470 c 56089 g 68066 t 502 others
ORIGIN

Query Match
Best Local Similarity 1.3%; Score 54; DB 2; Length 260266;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2435 gcagacatcaagacgggtacctgtccatcatcatcgagcccgaggagttuett 2488
|||||
Db 161514 GCAGACATCAAGACGGGTACCTGTCCTCATCATCGAGCCCGGGAGGTGCTT 161567

RESULT 34
AC022095 127488 bp DNA linear HTG 20-APR-2001
LOCUS Homo sapiens chromosome 5 clone CTB-36B8, WORKING DRAFT SEQUENCE,
DEFINITION 13 unordered pieces.
ACCESSION AC022095
VERSION HTG: HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 127488)
AUTHORS DOE Joint Genome Institute.
TITLE Sequencing of Human Chromosome 5
JOURNAL Unpublished
AUTHORS DOE Joint Genome Institute.
TITLE Direct Submission
JOURNAL Submitted (26-JAN-2000) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
COMMENT On Apr 20, 2001 this sequence version replaced gi:7711676.
-----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov
-----
Project Information
Center Project Name: 78060
Center clone name: CIT978SKB_36B8
-----
Summary Statistics
Consensus quality: 110477 bases at least Q40
Consensus quality: 117221 bases at least Q30
Consensus quality: 120225 bases at least Q20
Estimated insert size: 131000; pulse field gel estimation
Estimated insert size: 126288; sum-of-contigs estimation
Quality coverage: 7.48 in Q20 bases; pulse field gel estimation
Quality coverage: 7.76 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 13 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 1116: contig of 1116 bp in length
* 1117 1216: gap of unknown length
* 1217 2254: contig of 1038 bp in length
* 2255 2354: gap of unknown length
* 2355 3412: contig of 1058 bp in length
* 3413 3512: gap of unknown length
* 3513 5005: contig of 1493 bp in length
* 5006 5105: gap of unknown length
* 5106 7647: contig of 2542 bp in length
* 7648 7748 10237: contig of 2490 bp in length
```

```
* 10238 10337: gap of unknown length
* 10338 12440: contig of 2103 bp in length
* 12441 12540: gap of unknown length
* 12541 15935: contig of 3395 bp in length
* 15936 16035: gap of unknown length
* 16036 24396: contig of 8361 bp in length
* 24397 24496: gap of unknown length
* 24497 39085: contig of 14589 bp in length
* 39086 39185: gap of unknown length
* 39186 60545: contig of 21360 bp in length
* 60546 60645: gap of unknown length
* 60646 79490: contig of 18845 bp in length
* 79491 79591: gap of unknown length
* 79591 127488: contig of 47898 bp in length.
FEATURES
Location/Qualifiers
source 1..127488
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="5"
/clone="CTB-36B8"
/clone_lib="CalTech human BAC library B"
BASE COUNT 31643 a 32392 c 31616 g 30626 t 1211 others
ORIGIN

Query Match
Best Local Similarity 1.3%; Score 53; DB 2; Length 127488;
Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 26 cggggcgccgcgtgtgcctgcgacttgctcgtgcctggactcctggactcctggacgg 78
|||||
Db 65772 CGGGCGCGCGCTGTGCTGCGACTGTGGCTCTGCTGGGACTCCTGGACGG 65824

RESULT 35
AX056761 39 bp DNA linear PAT 17-JAN-2001
LOCUS Sequence 27 from Patent WO0075319.
DEFINITION AX056761
ACCESSION AX056761
VERSION AX056761.1 GI:12309736
KEYWORDS synthetic construct.
SOURCE synthetic construct.
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 39)
AUTHORS Papadopoulos,N.J., Davis,S. and Yancopoulos,G.D.
TITLE Modified chimeric polypeptides with improved pharmacokinetic
properties
JOURNAL Patent: WO 0075319-A 27 14-DEC-2000;
REGENERON PHARMACEUTICALS, INC. (US)
FEATURES
Location/Qualifiers
source 1..39
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="primer"
BASE COUNT 7 a 10 c 13 g 9 t
ORIGIN

Query Match
Best Local Similarity 0.9%; Score 39; DB 6; Length 39;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 713 atccagctgttgcacaggaatcgctgagctgctgata 751
|||||
Db 1 ATCCAGCTGTGTCGCCAGGAGTCGCTGAGCTGCTGGTA 39

RESULT 36
AX056762/c
LOCUS Sequence 28 from Patent WO0075319.
DEFINITION AX056762
ACCESSION AX056762
```

```

VERSION      AX056762.1  GI:12309737
KEYWORDS     .
SOURCE       synthetic construct.
ORGANISM     synthetic construct.
              artificial sequence.
REFERENCE    1 (bases 1 to 39)
AUTHORS      Papadopoulos,N.J., Davis,S. and Yancopoulos,G.D.
TITLE        Modified chimeric polypeptides with improved pharmacokinetic
              properties
JOURNAL      Patent: WO 0075319-A 28 14-DEC-2000;
              REGENERON PHARMACEUTICALS, INC. (US)
FEATURES     Location/Qualifiers
              source
              1..39
              /organism="synthetic construct"
              /db_xref="taxon:32630"
              /note="primer"
BASE COUNT   9 a 12 c 7 g 11 t
ORIGIN
Query Match      0.9%; Score 39; DB 6; Length 39;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 971 cgaattcgagagaccagcaggttcattgtcgcataaat 1009
Db 39 CGATTTCCGGGAGACCCGAGGTCATTGTGCATGAAAT 1

RESULT 37
LOCUS      HSA330946              777 bp      DNA      linear      PRI 01-OCT-2001
DEFINITION Homo sapiens genomic sequence surrounding NotI site, clone
              NL6-BC23RS.
ACCESSION   AJ330946
VERSION     AJ330946.1  GI:15875364
KEYWORDS    .
SOURCE      human.
ORGANISM    Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE   1 (bases 1 to 777)
AUTHORS     Kutsenko,A.S., Gizatullin,R.Z., Al-Amin,A.N., Wang,F.,
              Podowski,R.M., Matushkin,Y.G., Kvasha,S.M., Gyanchandani,A.,
              Muravenko,O.V., Protodopov,A.I., Kashuba,V.I., Kisselev,L.L.,
              Wasserman,W., Wahlestedt,C. and Zabarovsky,E.R.
TITLE       Analysis of NotI flanking sequences: a new tool for gene discovery
              and verification of the human genome
JOURNAL     Unpublished
REFERENCE   2 (bases 1 to 777)
AUTHORS     Zabarovsky,E.R.
TITLE       Direct Submission
JOURNAL     Submitted (16-MAY-2001) Microbiology and Tumorbiology Centre,
              Karolinska Institute, Theorells vag, 3, Box 280, Stockholm 171 77,
              Sweden
FEATURES     Location/Qualifiers
              source
              1..777
              /organism="Homo sapiens"
              /db_xref="taxon:9606"
              /clone="NL6-BC23RS"
BASE COUNT   161 a 180 c 223 g 209 t 4 others
ORIGIN

Query Match      0.8%; Score 34; DB 9; Length 777;
Best Local Similarity 100.0%; Pred. No. 4.3e-05;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 702 agctctatgacatccagctgttgcaggagtc 735
Db 342 AGCTTATGACATCCAGCTGTTGCCCAGGAAGTC 735

```

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RESULT 38
LOCUS      AF030379              420 bp      mRNA      linear      MAM 18-NOV-1998
DEFINITION Bos taurus tyrosine kinase receptor Fll4 mRNA, partial cds.
ACCESSION   AF030379
VERSION     AF030379.1  GI:2613138
KEYWORDS    .
SOURCE      cow.
ORGANISM    Bos taurus
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
              Bovidae; Bovinae; Bos.
REFERENCE   1 (bases 1 to 420)
AUTHORS     Pepper,M.S., Mandriota,S.J., Jeltsch,M., Kumar,V. and Alitalo,K.
TITLE       Vascular endothelial growth factor (VEGF)-C synergizes with basic
              fibroblast growth factor and VEGF in the induction of angiogenesis
              in vitro and alters endothelial cell extracellular proteolytic
              activity
JOURNAL     J. Cell. Physiol. 177 (3), 439-452 (1998)
MEDLINE     99023338
REFERENCE   2 (bases 1 to 420)
AUTHORS     Mandriota,S.J. and Pepper,M.S.
TITLE       Direct Submission
JOURNAL     Submitted (20-OCT-1997) Morphology, University Medical Center, 1,
              rue Michel Servet, 1211 Geneva 4, Switzerland
FEATURES     Location/Qualifiers
              source
              1..420
              /organism="Bos taurus"
              /db_xref="taxon:9913"
              /tissue_type="kidney"
              /dev_stage="adult"
              /note="RT-PCR product amplified from total RNA using
              degenerate primers; sequenced on both strands"
              cl..420
              /codon_start=1
              /product="tyrosine kinase receptor Flt4"
              /protein_id="AAC78244.1"
              /db_xref="GI:2613139"
              /translation="RCPVAGTHVPSIVMYKDEKLEPESGIDLADSNORLSIORVREE
              DAGHYLCSVNAKGCNVSSASVAVEGSEDKGMEIVILVGTGVIATVFWFVWLLLLLFCN
              MRRPTHADIKTYLSIIMDPCVEPLECEYLSYDASQ"
BASE COUNT   90 a 110 c 130 g 90 t
ORIGIN

Query Match      0.8%; Score 32; DB 4; Length 420;
Best Local Similarity 100.0%; Pred. No. 0.00046;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2457 tgctcatcatcatggaccccgaggagtgacct 2488
Db 347 TGTCATCATCATGACCCCGGAGGTGCCT 378

RESULT 39
LOCUS      AX056763              38 bp      DNA      linear      PAT 17-JAN-2001
DEFINITION Sequence 29 from Patent WO0075319.
ACCESSION   AX056763
VERSION     AX056763.1  GI:12309738
KEYWORDS    .
SOURCE      synthetic construct.
ORGANISM    synthetic construct.
              artificial sequence.
REFERENCE   1 (bases 1 to 38)
AUTHORS     Papadopoulos,N.J., Davis,S. and Yancopoulos,G.D.
TITLE       Modified chimeric polypeptides with improved pharmacokinetic
              properties
JOURNAL     Patent: WO 0075319-A 29 14-DEC-2000;
              REGENERON PHARMACEUTICALS, INC. (US)
FEATURES     Location/Qualifiers
              source
              1..38

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/organism="synthetic construct"
 /db_xref="taxon:32630"
 /note="primer"
 9 a 9 c 11 g 9 t
 BASE COUNT
 ORIGIN

Query Match 0.7% Score 30; DB 6; Length 38;
 Best Local Similarity 100.0%; Pred. No. 0.0063;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 713 atccagctgttgcaggaagtcgtgag 742

Db 9 ATCCAGCTGTGCGCAGGAGTCGTGGAG 38

RESULT 40

LOCUS AB017155 534 bp mRNA linear MAM 02-APR-1999
 DEFINITION Oryctolagus cuniculus mRNA for VEGF receptor-2/Fik-1, partial cds.
 ACCESSION AB017155
 VERSION AB017155.1 GI:4586885

KEYWORDS VEGF receptor-2/Fik-1.
 SOURCE Oryctolagus cuniculus (strain:Japanese white) liver cDNA to mRNA.
 ORGANISM Oryctolagus cuniculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Lacomorpha; Leporidae; Oryctolagus.

REFERENCE 1 (bases 1 to 534)

AUTHORS Umeki,K., Kon,K. and Ohtaki,S.
 TITLE Rabbit mRNA for vascular endothelial growth factor (VEGF) receptor-2/Fik-1, partial cds

JOURNAL Published Only in Database (1999) In press
 AUTHORS Umeki,K., Kon,K. and Ohtaki,S.
 TITLE Direct Submission

JOURNAL Department of Laboratory Medicine; Kihara 5200, Kiyotake, Miyazaki
 889-1602, Japan (E-mail:umeki@post1.miyazaki-med.ac.jp).
 Tel:+81-985-85-9400, Fax:+81-985-85-4709)
 Location/Qualifiers
 1..534

FEATURES source

/organism="Oryctolagus cuniculus"
 /strain="Japanese white"
 /db_xref="taxon:9986"
 /issue_type="liver"
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 /protein_id="BA076520.1"
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 /translation="LASRKC IHRDLAARNILLSEKNVVKICDFGLARDYKDPDYVRK
 GNARLPKWMAPETIFDRVYTIQSDVNSFGVLLWEIFSLGASPYGVKIDFECRRLK
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 PMSETLSMEEDSGLSLPT"
 128 a 132 c 156 g 118 t

BASE COUNT
ORIGIN

Query Match 0.7% Score 28; DB 4; Length 534;
 Best Local Similarity 100.0%; Pred. No. 0.042;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3165 acgtggtgaagactgtgactttggcct 3192

Db 65 ACCTGCTGAAGATCTCTGACTTTGGCCT 92

RESULT 41

LOCUS AC098957 161580 bp DNA linear HTG 20-DEC-2001
 DEFINITION Rattus norvegicus clone CH230-193G14, *** SEQUENCING IN PROGRESS
 *** 75 unordered pieces.

ACCESSION AC098957

VERSION AC098957.2 GI:17973745
 KEYWORDS HTGS_PHASE1.
 SOURCE Norway rat.

ORGANISM

Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Sciurognathi; Muridae; Murinae;
 Rattus.

1 (bases 1 to 161580)

Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,
 Alsbrooks,S.L., Amaral-Lunge,H.C., Arc,J.R., Banks,T., Barbara,J.,
 Benton,J., Bimaga,K., Blankenburg,K., Bonnin,D., Bouck,J.,
 Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P., Buhay,C.,
 Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C., Carron,T.F.,
 Carter,M., Cavazos,S.R., Chacko,J., Chavez,D., Chen,G., Chen,R.,
 Chen,Z., Chowdhry,I., Christopoulos,C., Cleveland,C.D., Cox,C.,
 Coyle,M.D., Dathorne,S.R., David,R., Davila,M.L., Davis,C.,
 Davy-Carroll,L., Dederich,D.A., Delaney,K.R., Delgado,O.,
 Dunn,A.L., Ding,Y., Dinh,H.H., Douthwaite,K.J., Draper,H.,
 Duggan-Rocha,S., Durbin,K.J., Earnhart,C., Edgar,D., Edwards,C.C.,
 Elhaj,C., Escotto,M., Falls,T., Ferraguto,D., Flagg,N., Ford,J.,
 Foster,P., Frantz,P., Gabisi,A., Gao,J., Garcia,A., Garner,T.,
 Garza,N., Gill,R., Gorrell,J.H., Guevara,W., Gunaratne,P., Hale,S.,
 Hamilton,K., Harris,C., Harris,K., Hart,M., Havlak,P., Hawes,A.,
 Hernandez,J., Hernandez,O., Hodgson,A., Hogues,M., Holloway,C.,
 Hollins,B., Honsi,F., Howard,S., Huber,J., Hulyk,S., Hume,J.,
 Jackson,L.E., Jacobson,B., Jia,Y., Johnson,R., Jolivet,S.,
 Joudah,S., Karlsson,E., Kelly,S., Khan,U., King,L., Korvah,J.,
 Kovar,C., Kratovic,J., Kureshi,A., Landry,N., Leal,B., Lewis,L.C.,
 Lewis,L., Li,J., Li,Z., Lichtarge,O., Lieu,C., Liu,J., Liu,W.,
 Loulseged,H., Lozano,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R.,
 Ma,J., Maheshwari,M., Mapua,P., Martin,R., Martindale,A.,
 Martinez,E., Massey,E., Mawhiney,E., McLeod,M.P., Meador,M.,
 Mei,G., Metzker,M., Miner,G., Miner,Z., Mitchell,T., Mohabbat,K.,
 Morgan,M., Morris,S., Moser,M., Neal,D., Newton,J., Newton,N.,
 Nguyen,A., Nguyen,N., Nguyen,N., Nickerson,E., Nwokenkwo,S.,
 Ogihara,M., Okuno,G., Oragunye,N., Oviedo,R., Pace,A., Payton,B.,
 Peery,J., Perez,L., Peters,L., Pickens,R., Primus,E., Pu,L.L.,
 Quiles,M., Ren,Y., Rives,M., Rojas,A., Rojibokan,I., Rolfe,M.,
 Ruiz,S., Savary,G., Scherer,S., Scott,G., Shen,H., Shooshtari,N.,
 Sisson,I., Sodergren,E., Sonaike,T., Sparks,A., Stanley,H.,
 Stone,H., Sutton,A., Svatek,A., Tabor,P., Tamerisa,A., Tamerisa,K.,
 Tang,H., Tansey,J., Taylor,C., Taylor,T., Telford,B., Thomas,N.,
 Thomas,S., Usmani,K., Vasquez,L., Vera,V., Villalobon,D., Vinson,R.,
 Wall,R., Wang,S., Ward-Moore,S., Warren,R., Washington,C.,
 Watlington,S., Williams,G., Williamson,A., Wleczek,R., Wooden,S.,
 Worley,K., Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D.,
 Weinstock,G. and Gibbs,R.

Direct Submission

Unpublished

2 (bases 1 to 161580)

Worley,K.C.

Direct Submission

Submitted (07-NOV-2001) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA

On Dec 20, 2001 this sequence version replaced gi:16756151.

----- Genome Center

Center: Baylor College of Medicine

Center code: BCM

Web site: <http://www.hgsc.bcm.tmc.edu/>

Contact: hgsc-help@bcm.tmc.edu

----- Project Information

Center project name: GJFR

Center clone name: CH230-193G14

----- Summary Statistics

Assembly program: Phrap; version 0.990329First call to

findPhrapList

Consensus quality: 121539 bases at least Q40

Consensus quality: 129496 bases at least Q30

Consensus quality: 136265 bases at least Q20

Estimated insert size: 111412; sum-of-contigs estimation

Quality coverage: 0x in Q20 bases; agarose-fp estimation

Quality coverage: 1.5x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 75 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1 5831: contig of 5831 bp in length
* 5832 5931: gap of unknown length
* 5932 11384: contig of 5453 bp in length
* 11385 11484: gap of unknown length
* 11485 16895: contig of 5411 bp in length
* 16896 16995: gap of unknown length
* 16996 21784: contig of 4789 bp in length
* 21785 21884: gap of unknown length
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* 25355 25454: gap of unknown length
* 25455 29460: contig of 4006 bp in length
* 29461 29560: gap of unknown length
* 29561 32307: contig of 2747 bp in length
* 32308 32407: gap of unknown length
* 32409 35343: contig of 2936 bp in length
* 35344 35443: gap of unknown length
* 35444 38216: contig of 2773 bp in length
* 38217 38316: gap of unknown length
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* 60506 60605: gap of unknown length
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* 62901 63000: gap of unknown length
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* 70778 70877: gap of unknown length
* 70878 73509: contig of 2632 bp in length
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* 87807 87906: gap of unknown length
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* 95739 97396: contig of 1657 bp in length
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* 99146 99245: gap of unknown length
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* 132212 133294: contig of 1083 bp in length
* 133295 133394: gap of unknown length
* 133395 134851: contig of 1457 bp in length
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* 134952 136002: contig of 1051 bp in length
* 136003 136102: gap of unknown length

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Best Local Similarity 100.0%; Pred. No. 0.019;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Caps 0;

Oy 1649 gagcggtccatctactctatgtgacca 1676
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Db 61372 GAGCGGCTCATCTACTTCTATGTGACCA 61399

RESULT 42
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LOCUS XELXFGFRA2
DEFINITION Xenopus laevis fibroblast growth factor receptor mRNA, complete cds.
ACCESSION MG2322
VERSION MG2322.1 GI:214899
KEYWORDS fibroblast growth factor receptor; tyrosine kinase receptor.
SOURCE X.laevis, cDNA to mRNA.

ORGANISM Xenopus laevis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
Xenopodinae; Xenopus.

XELXFGFRA2 2753 bp mRNA linear VRT 28-APR-1993
Xenopus laevis fibroblast growth factor receptor mRNA, complete

REFERENCE 1 (bases 1 to 2753)
AUTHORS Friesel,R.E. and David,I.B.
TITLE cDNA cloning and developmental expression of fibroblast growth factor receptors from Xenopus laevis
JOURNAL Mol. Cell. Biol. 11, 2481-2488 (1991)
MEDLINE 91203867
FEATURES
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154..2328 /gene="XFGFRA2"
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154..216
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217..2325
mat_peptide /gene="XFGFRA2"
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Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3112 aaagtgcattccacagagacctggctgc 3138
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Db 1722 AAAGTGCATCCACAGACCTGCCTGC 1748

RESULT 43
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LOCUS xenopus laevis fibroblast growth factor receptor-1 mRNA, complete
cvs
DEFINITION
ACCESSION U24491 M61687 M37201
VERSION U24491.1 GI:857677
KEYWORDS
SOURCE African clawed frog.
ORGANISM xenopus laevis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
Xenopodinae; Xenopus.
1 (bases 1 to 2439)
Musci.T.J., Amaya,E. and Kirschner,M.W.
Regulation of the fibroblast growth factor receptor in early
Xenopus embryos
Proc. Natl. Acad. Sci. U.S.A. 87 (21), 8365-8369 (1990)
JOURNAL 9104598
MEDLINE 2 (bases 2440 to 3634)
Robbie.F.P., Peterson,M., Amaya,E. and Musci,T.J.
Temporal regulation of the Xenopus fgf receptor in development: a
translation inhibitory element in the 3' untranslated region
Development 121 (6), 1775-1785 (1995)
JOURNAL

95324403
3 (bases 1 to 3634)
Musci.T.J.
Direct Submission
Submitted (11-APR-1995) Thomas J. Musci, Dept. of OB/GYN,
University of California, San Francisco, Box 0556, San Francisco,
CA 94143, USA
On Jun 12, 1995 this sequence version replaced gi:214137.
FEATURES
source Location/Qualifiers
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/db_xref="taxon:8355"
1..2439 /codon_start=1
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ORIGIN

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Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3112 aaagtgcattccacagagacctggctgc 3138
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Db 1833 AAAGTGCATCCACAGACCTGCCTGC 1859

RESULT 44
XELX1FGFR
LOCUS xenopus laevis fibroblast growth factor receptor mRNA, complete
cvs
DEFINITION
ACCESSION M55163
VERSION M55163.1 GI:214893
KEYWORDS fibroblast growth factor receptor.
SOURCE xenopus laevis XTC cell line, cDNA to mRNA.
ORGANISM xenopus laevis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
Xenopodinae; Xenopus.
1 (bases 1 to 3815)
Friesel,R.E. and David,I.B.
cDNA cloning and developmental expression of fibroblast growth
factor receptors from Xenopus laevis
Mol. Cell. Biol. 11, 2481-2488 (1991)
JOURNAL 91203867
MEDLINE Location/Qualifiers
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/db_xref="GI:214894"

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/product="fibroblast growth factor receptor"
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ORIGIN

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Best Local Similarity 100.0%; Pred. No. 0.1;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 3112 aaatgcacacagagacctggctgc 3138
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Db 1975 AAAGTCCATCCACAGACCTGGCTGC 2001

RESULT 45
MMAPK42
LOCUS Mouse MAPK mRNA for mitogen-activated protein kinase (p42).
DEFINITION X58712
ACCESSION X58712
VERSION x58712.1 GI:53001
KEYWORDS mitogen-activated protein kinase; protein kinase.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Her, J. H.
Direct Submission
Submitted (03-APR-1991) J. H. Her, University of Virginia, Dept of
Microbiology and, Cancer Center Box 441, School of Medicine,
Charlottesville VA 22908, USA
2 (bases 1 to 1256)
Her, J. H., Wu, J., Rall, T. B., Sturgill, T. W. and Weber, M. J.
Sequence of pp42/MAP kinase, a serine/threonine kinase regulated by
tyrosine phosphorylation
Nucleic Acids Res. 19 (13), 3743 (1991)
91305126
Location/Qualifiers
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19. .1095
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ORIGIN

Query Match 0.6%: Score 26; DB 10; Length 1256;
Best Local Similarity 100.0%; Pred. No. 0.37;
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Db 502 AAGATCTGTGACTTTGGCCTTGCCCG 527

Search completed: July 15, 2002, 23:22:29
Job time: 24202 sec

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Db 3404 AGACACGCACAGCATGAGGCGCCCGAGCTGCCACTCCCGCATACGCGCATCATG 3463
Qy 421 ctgaactgctggtccggagagaccccaaggcgagacctcattctcgagagctg 471
Db 3464 CTGAACCTGCTGCTCGGAGAGACCCCAAGCGAGACCTGCTGCTCGGAGCTG 3514

RESULT 4
HSFLT4 411 bp mRNA linear PRI 30-NOV-1993
LOCUS H.sapiens mRNA for FLT4, class III receptor tyrosine kinase.
DEFINITION X68203
ACCESSION X68203
VERSION X68203.1 GI:31433
KEYWORDS FLT4; tyrosine kinase receptor.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
Aprelikova, O.
Direct Submission
Submitted (01-SEP-1992) O. Aprelikova, University of Helsinki,
Cancer Biology Laboratory, Dept of Pathology, Haartmaninkatu 3,
00290 Helsinki, FINLAND
2 (bases 1 to 416)
Aprelikova, O., Pajusola, K., Partanen, J., Armstrong, E., Alitalo, R.,
Bailey, S.K., McMahon, J., Wasmuth, J., Huebner, K. and Alitalo, K.
FLT4, a novel class III receptor tyrosine kinase is on chromosome
5q33-qter
Cancer Res. 52 (3), 746-748 (1992)
JOURNAL Cancer Res. 52 (3), 746-748 (1992)
MEDLINE 92119639
COMMENT Related sequence: X51602.
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ORIGIN
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Qy 61 gcttccgaaagtgcattccacagagacgtgctgctcggaacattctgctgctggaagc 120
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Db 3104 GCTTCCGAAAGTGCAATCCACAGAGACCTGCTGCTCGGAACATCTGCTGTGCGGAAGC 3163
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Db 3164 GAGTGTGTGAAGATCTGTGACTTTGGCTTTGCCGGGACATCTACAAAGACCCCTGACTAC 3223
Qy 181 gtccgaaggcgagtgcccggtgccccctgaagtggatggcggccttgaagacatcttcgac 240
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Qy 301 tctctgggggctctcccgctaccctggggtgcagatcaatgagaggtctccagcgagctg 360
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Db 3344 TCTCTGGGGGCTCTCCCGTACCCTGGGTGCAGATCAATGAGGAGTTCTGCCAGCGGCTG 3403
Qy 361 agagacggcacaaggatgagggccccggaggctggccactccgccataccgcgcacatcg 420
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Db 3404 AGAGACGGCACAAAGATGAGGGGCCCGGAGCTGGCCACTCCCGGCATACGCGGCATCATG 3463
Qy 421 ctgaactgctggtccggagagaccccaaggcgagacctcattctcgagagctg 471
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Db 3464 CTGAACCTGCTGCTCGGAGAGACCCCAAGCGAGACCTGCTGCTCGGAGCTG 3514

RESULT 5
LOCUS I44520
DEFINITION Sequence 31 from patent US 5635177.
ACCESSION I44520
VERSION I44520.1 GI:2469233
KEYWORDS .
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 4425)
AUTHORS Bennett,B.D., Goeddel,D. and Matthews,W.
TITLE Protein tyrosine kinase agonist antibodies
JOURNAL Patent: US 5635177-A 31 03-JUN-1997;
FEATURES
source
1..4425
/organism="unknown"
BASE COUNT 939 a 1348 c 1361 g 777 t
ORIGIN
Query Match 100.0%; Score 471; DB 6; Length 4425;
Best Local Similarity 100.0%; Pred. No. 2.1e-263;
Matches 471; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ctgaccatggaagatcttctgctacagcttccagggtggcagagggatggagttcctg 60
|||||
Db 3055 CTGACCATGGAAGATCTGTCTCTACAGTTCACAGTTCAGGTCGCGCAGAGGGATGGAGTTCTCTG 3114
Qy 61 gcttccgaaagtgcattccacagagacgtgctgctcggaacattctgctgctggaagc 120
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Oy 301 tctctggggcctccccgtaccctgggtgcagatcaatgaagattctgcagcgctg 360
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Db 2449 TCTCTGGGGCCTCCCCGTACCCTGGGTGCAGATCAATGAGAGTCTTGCACGGCGTG 2390
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Oy 361 agagacggcacaaagatgagggcccgagctggcactcccgccatcacgcgcgcatcg 420
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Db 2389 AGAGACGGCACAAAGATGAGGGCCCGGAGCTGGCCACTCCGCCATACGCCGCCATCATG 2330
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Oy 421 ctgaactgctgctcgagagaccccaaggcagagacctgattctcgagcgtg 471
|||||
Db 2329 CTGAACCTGCTGCTCGGAGACCCCAAGCGGAGACCTGCATCTTCGAGCTG 2279
|||||

RESULT 10
HSFLT4X HSFLT4X 4450 bp mRNA linear PRI 29-NOV-1993
LOCUS H.sapiens Flt4 mRNA for transmembrane tyrosine kinase.
ACCESSION X69878 S59182
VERSION X69878.1 GI:297049
KEYWORDS transmembrane tyrosine kinase; tyrosine kinase.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 4450)
AUTHORS Galland,F., Karamysheva,A., Pebusque,M.J., Borg,J.P., Rottapel,R.,
Dubreuil,P., Rosnet,O. and Birnbaum,D.
TITLE The Flt4 gene encodes a transmembrane tyrosine kinase related to
the vascular endothelial growth factor receptor
JOURNAL Oncogene 8 (5), 1233-1240 (1993)
MEDLINE 93241723
REFERENCE 2 (bases 776 to 1200)
AUTHORS Galland,F., Karamysheva,A., Mattei,M.G., Rosnet,O., Marchetto,S.
and Birnbaum,D.
TITLE Chromosomal localization of FLT4, a novel receptor-type tyrosine
kinase gene
JOURNAL Genomics 13 (2), 475-478 (1992)
MEDLINE 92307693
REFERENCE 3 (bases 1 to 4450)
AUTHORS Galland,F.
TITLE Direct Submission
JOURNAL Submitted (28-DEC-1992) F. Galland, INSERM, Unite 119, 27 Bd Lei
Roure, Marseille 13009, FRANCE
FEATURES
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/organism="Homo sapiens"
/db_xref="taxon:9606"
22..87
/protein_id="CAA49505.1"
/db_xref="GI:297050"
/translation="MKGAAALCLRLMLCLGLDLGLSDYSMTPTPLNITESHVIDTG
DLSLISCRGQDPLWMPGAQEPATGDKDSEDTGVVRDCEGTDAREYCKVLLLHVH
ANDTGYCYVYKIKARIECTTAASSYFVRDFEQPINRPDTLLVNRKDMWVPCLV
SIPGLNVLTRSSQSLWMPDGEVYVDDRRGLVSTPLLDHALYLQCEITWGDQDFLSN
PFLVHTIGNELYDIOLPRKSLLELVGKELVINCTVWAEFNSGYTFDWDYPGKAERG
KWVPRSQOHTHELSSILTTHNSQHDGLGYSYCKANNQIQRFRFSEVIVHENPFI
VEMLKGPLETEAGDELVKLPVLAAYPPPEFOWYKDGKALSGRHSPLALVLEKTEA
STGNTYTLALNSAAGLRNLSLELVNVPQIHEKEASSPIYSRHSRQALCTAYGV
PLPLSIQHWRPWPCKNFAQSLRRRQQQDLMPQCRDRAVTTQDAVNPIESLDWT
EFVGGKNTYSLKVIQNAVSAWKCVVSNKVGQDERLIYFVTTIPDGTIESKPS
ELLEQPVLLSCQADSYKYEHLRWYRLNSTLDAHGNPLLLDCKNVHLFATPLAAL
EVAPARHATLSLSIPRPAVECHYCYEQVDRRSHDKHKKYLVSQALEAPRLQ
NLDTLLNVNDSLMQCLVAGAHAPSIWYKDERLLEKSGVDLADSNOKLSIORVE
EDAGPYLCSVCRPKGVNSASVAVEGSDKSMELVILVCTGVIAVFFNVLLILFC
NMRRPAHDIKTGYLSLIMDPGEVPLEQCEYLSYDASQSEFFPRERHLRGLYGAF
GKYVEASAFGIHKSSDVTAVKMLKEGATASEQALMSELKILIHGNHVNVLIG
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RPGSSDRVLFARESKTEGGARRASPDQEAEDLWLSPLTMEDLVCSYFQVARGMEFLAS
RKCHRLDLAARNILLSESVDYKICDFGLARDLIYKDPDYVRKGSARLPLKMKWAPESIFD
KYVTTQSDVNSFGVLLWEIFSLGAPYPGVQIINEEFCQVRDGTMRMRAPELATPAIRH
IMLNCWSGDPKARPAPFSDLVEILGLDLQGRGLQEEVEVCMAPKSSOSSEGSFSQVST
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22..2346
/citation=[1]
/product="extracellular domain"
misc_structure 160..366
/citation=[1]
/citation="IG-like domain 1"
misc_structure 481..651
/citation=[1]
/citation="IG-like domain 2"
misc_structure 763..963
/citation=[1]
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/citation=[1]
/citation="IG-like domain 4"
misc_structure 1342..1635
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/citation="IG-like domain 5"
misc_structure 1741..1992
/citation=[1]
/citation="IG-like domain 6"
misc_feature 2104..2277
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/product="IG-like domain 7"
misc_feature 2347..2412
/citation=[2]
/product="transmembrane domain"
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/citation=[1]
/citation=[2]
/product="kinase insert"
misc_feature 3049..3558
/citation=[2]
/citation=[1]
/product="tyrosine kinase domain 2"
BASE COUNT 960 a 1350 c 1354 g 786 t
ORIGIN

Query Match 64.8%; Score 305; DB 9; Length 4450;
Best Local Similarity 99.7%; Pred. No. 1.8e-166;
Matches 355; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 ctgaccatggaagattctgtctgtctacagcttcacagtgccagggatggagttcctg 60
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Db 3046 CTGACCATGGAAGATCTTGTCTGTACAGCTTCCAGGTGGCCAGAGGGATGGAGTTCTG 3105
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Oy 61 gcttcccgaaagtgcattccacagagacctgctgctcggaacattctgctcgaaagc 120
|||||
Db 3106 GTTCCCCAAAAGTGCATCCACAGAGACTGGCTGCTCGGAACATCTGCTGTCGGAAGC 3155
|||||

Oy 121 gacgtggtgaagattctgactttggcttggccttggcctgggacattctacaagaccctgactac 180
|||||
Db 3166 GACGTGTTGAAGATCTGTGACTTTGGCTTCCCGGGGACATCTACAAGACCCCGACTAC 3225
|||||

Oy 181 gtcgcgaaggcagtgcccgctgcccctgaagtggatggccctgaaagcattcttcgac 240
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Db 3226 GTCCGCAAGGGCAGTGGCCCGCTGCCCTGAAAGTGGATGGCCCTGAAAGCATCTTCGAC 3285
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Qy 241 aagtggtacacacagacagtgagctggtgctcttgggtgctctctggagatcttc 300
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Db 3286 AAGGTGTACACACACAGTACAGTGTGGTCTTTGGGGTCTCTCTGGAGATCTTC 3345
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Qy 301 tctctgggggctccctacacctgagctgggtgcagatcaatgagggtctctgccagc 356
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Db 3346 TCCTCGGGGGCTCCCGCTACCTGGGTGAGATCAATGAGGAGTTCTGCCAGCG 3401
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RESULT 11
AC022095/c 127488 bp DNA linear HTG 20-APR-2001
LOCUS Homo sapiens chromosome 5 clone CTB-36B8, WORKING DRAFT SEQUENCE,
DEFINITION 13 unordered pieces.
ACCESSION AC022095
VERSION AC022095.5 GI:13699618
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 127488)
AUTHORS DOE Joint Genome Institute.
TITLE Sequencing of Human Chromosome 5
JOURNAL Unpublished
AUTHORS DOE Joint Genome Institute.
REFERENCE 2 (bases 1 to 127488)
AUTHORS DOE Joint Genome Institute.
TITLE Direct Submission
JOURNAL Submitted (26-JAN-2000) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
On Apr 20, 2001 this sequence version replaced gi:7711676.
-----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov
-----
Project Information
Center Project Name: 78060
Center clone name: CIT978SKB_36B8
-----
Summary Statistics
Consensus quality: 110477 bases at least Q40
Consensus quality: 117221 bases at least Q30
Consensus quality: 120225 bases at least Q20
Estimated insert size: 131000; pulse field gel estimation
Estimated insert size: 126288; sum-of-contigs estimation
Quality coverage: 7.48 in Q20 bases; pulse field gel estimation
Quality coverage: 7.76 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 13 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 1116: contig of 1116 bp in length
* 1117 1216: gap of unknown length
* 1217 2254: contig of 1038 bp in length
* 2255 2354: gap of unknown length
* 2355 3412: contig of 1058 bp in length
* 3413 3512: gap of unknown length
* 3513 5005: contig of 1493 bp in length
* 5006 5105: gap of unknown length
* 5106 7647: contig of 2542 bp in length
* 7648 7747: gap of unknown length
* 7748 10237: contig of 2490 bp in length
* 10238 10337: gap of unknown length
* 10338 12440: contig of 2103 bp in length
* 12441 12540: gap of unknown length
* 12541 15935: contig of 3395 bp in length
* 15936 16035: gap of unknown length

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* 16036 24396: contig of 8361 bp in length
* 24397 24496: gap of unknown length
* 24497 39085: contig of 14589 bp in length
* 39086 39185: gap of unknown length
* 39186 60545: contig of 21360 bp in length
* 60546 60645: gap of unknown length
* 60646 79490: contig of 18845 bp in length
* 79491 79590: gap of unknown length
* 79591 127488: contig of 47898 bp in length.

FEATURES
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         source          1..127488
                        /organism="Homo sapiens"
                        /db_xref="taxon:9606"
                        /chromosome="5"
                        /clone_lib="CTB-36B8"
                        /clone_lib="CalTech human BAC library B"
BASE COUNT 31643 a 32392 c 31616 g 30626 t 1211 others
ORIGIN

Query Match      24.0%; Score 113; DB 2: Length 127488;
Best Local Similarity 100.0%; Pred. No. 2.3e-54;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 196 gcccggtgccccctgaagtgagtgagccctgaaagcattctcgacaaggtgtacaccacg 255
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Db 106477 GCCCGGTGCCCCCTGAAGTGGATGCGCCCTCGAAAGCATCTTCGACAAAGGTGTACACCACG 106418
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Qy 256 cagagtgcactgtgtctctttgggtgctctctctggtgagatctctctctctggtg 308
|||||
Db 106417 CAGAGTACGCTGTGCTCTTTGGGTGCTTCTCTCGGAGATCTTCTCTCTGGG 106365
|||||

RESULT 12
AC108083/c 130129 bp DNA linear HTG 25-JAN-2002
LOCUS Homo sapiens chromosome 5 clone CTD-2013L15, WORKING DRAFT
DEFINITION SEQUENCE, 4 unordered pieces.
ACCESSION AC108083
VERSION AC108083.1 GI:18369929
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 130129)
AUTHORS DOE Joint Genome Institute.
TITLE Sequencing of Human Chromosome 5
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 130129)
AUTHORS DOE Joint Genome Institute.
TITLE Direct Submission
JOURNAL Submitted (25-JAN-2002) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
-----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov
-----
Project Information
Center Project Name: 632820
Center clone name: CITB-H1_2013L15
-----
Summary Statistics
Consensus quality: 124488 bases at least Q40
Consensus quality: 128031 bases at least Q30
Consensus quality: 128842 bases at least Q20
Estimated insert size: 135000; agarose-fp estimation
Estimated insert size: 129829; sum-of-contigs estimation
Quality coverage: 7.66 in Q20 bases; agarose-fp estimation
Quality coverage: 7.97 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 4 contigs. The true order of the pieces

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* is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

1 4320: contig of 4320 bp in length
 * 4321 4420: gap of unknown length
 * 4421 23712: contig of 19292 bp in length
 * 23713 23812: gap of unknown length
 * 23813 48602: contig of 24790 bp in length
 * 48603 48702: gap of unknown length
 * 48703 130129: contig of 81427 bp in length.

FEATURES

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1. 130129
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /chromosome="5"
 /clone="CTD-2013L15"

/clone_lib="Caltech human BAC library D"
 /base 35337 a 32397 c 30949 g 31146 t 300 others

BASE COUNT

ORIGIN

Query Match 24.0%; Score 113; DB 2: Length 130129;
 Best Local Similarity 100.0%; Pred. No. 2.3e-54;
 Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 196 gccgcgtgccctgaagtgcctgagccctgaaagcattctgcacaagtgatcacccacg 255
 |||||
 Db 46759 GCCCGCTGCCCTCAAGTGGATGCCCTGAAAGCATCTTCGACAAAGTGTACACACG 46700
 |||||
 Qy 256 caagatgcgcgtgctcttcttggggctctctctctctctctctctctctctctggg 308
 |||||
 Db 46699 CAGACTGACGTGTGCTCTTTGGGTGCTTCTCTGGAGATCTTCTCTCTGGG 46647

RESULT 13

AC025336

LOCUS

DEFINITION Homo sapiens chromosome 5 clone RP11-451H23 map 5, WORKING DRAFT
 SEQUENCE, 32 unordered pieces.

ACCESSION

AC025336

VERSION

AC025336.2 GI:7328761

KEYWORDS

HTG; HTGS_PHASE1; HTGS_DRAFT.

SOURCE

human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 168347)

Birren,B., Linton,L., Nusbaum,C. and Lander,E.

Homo sapiens chromosome 5, clone RP11-451H23

Unpublished

2 (bases 1 to 168347)

Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,

Anderson,S., Baldwin,J., Barna,N., Bastien,V., Beda,F.,

Boguslavsky,L., Boukhgalter,B., Brown,A., Burkett,G.,

Campolano,A., Castle,A., Choepel,Y., Colangelo,M., Collins,S.,

Collins,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S.,

Dodge,S., Domino,M., Doyle,M., Ferreira,P., Fitzhugh,W., Gage,D.,

Galagan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L.,

Graland-Pierre,N., Grant,G., Hagos,B., Heaford,A., Horton,L.,

Howland,J.C., Iliev,I., Johnson,R., Jones,C., Kann,L., Karatas,A.,

Klein,J., LaRocque,K., Lamazares,R., Landers,T., Lehoczy,J.,

Levine,R., Lieu,C., Liu,G., Locke,K., Macdonald,P., Marquis,N.,

McCarthy,M., McEwan,P., McGurk,A., McKernan,K., McPheeters,R.,

Meldrim,J., Meneus,L., Mihova,T., Miranda,C., Mlenga,V., Morrow,J.,

Murphy,T., Naylor,J., Norman,C.H., O'Connor,K., O'Donnell,P.,

O'Neill,D., Oliver,T.M., Oliver,J., Peterson,T., Pierre,N.,

Pisani,C., Pollara,Y., Raymond,C., Riley,R., Rogov,P., Rothman,D.,

Roy,A., Santos,R., Schauer,S., Severy,P., Spencer,B.,

Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,

Tesfaye,S., Theodore,J., Tirtell,A., Travers,M., Trigilio,J.,

TITLE

JOURNAL

COMMENT

Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J.,
 Young,G., Zainoun,J., Zimmer,A. and Zody,M.

Direct Submission
 Submitted (08-MAR-2000) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA

On Mar 25, 2000 this sequence version replaced gi:7210017.
 All repeats were identified using RepeatMasker:

Smit, A.F.A. & Green, P. (1996-1997)
 http://ftp.genome.washington.edu/RM/RepeatMasker.html

----- Genome Center
 Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIBR
 Web site: http://www-seq.wi.mit.edu

Contact: sequence_submissions@genome.wi.mit.edu
 ----- Project Information

Center project name: L6686
 Center clone name: 451_H_23

----- Summary Statistics
 Sequencing vector: M13; M77815; 100% of reads

Chemistry: Dye-terminator Big Dye; 100% of reads
 Assembly program: Phrap; version 0.960731

Consensus quality: 150422 bases at least Q40
 Consensus quality: 159524 bases at least Q30

Consensus quality: 163013 bases at least Q20
 Insert size: 165247; sum-of-contigs

Quality coverage: 3.6 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently
 * consists of 32 contigs. The true order of the pieces
 * is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

1 1389: contig of 1389 bp in length
 * 1390 1489: gap of 100 bp

* 1490 3130: contig of 1641 bp in length
 * 3131 3230: gap of 100 bp

* 3231 4942: contig of 1712 bp in length
 * 4943 5042: gap of 100 bp

* 5043 6981: contig of 1939 bp in length
 * 6982 7081: gap of 100 bp

* 7082 8708: contig of 1627 bp in length
 * 8709 8808: gap of 100 bp

* 8809 10286: contig of 1478 bp in length
 * 10287 10386: gap of 100 bp

* 10387 12212: contig of 1826 bp in length
 * 12213 12312: gap of 100 bp

* 12313 14658: contig of 2346 bp in length
 * 14659 14758: gap of 100 bp

* 14759 17941: contig of 3183 bp in length
 * 17942 18041: gap of 100 bp

* 18042 21297: contig of 3256 bp in length
 * 21298 21397: gap of 100 bp

* 21398 24992: contig of 3595 bp in length
 * 24993 25092: gap of 100 bp

* 25093 27768: contig of 2676 bp in length
 * 27769 27868: gap of 100 bp

* 27869 31188: contig of 3320 bp in length
 * 31189 31288: gap of 100 bp

* 31289 33714: contig of 2426 bp in length
 * 33715 33814: gap of 100 bp

* 33815 37277: contig of 3463 bp in length
 * 37278 37377: gap of 100 bp

* 37378 42302: contig of 4925 bp in length
 * 42303 42402: gap of 100 bp

* 42403 47816: contig of 5414 bp in length
 * 47817 47916: gap of 100 bp

* 47917 52586: contig of 4670 bp in length
 * 52587 52686: gap of 100 bp

* 52687 56567: contig of 3881 bp in length
 * 56568 56667: gap of 100 bp

FEATURES
source
* 56668 61557: contig of 4890 bp in length
* 61558 61657: gap of 100 bp
* 61658 66724: contig of 5067 bp in length
* 66725 66824: gap of 100 bp
* 66825 71568: contig of 4744 bp in length
* 71569 71668: gap of 100 bp
* 71669 76578: contig of 4910 bp in length
* 76579 76678: gap of 100 bp
* 76679 83312: contig of 6634 bp in length
* 83313 83412: gap of 100 bp
* 83413 90053: contig of 6641 bp in length
* 90054 90153: gap of 100 bp
* 90154 99426: contig of 9273 bp in length
* 99427 99526: gap of 100 bp
* 99527 108015: contig of 8489 bp in length
* 108016 108115: gap of 100 bp
* 108116 118144: contig of 10029 bp in length
* 118145 118244: gap of 100 bp
* 118245 130468: contig of 12224 bp in length
* 130469 130568: gap of 100 bp
* 130569 142239: contig of 11671 bp in length
* 142240 142339: gap of 100 bp
* 142340 157135: contig of 14796 bp in length
* 157136 157235: gap of 100 bp
* 157236 168347: contig of 11112 bp in length.
Location/Qualifiers
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="5"
/map="5"
/clone_lib="RPCI-11 Human Male BAC"
1. .1389
/note="assembly_fragment"
misc_feature
1490. .3130
/note="assembly_fragment"
misc_feature
3231. .4942
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5043. .6981
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42403. .47816
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misc_feature 118245. .130468
/note="assembly_fragment"
misc_feature 130569. .142239
/note="assembly_fragment"
Query Match 24.0%; Score 113; DB 2; Length 168347;
Best Local Similarity 100.0%; Pred No. 2.3e-54;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 196 gccggcgctgccctgaagtgtgctcttgggggtctctctgagatctctctcggg 308
|||||
Db 41551 GCCCGGCTGCCCTGAAGTGTGATGCCCTCGAACATCTTCGACAAAGGTGTACACACG 41610
|||||
QY 256 cagagtgcctgtgtctcttgggggtctctctgagatctctctcggg 308
|||||
Db 41611 CAGAGTACGCTGTGCTCTTGGGGTGTCTCTCGGAGATCTTCTCTCTGGG 41663
|||||
RESULT 14
AC106813 173341 bp DNA linear HTG 25-JAN-2002
LOCATION Homo sapiens chromosome 5 clone RP11-586L9, WORKING DRAFT SEQUENCE,
DEFINITION 7 unordered pieces.
ACCESSION AC106813
VERSION AC106813.2 GI:18369924
KEYWORDS HTG: HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 173341)
AUTHORS DOE Joint Genome Institute.
TITLE Sequencing of Human Chromosome 5
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 173341)
AUTHORS DOE Joint Genome Institute.
TITLE Direct Submission
JOURNAL Submitted (12-JAN-2002) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
On Jan 25, 2002 this sequence version replaced gi:18139363.
COMMENT
-----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: <http://www.jgi.doe.gov>

Project Information
Center Project Name: 1519801
Center clone name: RPCI-11_586L9

Summary Statistics
Consensus quality: 164442 bases at least Q40
Consensus quality: 167261 bases at least Q30
Consensus quality: 167771 bases at least Q20
Estimated insert size: 186250; agarose-fp estimation
Estimated insert size: 172741; sum-of-contigs estimation
Quality coverage: 10.29 in Q20 bases; agarose-fp estimation
Quality coverage: 11.1 in Q20 bases; sum-of-contigs estimation.

Oy 98 ggaacattctgtcgtggaagcagcgtggtgaagatctgtgacttttgcccttaccgccggg 157
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Db 30 GGAACATTTCTGCTGCGAAGACGACGCGTGAAGATCTGTGACTTTGGCCTTGCCCGGG 89
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Oy 158 acatctacaaagacc 173
|||||
Db 90 ACATCTACAAGACCC 105
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RESULT 17
MUSRTKA
LOCUS MUSRTKA 5284 bp mRNA linear ROD 09-AUG-1993
DEFINITION Mus musculus receptor tyrosine kinase (FLT4) mRNA, complete cds.
ACCESSION L07296
VERSION L07296.1 GI:293780
KEYWORDS receptor protein tyrosine kinase.
SOURCE Mus musculus (strain C57BL/6J, sub_species domesticus) cDNA to
mRNA.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 5284)
AUTHORS Finnerty,H., Kelleher,K., Morris,G.E., Bean,K., Merberg,D.M.,
Kriz,R., Morris,J.C., Sookdeo,H., Turner,K.J. and Wood,C.R.
TITLE Molecular cloning of murine FLT and FLT4
JOURNAL Oncogene 8, 2293-2298 (1993)
MEDLINE 93330572
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source Location/Qualifiers
1..5284
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/db_xref="taxon:10090"
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45..4136
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KWPPERSQOQTHTELSLTITHNVSQNDLGPYCEANNQIRFRESTEVIIVHEKPFIS
VEMLKGPVLEATAGDELVKLPVLAAYPPPEFQWYKDKAVTGRNHPHALVKEVTEA
SAGVYTLALNNSAAGLRONISLELVNVPVPHIHEKEASSPSIYSRHSROTUTCTAGVT
EFVECKNTYSKLVIQDANVSNMYKCVVNVKGDERLIYFYVTIIPDGFSESEPE
DPLEGQSVRLSCRADNYTYEHLRWTLNLSTLHDAQGNPLLDCKNNHLFATPLEANL
EEAEPGRHATLSLNIIPRAVEDGDEGVYVODRRSQDKHKKYLSVQALEAPRLTQ
NLDLLVNSDSLEMRCPVAGHPVSIWYKDRLEKESGIDLADSNQRLSIQVRRE
EDAGRYLCVSNKAGVSSASVAVEGDEKSGMEIVILIGTVIAVFFVLLLLIFC
NKRPAHADIKTGYLSIIMDPEVPLEQCEVLSYDASOWEFPFRHLGLVGLGHGAF
CKVNFSAFGLNKSSCDTVAKMLKCATASEHRAIMSELKILIHGNHLNVNLLG
ACTPENGPLMWIVECKYGNLSNELRVKEDTFNPYAEKSPQERFRFAMVSGAKADR
RPGSDRALFTRLMGKSARAPLVQAEIDLWLSPLTWEDLVICYSFQVARGMFLAS
RKC1HRDLAARNILLESDEIVIKCDFGLARDIYKDPDYVRKGSARLPLKWAPESIFD
KYVTTQSDVSWFGVLLWEIFSLGASPYPGVQINEEFCQRLKDGTRMRAPELATPAIRH
IMQSCWSDPKARPAFSDLVETIIGDLLOGQWQEEEREMALHSQSSEEDGFQMAST
TALH1TEADADSPSPMHSCHSLAARYNCVSPGRLARGTKTPGSSRMKTFEELPMTP
TTYKASMDNOTDSGMVLASEEERFELESRRPREGSFSCKPGQHMDIPRGHPDPQGRRR
RPTQAGCGKVFYNNHEYGEVSQPTGEGCCPSAGSTFFADSSY"

BASE COUNT 1221 a 1533 c 1466 g 1064 t

Query Match 6.6%; Score 31; DB 10; Length 5284;
Best Local Similarity 100.0%; Pred. No. 1.8e-06;

Matches 31; Conservative 0; Mismatches 0; Indels 0; Caps 0;
Oy 331 cagatcaatgaggaggttcttccagcggctga 361
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Db 3399 CAGATCAATGAGGAGTTCCTCCACGGGCTGA 3429
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RESULT 18
AL646088 260266 bp DNA linear HTG 30-JAN-2002
LOCUS Mus musculus chromosome 11 clone RP23-58E13, *** SEQUENCING IN
DEFINITION PROGRESS ***, in unordered pieces.
ACCESSION AL646088
VERSION AL646088.11 GI:18476932
KEYWORDS HTG; HTGS_PHASE1; HTGS_ACTIVEFIN; HTGS_DRAFT; HTGS_FULLLTOP.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (sites)
AUTHORS Clark,S
TITLE Direct Submission
JOURNAL Submitted (28-JAN-2002) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Feb 1, 2002 this sequence version replaced gi:18151535.
COMMENT ----- Genome Center
Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
----- Project Information
Center project name: BW58E13
----- Summary Statistics
Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid; L08752; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality: 258539 bases at least Q40
Consensus quality: 258926 bases at least Q30
Consensus quality: 259227 bases at least Q20
Insert size: 259766; sum-of-contigs
Insert size: 225486; 6.3% error; agarose-fp
Quality coverage: 9.68x in Q20 bases; sum-of-contigs Quality
coverage: 11.43x in Q20 bases; agarose-fp

* NOTE: This is a 'working draft' sequence.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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1..8902
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fragment_chain:1"
9003..87162
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87263..123670
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123771..188404
/note="assembly_fragment:00429"
188505..214152
/note="assembly_fragment:05868"
214253..260266
/note="assembly_fragment:05872"
BASE COUNT 80139 a 55470 c 56089 g 68066 t 502 others
ORIGIN

/product="SEA protein (oncogene)"

LTR

2016..2338

/note="3' LTR"

BASE COUNT 564 a 659 c 757 g 558 t

ORIGIN 1 bp upstream of HindIII site.

Query Match 4.9% Score 23; DB 14; Length 2538;

Best Local Similarity 100.0%; Pred. NO. 0.084;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 262 gacgtgtggtcctttggggtgct 284

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Db 1417 GACGTGTGCTCCTTTGGGTGCT 1439

Search completed: July 15, 2002, 23:28:07

Job time: 24540 sec

Query Match 6.6%; Score 31; DB 2; Length 260266;
Best Local Similarity 100.0%; Pred. No. 1.7e-06;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 331 cagatcaatgaggaattctgccagcgctga 361
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Db 168147 CAGATCAATGAGGAGTCTGCCAGCGCTGA 168177

RESULT 19
LOCUS AB017155 534 bp mRNA linear MAM 02-APR-1999
DEFINITION Oryctolagus cuniculus mRNA for VEGF receptor-2/Flk-1, partial cds.
ACCESSION AB017155
VERSION AB017155.1 GI:4586885
KEYWORDS VEGF receptor-2/Flk-1.
SOURCE Oryctolagus cuniculus (strain:Japanese white) liver cDNA to mRNA.
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
REFERENCE 1 (bases 1 to 534)
AUTHORS Umeki,K., Kon,K. and Ohtaki,S.
TITLE Rabbit mRNA for vascular endothelial growth factor (VEGF) receptor-2/Flk-1, partial cds
JOURNAL Published Only in Database (1999) In press
AUTHORS 2 (bases 1 to 534)
TITLE Umeki,K., Kon,K. and Ohtaki,S.
JOURNAL Direct Submission
AUTHORS Submitted (26-AUG-1998) Kazumi Umeki, Miyazaki Medical College,
TITLE Department of Laboratory Medicine; Kihara 5200, Kiyotake, Miyazaki
889-1692, Japan (E-mail:umeki@post1.miyazaki-med.ac.jp,
Tel:+81-985-85-9400, Fax:+81-985-85-4709)

FEATURES
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BASE COUNT 128 a 132 c 156 g 118 t
ORIGIN

Query Match 5.9%; Score 28; DB 4; Length 534;
Best Local Similarity 100.0%; Pred. No. 0.0001;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 122 acgtggtgaagactctgactttggcct 149
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Db 65 ACCTGCTGAAGATCTGTGACTTTGGCCT 92

RESULT 20
LOCUS XELXFGFRA2 2753 bp mRNA linear VRT 28-APR-1993
DEFINITION Xenopus laevis fibroblast growth factor receptor mRNA, complete cds.
ACCESSION M62322
VERSION M62322.1 GI:214899
KEYWORDS fibroblast growth factor receptor; tyrosine kinase receptor.
SOURCE X.laevis, cDNA to mRNA.
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae; Pipidae; Xenopodinae; Xenopus.
REFERENCE 1 (bases 1 to 2753)
AUTHORS Friesel,R.E. and David,I.B.
TITLE cDNA cloning and developmental expression of fibroblast growth factor receptors from Xenopus laevis
JOURNAL Mol. Cell. Biol. 11, 2481-2488 (1991)
MEDLINE 91203867
FEATURES
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CAYOVARGMDYLSKSKCIHRDLAARNVLLVEDNIMKTADFERLARDIHIHDIYKKTNG
RLPYKMAPEALFDRIYTHQSDVMSFGVLLWEITFGGSPYGPVPMEEFLKLLKEGHR
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154..216
/gene="XFGFRA2"
217..2325
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/product="fibroblast growth factor receptor"
BASE COUNT 740 a 672 c 635 g 706 t
ORIGIN

sig_peptide 154..216
mat_peptide 217..2325

Query Match 5.7%; Score 27; DB 5; Length 2753;
Best Local Similarity 100.0%; Pred. No. 0.00039;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 69 aaagtgcacacagacacgtggctgc 95
|||||
Db 1722 AAAGTGCATCCACAGACCTGGCTGC 1748

RESULT 21
LOCUS XLU24491 3634 bp mRNA linear VRT 02-FEB-1996
DEFINITION Xenopus laevis fibroblast growth factor receptor-1 mRNA, complete cds.
ACCESSION U24491 M61687 M37201
VERSION U24491.1 GI:857677
KEYWORDS
SOURCE African clawed frog.
ORGANISM Xenopus laevis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
Xenopodinae; Xenopus.
REFERENCE 1 (bases 1 to 2439)
AUTHORS Musci,T.J., Amaya,E. and Kirschner,M.W.
TITLE Regulation of the fibroblast growth factor receptor in early
Xenopus embryos
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 87 (21), 8365-8369 (1990)
MEDLINE 91045998
REFERENCE 2 (bases 2440 to 3634)
AUTHORS Robbie,E.P., Peterson,M., Amaya,E. and Musci,T.J.
TITLE Temporal regulation of the Xenopus FGF receptor in development: a

translation inhibitory element in the 3' untranslated region
 Development 121 (6), 1775-1785 (1995)
 95324403
 3 (bases 1 to 3634)
 Musci.T.J.
 Direct Submission
 Submitted (11-APR-1995) Thomas J. Musci, Dept. of OB/GYN,
 University of California, San Francisco, Box 0556, San Francisco,
 CA 94143, USA
 On Jun 12, 1995 this sequence version replaced gi:214137.

Location/Qualifiers
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 YTCLAANSIGISHSASLWJVLKVEDNKPALLASPLETIIIVCTGAAPYSAMVVTTII
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 LRARRPPAMEYCYNPTCPVDQLLSFKDLVSCAYOAVGMDYLASKKCIHRDLAARNVL
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 2440. .2619
 /note="translational inhibitory regulatory element
 contained within the 3' UTR"

BASE COUNT 1015 a 827 c 806 g 986 t
 ORIGIN

3'UTR
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Query Match 5.7%; Score 27; DB 5; Length 3634;
 Best Local Similarity 100.0%; Pred. No. 0.00039;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 69 aagtgcatcacagagacctggctgc 95
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 Db 1833 AAAGTGCATCACAGACCTGGCTGC 1859

RESULT 22
 XELX1FGFR
 LOCUS
 DEFINITION
 XELX1FGFR 3815 bp mRNA linear VRT 28-APR-1993
 Xenopus laevis fibroblast growth factor receptor mRNA, complete
 cds.

ACCESSION M55163
 VERSION M55163.1 GI:214893
 KEYWORDS fibroblast growth factor receptor.
 SOURCE Xenopus laevis XTC cell line, cDNA to mRNA.
 ORGANISM Xenopus laevis
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
 Xenopodinae; Xenopus.
 1 (bases 1 to 3815)
 Friesel,R.E. and Dawid,I.B.
 cDNA cloning and developmental expression of fibroblast growth
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 Mol. Cell. Biol. 11, 2481-2488 (1991)
 91203867 Location/Qualifiers
 1. .3815
 /organism="Xenopus laevis"

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137..199
mat_peptide
200..2578
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/product="fibroblast growth factor receptor"
BASE COUNT 1030 a 879 c 881 g 1025 t
ORIGIN

Query Match 5.7% Score 27; DB 5; Length 3815;
Best Local Similarity 100.0%; Pred. No. 0.00039;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 69 aaagtgcacacagagacctgctgc 95
|||||
Db 1975 AAAGTCATCCACAGACCTGCTGC 2001

RESULT 23
AF402786
LOCUS
DEFINITION
Rattus norvegicus receptor tyrosine kinase VEGFR-3kt (Vegfr3) mRNA,
complete cds, alternatively spliced.
AF402786
AF402786.1 GI:16033529
Norway rat.
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE
1 (bases 1 to 4254)
Krisnan,J. and Sleeman,J.P.
Characterization of a novel alternatively spliced form of VEGFR-3
Unpublished
REFERENCE
2 (bases 1 to 4254)
Krisnan,J. and Sleeman,J.P.
Direct Submission
Submitted (25-JUL-2001) Institut fuer Toxikologie und Genetik,
Forschungszentrum Karlsruhe, Postfach 3640, Karlsruhe 76021,
Germany
FEATURES
source
1..4254
/organism="Rattus norvegicus"
/strain="Sprague-Dawley"
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alternatively spliced"
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/ product="receptor tyrosine kinase VEGFR-3kt"
/ db_xref="GI:16033530"
/ translation="MOPGAALNRRLWLCGLGLOGLANGYSWTPPTLNITEDSYVIDTG
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BASE COUNT 989 a 1236 c 1224 g 805 t
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Query Match 5.7%; Score 27; DB 10; Length 4254;
Best Local Similarity 100.0%; Pred. No. 0.00039;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 79 cacagagacctggctgctcggaacatt 105
|||||
Db 3103 CACAGAGACCTGGCTGCTCGGAACATT 3129
RESULT 24
AF402785 4360 bp mRNA linear ROD 11-OCT-2001
LOCUS Rattus norvegicus receptor tyrosine kinase VEGFR-3 (vegfr3) mRNA,
DEFINITION complete cds, alternatively spliced.
ACCESSION AF402785
VERSION AF402785.1 GI:16033526
KEYWORDS Norway rat.
SOURCE Rattus norvegicus
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE
1 (bases 1 to 4360)
Krishnan,J. and Sleeman,J.P.
Characterization of a novel alternatively spliced form of VEGFR-3
Unpublished
REFERENCE
2 (bases 1 to 4360)
Krishnan,J. and Sleeman,J.P.
Direct Submission
Submitted (25-JUL-2001) Institut fuer Toxikologie und Genetik,
Forschungszentrum Karlsruhe, Postfach 3640, Karlsruhe 76021,
Germany
FEATURES
Location/Qualifiers
1. 4360
/organism="Rattus norvegicus"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
1..4360
/ gene="vegfr3"
1..4092
/ gene="vegfr3"
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/note="VEGFR-3 long form; activated by VEGF-C and VEGF-D;
alternatively spliced"
/ codon_start=1
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/ protein_id="AAL13269.1"
/ db_xref="GI:16033527"
/ translation="MOPGAALNRRLWLCGLGLOGLANGYSWTPPTLNITEDSYVIDTG
DSLISCRGHPLEWTRGAQEVLTITGGKSEDTQVVDCEGTEARPYCKVLSLAQTH
ANNTGSYCYKYIKARIEGTTAASTYVVRDFEQPINAKPTDLLNVRKDSMWVPCLV
SIPGLNITLRSSQSVLHPDGOEVLDDRRGMRVPTLLLRDALYLQCEETWGDODFLSN
PFLVHITGNELYDIQLYPKKSLELLVGEKLVNCTVMAEFDGVTFDMDYPGKOAERA
KWPERSOOTHTELSLITLHNVSQHDLPYVCEANNGIQQFRESTEVIIVHEKPFIS
VENLKGVPLEATAGDEMVKLPVLAAPPEFQWKDKKAVTGRHNPALVLEKVEA
SAGVYTTALNWSAAGLRONTISLELVNVPPIHEKEASSPSIYSRHSROTLCCTYGV
POPUSVQWHRPMTPTCKTFAQRSLRRQRQDMPQCRDKWEVTTQDAVNPIESLDWT
ESVEGKNKTVSKLVIQDANVSAMTKCVFNKVGQDERLIYFYVTIPDGFSIESEPE
DPLEGQSVRLSCRADNTYEHURWYRLNLSLTHDAQGNPLLLDCKNVHLFATPLEANL
EAEAPGARHATLSLNIIPVAPEDGDDYCEVQDRRSQDKHCKKYLVSQALFAPRLTQ
NLTDLNVRVTSLEMRCPVAGAHVPSIWKYKDERLLEKESGIDLADSNQRLSIORVRE
EDAGRYLCSVNAKGCNVSSAVAGESEDKGSMEIVLIGTGVIAVFFVWVLLLIIFC
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RLGSTDRALTRFLMGKSARRAPVQOEADLWLSPLTMEDLVCSYQVARGMEFLAS
KVYTTOSDVMSFGVLLWEIFSLGASYPYGVQINEEFCORLKDCTRMKHAPELATPIRH
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BASE COUNT 1008 a 1260 c 1259 g 833 t
ORIGIN
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Best Local Similarity 100.0%; Pred. No. 0.00039;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 79 cacagagacctggctgctcggaacatt 105
|||||
Db 3103 CACAGAGACCTGGCTGCTCGGAACATT 3129
RESULT 25
AC098957/c 161580 bp DNA linear HTG 20-DEC-2001
LOCUS Rattus norvegicus clone CH230-193G14, *** SEQUENCING IN PROGRESS
DEFINITION ***; 75 unordered clones.
ACCESSION AC098957
VERSION AC098957.2 GI:17973745
KEYWORDS HTG; HTGS, PHASE1.
SOURCE Norway rat.
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE
1 (bases 1 to 161580)
Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-Osman,F.R., Allen,C.,
Alsbrooks,S.L., Amaratunga,H.C., Are,J.R., Banks,T., Barbara,J.,
Benton,J., Bimage,K., Blankenbury,K., Bonnin,D., Bouck,J.,
Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P., Buhay,C.,
Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C., Carron,T.F.,
Carter,M., Cavazos,S.R., Chacko,J., Chavez,D., Chen,G., Chen,R.,
Chen,Z., Chowdhry,I., Christopoulos,C., Cleveland,C.D., Cox,C.,
Coyle,M.D., Dathorne,S.R., David,R., Davila,M.L., Davis,C.,
Davy-Carroll,L., Dederich,D.A., Delaney,K.R., Delgado,O.,
Denn,A.L., Ding,Y., Dinh,H.H., Douthwaite,K.J., Draper,H.,
Dugan-Rocha,S., Durbin,K.J., Earnhart,C., Edgar,D., Edwards,C.C.,
Elhaj,C., Escotto,M., Falls,T., Ferraguto,D., Flagg,N., Ford,J.,
Foster,P., Frantz,P., Gabisi,A., Gao,J., Garcia,A., Garner,T.,
Garza,N., Gill,R., Gorrell,J.H., Guevara,W., Gunaratne,P., Hale,S.,
Hamilton,K., Harris,C., Harris,K., Hart,M., Havlak,P., Hawes,A.,
Hernandez,J., Hernandez,O., Hodgson,A., Hogues,M., Holloway,C.,
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Hollins, B., Homs, F., Howard, S., Huber, J., Hulyk, S., Hume, J.,
 Jackson, L. E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S.,
 Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, R., Korvah, J.,
 Kovar, C., Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L. C.,
 Lewis, L., Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W.,
 Loulseghe, H., Lozado, R. J., Lu, X., Lucier, A., Lucier, R., Luna, R.,
 Ma, J., Maheshwari, M., Mapua, P., Martin, R., Martindale, A.,
 Martinez, E., Massey, E., Mawhney, E., McLeod, M. P., Meador, M.,
 Mel, G., Metzker, M., Miner, G., Miner, Z., Mitchell, T., Mohabbat, K.,
 Morgan, M., Morris, S., Moser, M., Neal, D., Newton, J., Newton, N.,
 Nguyen, A., Nguyen, N., Nguyen, N., Nickerson, E., Nwokenkwo, S.,
 Ogulu, M., Okwuonu, G., Otaguay, N., Oviedo, R., Pace, A., Payton, B.,
 Peery, J., Perez, L., Peters, L., Pickens, R., Primus, E., Pu, L. L.,
 Quiles, M., Ren, Y., Rives, M., Rojas, A., Rojibokan, I., Rolfe, M.,
 Ruiz, S., Savary, G., Scherer, S., Scott, G., Shen, H., Shooshtari, N.,
 Stinson, I., Sodergren, E., Sonaik, T., Sparks, A., Stanley, H.,
 Stone, H., Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K.,
 Tang, H., Tansey, J., Taylor, C., Taylor, T., Telford, B., Thomas, N.,
 Thomas, S., Usmani, K., Vasquez, L., Vera, V., Villalón, D., Vinson, R.,
 Wall, R., Wang, S., Ward-Moore, S., Warren, R., Washington, C.,
 Watlington, S., Williams, G., Williamson, A., Wleczek, R., Wooden, S.,
 Worley, K., Wu, C., Wu, Y., Wu, Y. F., Zhou, J., Zorrilla, S., Nelson, D.,
 Weinstein, G., and Gibbs, R.
 Direct Submission
 Unpublished
 2 (bases 1 to 161580)
 Worley, K. C.
 Direct Submission
 Submitted (07-NOV-2001) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 On Dec 20, 2001 this sequence version replaced gi:16756151.
 ----- Genome Center
 Center: Baylor College of Medicine
 Center code: BCM
 Web site: <http://www.hgsc.bcm.tmc.edu/>
 Contact: hgsc-help@bcm.tmc.edu
 ----- Project Information
 Center project name: GJBR
 Center clone name: CH230-193G14
 ----- Summary Statistics
 Assembly program: Phrap; version 0.990329First call to
 findPhrapList
 Consensus quality: 121539 bases at least Q40
 Consensus quality: 129496 bases at least Q30
 Consensus quality: 136265 bases at least Q20
 Estimated insert size: 111412; sum-of-contigs estimation
 Quality coverage: 0x in Q20 bases; agarose-fp estimation
 Quality coverage: 1.5x in Q20 bases; sum-of-contigs estimation

 * NOTE: Estimated insert size may differ from sequence length
 (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 75 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.
 *
 * 1 5831: contig of 5831 bp in length
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 * 16896 16995: gap of unknown length
 * 16996 21784: contig of 4789 bp in length
 * 21785 21884: gap of unknown length
 * 21885 25354: contig of 3470 bp in length
 * 25355 25454: gap of unknown length
 * 25455 29460: contig of 4006 bp in length
 * 29461 29560: gap of unknown length
 * 29561 32307: contig of 2747 bp in length

32407: gap of unknown length
 35343: contig of 2936 bp in length
 35344 35443: gap of unknown length
 38216: contig of 2773 bp in length
 38316: gap of unknown length
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 43959: contig of 2676 bp in length
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 47385: gap of unknown length
 50539: contig of 3154 bp in length
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 54376: gap of unknown length
 57920: contig of 3544 bp in length
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 62900: contig of 2295 bp in length
 63000: gap of unknown length
 64914: contig of 1914 bp in length
 65014: gap of unknown length
 67533: contig of 2519 bp in length
 67633: gap of unknown length
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 70877: gap of unknown length
 73509: contig of 2632 bp in length
 73609: gap of unknown length
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 78450: contig of 2294 bp in length
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 80050: contig of 1500 bp in length
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 87906: gap of unknown length
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 99145: contig of 1649 bp in length
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 104468: contig of 1413 bp in length
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 108692: gap of unknown length
 110626: contig of 1835 bp in length
 110726: gap of unknown length
 111801: contig of 1075 bp in length
 111901: gap of unknown length
 113358: contig of 1457 bp in length
 113458: gap of unknown length
 114629: contig of 1171 bp in length
 114729: gap of unknown length

TITLE
 JOURNAL
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL

COMMENT

* 114730 116364: contig of 1635 bp in length
* 116365 116464: gap of unknown length
* 116465 118200: contig of 1736 bp in length
* 118201 118300: gap of unknown length
* 118301 119530: contig of 1230 bp in length
* 119531 119630: gap of unknown length
* 119631 121318: contig of 1688 bp in length
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* 121419 122620: contig of 1202 bp in length
* 122621 122720: gap of unknown length
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* 126160 126259: gap of unknown length
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* 133295 133394: gap of unknown length
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* 136003 136102: gap of unknown length

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Best Local Similarity 100.0%; Pred. No. 0.00038;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 25724 CACAGAGACTGGCTGCTCGGAACATT 25698

RESULT 26
MMAPK42
LOCUS Mouse MAPK mRNA for mitogen-activated protein kinase (p42). 1256 bp mRNA linear ROD 02-FEB-1999
DEFINITION X58712
ACCESSION X58712
VERSION X58712.1 GI:53001
KEYWORDS mitogen-activated protein kinase; protein kinase.
SOURCE house mouse.
ORGANISM Mus musculus.
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 1256)
Her.J.H.
Direct Submission
Submitted (03-APR-1991) J.H. Her, University of Virginia, Dept of Microbiology and, Cancer Center Box 441, School of Medicine, Charlottesville VA 22908, USA
2 (bases 1 to 1256)
Her,J.H., Wu,J., Rall,T.B., Sturgill,T.W. and Weber,M.J.
Sequence of pp42/MAP kinase, a serine/threonine kinase regulated by tyrosine phosphorylation
Nucleic Acids Res. 19 (13), 3743 (1991)
91305126
Location/Qualifiers
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LKICDFGLARVADPDHDTGFLTEVATRWYRAPEIMLSKNGYTKSIDINSGVGCILAE
MLSNRP1FPGCKHYLDOLNHLILGILGSPQEDLNCIINLKARNYLLSLPHKNKVPWNRLL
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ORIGIN

Query Match 5.5%; Score 26; DB 10; Length 1256;
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Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 130 aagatctgtgacttggccttgcccg 155
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Db 502 AAGATCTGTGACTTTGGCCTTGCCCG 527

RESULT 27
AR016532
LOCUS AR016532 1467 bp DNA linear PAT 05-DEC-1998
DEFINITION Sequence 3 from patent US 5776751.
ACCESSION AR016532
VERSION AR016532.1 GI:3972809
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1467)
AUTHORS Boulton,T.G., Cobb,M.H., Yancopoulos,G.D., Nye,S. and Panayotatos,N.
TITLE Family of MAP2 protein kinases
JOURNAL Patent: US 5776751-A 3 07-JUL-1998;
FEATURES Location/Qualifiers
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source
BASE COUNT 365 a 382 c 355 g 365 t
ORIGIN

Query Match 5.5%; Score 26; DB 6; Length 1467;
Best Local Similarity 100.0%; Pred. No. 0.0015;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 655 AAGATCTGTGACTTTGGCCTTGCCCG 680

RESULT 28
AR036245
LOCUS AR036245 1467 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 3 from patent US 5872006.
ACCESSION AR036245
VERSION AR036245.1 GI:5952913
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1467)
AUTHORS Boulton,T.G., Cobb,M.H., Yancopoulos,G.D., Nye,S. and Panayotatos,N.
TITLE Family of MAP2 protein kinases
JOURNAL Patent: US 5872006-A 3 16-FEB-1999;

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FEATURES
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ORIGIN

Query Match      5.5%; Score 26; DB 6; Length 1467;
Best Local Similarity 100.0%; Pred. No. 0.0015;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 655 AAGATCTGTGACTTTGGCCTTGCCCG 680

RESULT 31
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LOCUS      I34200      1467 bp      DNA      linear      PAT 06-FEB-1997
DEFINITION Sequence 3 from patent US 5595904.
ACCESSION  I34200
VERSION    I34200.1 GI:1824991
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 1467)
AUTHORS   Boulton,T.G., Cobb,M.H., Yancopoulos,G.D., Nye,S. and
Panayotatos,N.
TITLE     Family of map2 protein kinases
JOURNAL   Patent: US 5595904-A 3 21-JAN-1997;
FEATURES   Location/Qualifiers
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           source      /organism="unknown"
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Query Match      5.5%; Score 26; DB 6; Length 1467;
Best Local Similarity 100.0%; Pred. No. 0.0015;
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RESULT 32
RATERK2
LOCUS      Rat extracellular signal-related kinase (ERK2) mRNA      ROD 27-APR-1993
DEFINITION M64300
ACCESSION  M64300
VERSION    M64300.1 GI:204055
KEYWORDS   extracellular signal-related kinase; protein kinase; protein
serine/threonine kinase.
SOURCE     Rat adult brain, cDNA to mRNA.
ORGANISM   Rattus norvegicus
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
           Rattus.
REFERENCE  1 (bases 1 to 1467)
AUTHORS   Boulton,T.G., Nye,S.H., Robbins,D.J., Ip,N.Y., Radziejewska,E.,
Morgenbesser,S.D., Depinho,R.A., Panayotatos,N., Cobb,M.H. and
Yancopoulos,G.D.
TITLE     ERKs: A family of protein-serine/threonine kinases that are
activated and tyrosine phosphorylated in response to insulin and
NGF
JOURNAL   Cell 65, 663-675 (1991)
MEDLINE   91235302
FEATURES   Location/Qualifiers
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Qy 130 aagatctgtgactttggccttgcccg 155
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Db 655 AAGATCTGTGACTTTGGCCTTGCCCG 680

RESULT 30
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LOCUS      AR172792      1467 bp      DNA      linear      PAT 17-DEC-2001
DEFINITION Sequence 3 from patent US 6303358.
ACCESSION  AR172792
VERSION    AR172792.1 GI:17912283
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 1467)
AUTHORS   Boulton,T.G., Cobb,M.H., Yancopoulos,G.D., Nye,S. and
Panayotatos,N.
TITLE     ERK3 MAP2 protein kinase
JOURNAL   Patent: US 6303358-A 3 16-OCT-2001;
FEATURES   Location/Qualifiers
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           /organism="unknown"
BASE COUNT 365 a 382 c 355 g 365 t
ORIGIN

Query Match      5.5%; Score 26; DB 6; Length 1467;
Best Local Similarity 100.0%; Pred. No. 0.0015;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 130 aagatctgtgactttggccttgcccg 155
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QDLMETDLYKLLKTOHSDNHICYFLYQILRGLKYIHSANLHRLKPSNLLNTTCD
LKICDFGLARVADPDHDTGFLTEYVATRWYRAPEIMLNSKGYTKSIDTWSVCILAE
MLSNRPIFPCKKHVLDOLNHLTGLGSPSOEDLNCIINLKARNYLLSLPHKNKVPWNRLL
FPNADSKALDLDLKMILTFNPHKRIEVEQALAIUPLYEQYYDPSDEPIAEAFKDFMELD
DLPKELKELIFEETARFPQYRS"
BASE COUNT 365 a 382 c 355 g 365 t
ORIGIN

Query Match 5.5%; Score 26; DB 10; Length 1467;
Best Local Similarity 100.0%; Pred. No. 0.0015;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 130 aagatctgtgacttggccttgccg 155
|||||
Db 655 AAGATCTGTGACTTTGGCCTTGCCCG 680
|||||

RESULT 33
LOCUS S65207 1534 bp mRNA linear VRT 02-NOV-1993
DEFINITION endothelial kinase Quek2-vascular endothelial growth factor
receptor homolog [Coturnix coturnix-queals, ssp. japonica, E4
embryo, mRNA Partial, 1534 nt].
ACCESSION S65207
VERSION S65207.1 GI:410682
KEYWORDS common quail E4 embryo ssp. japonica.
SOURCE Coturnix coturnix
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Coturnix.

REFERENCE 1 (bases 1 to 1534)
AUTHORS Eichmann,A., Marcelle,C., Breant,C. and Le Douarin,N.M.
TITLE Two molecules related to the VEGF receptor are expressed in early
endothelial cells during avian embryonic development
JOURNAL Mech. Dev. 42 (1-2), 33-48 (1993)
MEDLINE 93378866
REMARK GenBank staff at the National Library of Medicine created this
entry [NCBI gibbsq 137164] from the original journal article.
This sequence comes from Fig. 2.

FEATURES
source Location/Qualifiers
1..1534
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TFSDLVLEILNLLQENVOOEKDYIPLNDSHSEDGFSQVPSQAQNSDEEDFDHRI
RCHSLAARYNCVSPFCGLTGNOIRCSSRIKTFEFPMTHTMKKAPDNQDTSGMWL
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BASE COUNT 388 a 417 c 389 g 340 t
ORIGIN

Query Match 5.5%; Score 26; DB 5; Length 1534;

Best Local Similarity 100.0%; Pred. No. 0.0015;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 64 tccgaaagtgcacacagagacct 89
|||||
Db 88 TCCCGAAGTGCATCCACAGAGACCT 113
|||||

RESULT 34
MUSERK2
LOCUS MUSERK2 1747 bp mRNA linear ROD 03-FEB-1999
DEFINITION Mouse mRNA for ERK2, complete cds.
ACCESSION D10939
VERSION D10939.1 GI:220994
KEYWORDS ERK2; Ser/Thr kinase.
SOURCE Mus musculus (strain C57 black B6) brain (cell line mouse whole
brain) cDNA to mRNA, clone G1A.

ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 1747)
AUTHORS Takishima,K.
TITLE Direct Submission
JOURNAL Submitted (10-APR-1993) Kunio Takishima, National Defense Medical
College; Namiki 3-2, Tokorozawa, Saitama 359, Japan
(Tel:0429-95-1211(ex.2294), Fax:0429-95-0638)

REFERENCE 2 (bases 1 to 1747)
AUTHORS Her,J.H., Wu,J., Hall,T.B., Sturgill,T.W. and Weber,M.J.
TITLE Sequence of pp42/MAP kinase, a serine/threonine kinase regulated by
tyrosine phosphorylation
JOURNAL Nucleic Acids Res. 19 (13), 3743 (1991)
MEDLINE 91305126
REFERENCE 3 (bases 1 to 1747)
AUTHORS Takishima,K.
TITLE untitled
JOURNAL Unpublished (1992)

COMMENT Submitted (10-Apr-1993) to DDBJ by:
Kunio Takishima
National Defence Medical College
3-2 Namiki
Tokorozawa, Saitama 359
Japan
Phone: 0429-95-1211 x2294
Fax: 0429-95-0638.
Location/Qualifiers
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/cell_line="mouse whole brain"
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MLSNRPIFPCKKHVLDOLNHLTGLGSPSOEDLNCIINLKARNYLLSLPHKNKVPWNRLL
FPNADSKALDLDLKMILTFNPHKRIEVEQALAIUPLYEQYYDPSDEPIAEAFKDFMELD
DLPKELKELIFEETARFPQYRS"
BASE COUNT 502 a 364 c 413 g 468 t
ORIGIN

Query Match 5.5%; Score 26; DB 10; Length 1747;
Best Local Similarity 100.0%; Pred. No. 0.0015;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 130 aagatctgtgacttggccttgccg 155

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Db 544 AAGATCTGACTTTGGCCTTGCCCG 569

RESULT 35
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LOCUS       A84443       1815 bp      DNA      linear      PAT 21-JAN-2000
DEFINITION   Sequence 58 from Patent W09845704.
ACCESSION   A84443
VERSION      A84443.1  GI:67333362
KEYWORDS     .
SOURCE      unidentified.
ORGANISM     unclassified.
REFERENCE    1 (bases 1 to 1815)
AUTHORS      Tullin,S. and Kasper,A.
TITLE        A METHOD FOR EXTRACTING QUANTITATIVE INFORMATION RELATING TO AN
JOURNAL      INFLUENCE ON A CELLULAR RESPONSE
JOURNAL      Patent: WO 9845704-A 58 15-OCT-1998;
FEATURES     TULLIN SOEREN (DK); KASPER ALMHOLT (DK)
SOURCE       Location/Qualifiers
            1..1815
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CDS         1..1815
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            FVSQGEGBGATYKFLKFICTTGKLPVPWPTLTVTLTGYVQCFSRYPDQMKOHDF
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BASE COUNT  480 a 506 c 451 g 378 t
ORIGIN

Query Match      5.5%; Score 26; DB 6; Length 1815;
Best Local Similarity 100.0%; Pred. No. 0.0015;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 130 aagatctgtgactttggccttgcccg 155
|||||
Db 484 AAGATCTGACTTTGGCCTTGCCCG 509

RESULT 36
A84425
LOCUS       A84425       1818 bp      DNA      linear      PAT 21-JAN-2000
DEFINITION   Sequence 40 from Patent W09845704.
ACCESSION   A84425
VERSION      A84425.1  GI:67333344
KEYWORDS     .
SOURCE      unidentified.
ORGANISM     unclassified.
REFERENCE    1 (bases 1 to 1818)
AUTHORS      Tullin,S. and Kasper,A.
TITLE        A METHOD FOR EXTRACTING QUANTITATIVE INFORMATION RELATING TO AN
JOURNAL      INFLUENCE ON A CELLULAR RESPONSE
JOURNAL      Patent: WO 9845704-A 40 15-OCT-1998;
FEATURES     TULLIN SOEREN (DK); KASPER ALMHOLT (DK)
SOURCE       Location/Qualifiers
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TKSIDISVSGCILAEMLSNRPIFPCKHYLDOLNHLITGLGSPSQEDLACIINLKARNY
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BASE COUNT  482 a 505 c 451 g 380 t
ORIGIN

Query Match      5.5%; Score 26; DB 6; Length 1818;
Best Local Similarity 100.0%; Pred. No. 0.0015;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 130 aagatctgtgactttggccttgcccg 155
|||||
Db 1225 AAGATCTGACTTTGGCCTTGCCCG 1250

RESULT 37
CCQUEK2
LOCUS       Ccoturnix Quek2 mRNA for vascular endothelial growth factor
DEFINITION   Ccoturnix Quek2 mRNA for vascular endothelial growth factor
ACCESSION   X83287
VERSION      X83287.1  GI:619865
KEYWORDS     growth factor receptor; Quek2 gene.
SOURCE       common quail.
ORGANISM     Ccoturnix coturnix
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
            Phasianinae; Coturnix.
REFERENCE    1 (bases 1 to 4617)
AUTHORS      Eichmann,A., Marcelle,C., Breat,C. and Le Douarin,N.M.
TITLE        Molecular cloning of Quek 1 and 2, two quail vascular endothelial
JOURNAL      growth factor (VEGF) receptor-like molecules
JOURNAL      Gene 174 (1), 3-8 (1996)
MEDLINE      97017121
REFERENCE    2 (bases 1 to 4617)
AUTHORS      Marcelle,C.A.
TITLE        Direct Submission
JOURNAL      Submitted (02-DEC-1994) C.A. Marcelle, Univ. of California, Irvine.,
            Dept. of Developmental and Cell Biology, Irvine, California 92717,
            USA
FEATURES     Location/Qualifiers
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            /db_xref="SPTREMBL:P79701"
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BASE COUNT 1187 a 1233 c 1241 g 956 t

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mac_peptide

46..135
136..4155

/product="insulin-like growth factor 1 receptor"

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BASE COUNT
ORIGIN

Query Match 5.5%; Score 26; DB 5; Length 4617;
Best Local Similarity 100.0%; Pred. No. 0.0015;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 64 tcccaaaagtcatcacagagacct 89
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Db 3172 TCCCGAAGTGCATCACAGAGACCT 3197

RESULT 38
RATIGIRT
LOCUS Rattus norvegicus insulin-like growth factor 1 receptor mRNA, complete cds.
DEFINITION Rattus norvegicus insulin-like growth factor 1 receptor mRNA, complete cds.
ACCESSION L29232
VERSION L29232.1 GI:460333
KEYWORDS Norway rat.
SOURCE Rattus norvegicus
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

REFERENCE 1 (bases 1 to 4696)
Du,J. and Delafontaine,P.
TITLE Inhibition of vascular smooth muscle cell growth through antisense transcription of a rat insulin-like growth factor I receptor cDNA
JOURNAL Circ. Res. 76 (6), 963-972 (1995)
MEDLINE 95277910
PUBMED 7758167
COMMENT On Mar 15, 1994 this sequence version replaced gi:459940.
FEATURES
Location/Qualifiers
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/db_xref="taxon:10116"
/tissue_type="brain"
/dev_stage="adult"
46..4158
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protein cleavage site, RRRR; bp 2269-4158: beta subunit;
bp 2857-2907: putative trans-membrane domain; bp
3055-3825: putative tyrosine kinase domain; bp 658-838:
cysteine rich domain"

/codon_start=1

/product="insulin-like growth factor 1 receptor precursor"
/protein_id="AAA41392.1"

/db_xref="GI:460334

/translation="MKSGSGSGPTSLWGLVFLSAALSWMPTSGEICGPGIDIRNDYQ
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LTVIRGKFLYENALVIFEMTNLKDICGLYLRNITRGAIIRKNAADLCYLTIDWLSL
CDKASNNYIVGNKPPKPGDLCPTLEEKPMCKTTINNEYNYRWTNRCOKMCPSTV
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Query Match 5.5%; Score 26; DB 10; Length 4696;
Best Local Similarity 100.0%; Pred. No. 0.0015;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 77 tccacagagacctgcgtcgcgaac 102
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Db 3443 TCCACAGAGACCTGCCTCGGAAC 3468

RESULT 39
D87264S4
LOCUS D87264S4 786 bp DNA linear ROD 14-APR-2000
DEFINITION Mus musculus DNA for ERK2, exon 4.
ACCESSION D87267
VERSION D87267.1 GI:2506068
KEYWORDS Erk2; extracellular signal-regulated kinase 2.
SEGMENT 4 of 8
SOURCE Mus musculus DNA.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (sites)
REFERENCE
AUTHORS Sugiyama,N., Suga,T., Ozeki,Y., Mamiya,G. and Takishima,K.
TITLE The mouse extracellular signal-regulated kinase 2 gene. Gene
structure and characterization of the promoter
J. Biol. Chem. 272 (34), 21575-21581 (1997)
JOURNAL
MEDLINE 97407954
REFERENCE 2 (bases 1 to 786)
AUTHORS Takishima,K.
TITLE Direct Submission
Submitted (21-AUG-1996) Kunio Takishima, National Defense Medical
College, Department of Biochemistry I; Namiki 3-2, Tokorozawa,
Saitama 359, Japan (Tel:0429-95-1373, Fax:0429-96-5189)

FEATURES
source Location/Qualifiers
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exon 198..314
/number=4
intron 315..>786
/number=4
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Query Match 5.3%; Score 25; DB 10; Length 786;
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Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 131 agatctgtgacttggccttgcgcg 155
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Db 196 AGATCTGTGACTTTGGCCTTGCCCG 220

RESULT 40
AR062728 159 bp DNA linear PAT 29-SEP-1999
LOCUS
DEFINITION Sequence 19 from patent US 5843749.
ACCESSION AR062728
VERSION AR062728.1 GI:5990419
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 159)
AUTHORS Maisonnier,P.C., Masiakowski,P. and Yancopoulos,G.D.
TITLE Enh and Ror tyrosine kinases
JOURNAL Patent: US 5843749-A 19 01-DEC-1998;
Location/Qualifiers
FEATURES
source 1..159
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BASE COUNT 38 a 36 c 51 g 34 t
ORIGIN

Query Match 4.9%; Score 23; DB 6; Length 159;
Best Local Similarity 100.0%; Pred. No. 0.085;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 124 gtggtgaagatctgtgactttgg 146
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Db 22 GTGTTGAAGATCTGTGACTTTGG 44

RESULT 41
D50001S13 272 bp DNA linear PRI 14-APR-2000
LOCUS
DEFINITION Human DNA for alpha-platelet-derived growth factor receptor, exon 18.
ACCESSION D50013
VERSION D50013.1 GI:767793
KEYWORDS alpha-platelet-derived growth factor receptor; PDGFRA.
SEGMENT 13 of 17
SOURCE
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Primates; Catarrhini; Hominidae; Homo.
1 (sites)
REFERENCE Kawagishi,J., Kumabe,T., Yoshimoto,T. and Yamamoto,T.
AUTHORS Structure, organization, and transcription units of the human
TITLE alpha-platelet-derived growth factor receptor gene, PDGFRA
JOURNAL Genomics 30 (2), 224-232 (1995)
MEDLINE 96163874
REFERENCE 2 (bases 1 to 272)

AUTHORS Kawagishi,J.
JOURNAL Unpublished (1996)
REFERENCE 3 (bases 1 to 272)
AUTHORS Kawagishi,J.
TITLE Direct Submission
JOURNAL Submitted (03-APR-1995) Jun Kawagishi, Tohoku University, Gene Research Center; 1-1 Tsutsumidouri-Anamiyamachi, Aobaku, Sendai, Miyagi 981, Japan (Tel:022-272-4321(ex.388, 389), Fax:022-263-9295)
FEATURES
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ORIGIN

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Best Local Similarity 100.0%; Pred. No. 0.085;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 127 gtgaagatctgtgactttgcct 149
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Db 147 GTGAAGATCTGTGACTTTGCCT 169

RESULT 42
MUS3RTK 429 bp mRNA linear ROD 30-DEC-1996
LOCUS
DEFINITION Mus musculus (clone FTS) receptor tyrosine kinase type III (did)
mRNA, partial cds.
ACCESSION L36163
VERSION L36163.1 GI:537334
KEYWORDS receptor tyrosine kinase; tyrosine kinase.
SOURCE house mouse.
ORGANISM Mus musculus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 429)
AUTHORS Rosnet,O., Mattei,M.G., Marchetto,S. and Birnbaum,D.
TITLE Isolation and chromosomal localization of a novel FMS-like tyrosine kinase gene
JOURNAL Genomics 9, 380-385 (1991)
MEDLINE 91169547
FEATURES
source Location/Qualifiers
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VRGNARLPVKWMAPESLFEGITVTKSDVWSYGILLWEIFSLGVNPPGIPVDANFYKL
TQSGFKMEQPFYATEGIYFMQSWAFDSKRKPSFPNLFSF"

BASE COUNT ORIGIN	101 a	107 c	114 g	107 t	
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Best Local Similarity	100.0%; Pred. No. 0.085;				
Matches 23:	Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
Qy	124	gtggtgaagatctgtgactttgg	146		
Db	73	GTGGTGAAGATCTGTGACTTTGG	95		
RESULT 43					
LOCUS	AF178759	1525 bp	mrna	linear	VRT 01-OCT-1999
DEFINITION	Danio rerio flt4 protein mRNA, partial cds.				
ACCESSION	AF178759				
VERSION	AF178759.2 GI:6006041				
KEYWORDS	zebrafish				
SOURCE	Danio rerio				
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.				
REFERENCE	1 (bases 1 to 1525)				
AUTHORS	Thompson,M.A., Ransom,D.G., Pratt,S.J., MacLennan,H., Kieran,M.W., Detrich,H.W. III, Vail,B., Huber,T.L., Paw,B., Brownlie,A.J., Oates,A.C., Fritz,A., Gates,M.A., Amores,A., Bahary,N., Talbot,W.S., Her,H., Beier,D.R., Postlethwait,J.H. and Zon,L.I.				
TITLE	The cloche and spadetail genes differentially affect hematopoiesis and vasculogenesis				
JOURNAL	Dev. Biol. (NY) 197, 248-269 (1998)				
REFERENCE	2 (bases 1 to 1525)				
AUTHORS	Thompson,M.A., Ransom,D.G., Pratt,S.J., MacLennan,H., Kieran,M.W., Detrich,H.W. III, Vail,B., Huber,T.L., Paw,B., Brownlie,A.J., Oates,A.C., Fritz,A., Gates,M.A., Amores,A., Bahary,N., Talbot,W.S., Her,H., Beier,D.R., Postlethwait,J.H. and Zon,L.I.				
TITLE	Direct Submission				
JOURNAL	Submitted (18-AUG-1999) Hematology/Oncology, Children's Hospital, 300 Longwood Ave, Boston, MA 02115, USA				
COMMENT	On Oct 1, 1999 this sequence version replaced gi:5917727.				
FEATURES	Location/Qualifiers				
source	1..1525				
	/organism="Danio rerio"				
	/db_xref="taxon:7955"				
	/chromosome="14"				
	<1..1216				
	/codon_start=2				
	/product="flt4 protein"				
	/protein_id="AAD56011.2"				
	/db_xref="GI:6006042"				
CDS	/translation="GNSLNFRAKREFFFLPYRDRSPKTSQVRRMIAGQASQSEHQP STSTNPRVTVDLMKPTLIEDLCYSFQVARGMEFLASRKCIIHRDLAARNILISE NNVKICDFGLARDIYKDPYVRKGNARLPKWMAPESIFDKVYTSQSVMSFGVLLW EIFSLGSPGQIDEDCKRLKDGTRMRAPDNASPEIYIGIMLACWQGEPRPRPTFP ALVEILDLLQENSLPEIPFNVSOSSEDDGFSOASRPPSOEIRLACNTLPTRYNC VPAGCVMGVPSSTCHSRVKTFEELPMEMTSKHTQHDSDTDSGMVLASDELEFEKH RGAMLTTATTGOSTDRLISCPVSVSSGSGGLLRPVFPFTQLSQTFYNNYGHLSSEG VSYFSSDDAQ"				
BASE COUNT	442 a	376 c	352 g	355 t	
ORIGIN					
Query Match	4.9%; Score 23; DB 5; Length 1525;				
Best Local Similarity	100.0%; Pred. No. 0.084;				
Matches 23:	Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
Qy	124	gtggtgaagatctgtgactttgg	146		
Db	314	GTGGTGAAGATCTGTGACTTTGG	336		

RESULT 44					
LOCUS	AR149571	1894 bp	DNA	linear	PAT 08-AUG-2001
DEFINITION	Sequence 3 from patent US 6228609.				
ACCESSION	AR149571				
VERSION	AR149571.1 GI:15114162				
KEYWORDS	Unknown.				
SOURCE	Unknown.				
ORGANISM	Unclassified.				
REFERENCE	1 (bases 1 to 1894)				
AUTHORS	Yang,Z.				
TITLE	Soluble Flk-2 sequence				
JOURNAL	Patent: US 6228609-A 3 08-MAY-2001;				
FEATURES	Location/Qualifiers				
source	1..1894				
	/organism="unknown"				
BASE COUNT	494 a	465 c	496 g	439 t	
ORIGIN					
Query Match	4.9%; Score 23; DB 6; Length 1894;				
Best Local Similarity	100.0%; Pred. No. 0.084;				
Matches 23:	Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
Qy	124	gtggtgaagatctgtgactttgg	146		
Db	976	GTGGTGAAGATCTGTGACTTTGG	998		
RESULT 45					
LOCUS	AC2TKSEA	2538 bp	ss-rna	linear	URL 27-APR-1993
DEFINITION	Avian retrovirus proviral tyrosine kinase (ENV-SEA oncogene), 3'				
ACCESSION	M25158				
VERSION	M25158.1 GI:209658				
KEYWORDS	c-myc proto-oncogene; long terminal repeat (LTR); tyrosine kinase.				
SOURCE	Avian retrovirus (isolate SI3) RNA, from a chicken, passed in rat cells.				
ORGANISM	Avian carcinoma virus				
REFERENCE	1 (bases 1 to 2538)				
AUTHORS	Smith,D.R., Vogt,P.K. and Hayman,M.J.				
TITLE	The SEA oncogene of avian retrovirus SI3; A new member of the protein tyrosine kinase gene family				
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 86, 5291-5295 (1989)				
MEDLINE	89315783				
COMMENT	Draft entry and computer-readable sequence for [1] kindly provided by M.J.Hayman, 02-JUN-1989.				
FEATURES	Location/Qualifiers				
source	1..2538				
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	/db_xref="taxon:11958"				
	<1..1791				
	/note="ARV polyprotein"				
	/codon_start=1				
	/protein_id="AAA42392.1"				
	/translation="KLTMLAPNHTDLKVLANSRRTGIRRKNTSHLDDTCSDVOLW GPTARIFASILAPGVAATQALREIERLACKSVKQANLTLSLGLDLDVTSIRHAVLQ NRAAIDFLLAHGHGCEDIAGMCCFNLSHSEIOKKFOLMKKHVNKIGVSDPIGSM LRKFGGIGEMAVHLLKGLLGLVILLVCLPCLLOFVSSSIRKMI DNSLGYREEC RKLOEANRADSPCLARPHAFHASAGADAGGSPYLLLLTSCCLDLRPELLEVKD ILIPEERLITHRSVRIGRFGSVTHGTMDPLLGHCAVSKSLHRITYLEEVFELR EGLVMKGFFHPQVLSLLGVCLPRHGLPVLLPYMRHGDLRHFVRAQERSPTVKELIGF GLQVALGMEYLQAKFKFVRLAARNCLDETITVKVADFLGRADVFEGKEYYSIRQHRH AKLPVRMALESLOTQKFTTKSDVMSFGVLMWELLTRGASPYEVDPYDMARYLLKGR RLPOPCPDITLYGVMLSCWAPTPEERPSFGLVCLCELRVLSLEGEHYINNAVTVN LESGPPFPAPRGQLPDSEDEEEVAE"				
	/product="envelope protein"				
	<1..678				
	679..1788				
mat_peptide					
mat_peptide					

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: July 16, 2002, 02:57:00 ; Search time 808.35 Seconds
(without alignments)
2.105 Million cell updates/sec

Title: US-09-375-248-1_COPY_2588_2588

Perfect score: 1
Sequence: 1 g 1

Scoring table: OLIGO_NUC
Gapop 60.0 , Capext 60.0

Searched: 1163369 seqs, 850982142 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2326738

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Pending_Patents_NA_New:*
1: /cgn2_6/ptodata/2/pna/PCT_NEW_COMB.seq:*
2: /cgn2_6/ptodata/2/pna/US06_NEW_COMB.seq:*
3: /cgn2_6/ptodata/2/pna/US07_NEW_COMB.seq:*
4: /cgn2_6/ptodata/2/pna/US08_NEW_COMB.seq:*
5: /cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq:*
6: /cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq:*
7: /cgn2_6/ptodata/2/pna/US60_NEW_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	100.0	2	6	US-10-027-632-51869	Sequence 51869, A
C 2	100.0	2	6	US-10-027-632-52280	Sequence 52280, A
C 3	100.0	2	6	US-10-027-632-52357	Sequence 52357, A
C 4	100.0	2	6	US-10-027-632-53003	Sequence 53003, A
C 5	100.0	2	6	US-10-027-632-58305	Sequence 58305, A
6	100.0	2	6	US-10-027-632-175312	Sequence 175312, A
7	100.0	2	6	US-10-027-632-175337	Sequence 175337, A
8	100.0	2	6	US-10-027-632-175354	Sequence 175354, A
9	100.0	2	6	US-10-027-632-175401	Sequence 175401, A
10	100.0	2	6	US-10-027-632-175403	Sequence 175403, A
11	100.0	2	6	US-10-027-632-175415	Sequence 175415, A
12	100.0	2	6	US-10-027-632-175419	Sequence 175419, A
13	100.0	2	6	US-10-027-632-175426	Sequence 175426, A
14	100.0	2	6	US-10-027-632-175433	Sequence 175433, A
15	100.0	2	6	US-10-027-632-175849	Sequence 175849, A
16	100.0	2	6	US-10-027-632-176848	Sequence 176848, A
17	100.0	2	6	US-10-027-632-176849	Sequence 176849, A
18	100.0	2	6	US-10-027-632-176880	Sequence 176880, A
19	100.0	2	6	US-10-027-632-178420	Sequence 178420, A
20	100.0	2	6	US-10-027-632-178440	Sequence 178440, A
21	100.0	2	6	US-10-027-632-178440	Sequence 178440, A
22	100.0	2	6	US-10-027-632-178617	Sequence 178617, A
23	100.0	2	6	US-10-027-632-178640	Sequence 178640, A
C 24	100.0	3	1	PCT-US02-00351-20	Sequence 20, Appl
25	100.0	3	6	US-10-027-632-52136	Sequence 52136, A
C 26	100.0	3	6	US-10-027-632-52402	Sequence 52402, A

C 27	100.0	3	6	US-10-027-632-52403	Sequence 52403, A
C 28	100.0	3	6	US-10-027-632-52404	Sequence 52404, A
C 29	100.0	3	6	US-10-027-632-52410	Sequence 52410, A
C 30	100.0	3	6	US-10-027-632-52417	Sequence 52417, A
C 31	100.0	3	6	US-10-027-632-52418	Sequence 52418, A
C 32	100.0	3	6	US-10-027-632-52419	Sequence 52419, A
C 33	100.0	3	6	US-10-027-632-52425	Sequence 52425, A
C 34	100.0	3	6	US-10-027-632-52491	Sequence 52491, A
C 35	100.0	3	6	US-10-027-632-52495	Sequence 52495, A
36	100.0	3	6	US-10-027-632-52496	Sequence 52496, A
37	100.0	3	6	US-10-027-632-52508	Sequence 52508, A
C 38	100.0	3	6	US-10-027-632-52512	Sequence 52512, A
39	100.0	3	6	US-10-027-632-52513	Sequence 52513, A
40	100.0	3	6	US-10-027-632-52615	Sequence 52615, A
41	100.0	3	6	US-10-027-632-52633	Sequence 52633, A
42	100.0	3	6	US-10-027-632-52651	Sequence 52651, A
43	100.0	3	6	US-10-027-632-52753	Sequence 52753, A
C 44	100.0	3	6	US-10-027-632-52758	Sequence 52758, A
45	100.0	3	6	US-10-027-632-52761	Sequence 52761, A

ALIGNMENTS

RESULT 1
US-10-027-632-51869/c
; Sequence 51869, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027.632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 51869
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-51869

Query Match 100.0%; Score 1; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
Db 2 G 2

RESULT 2
US-10-027-632-52280/c
; Sequence 52280, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027.632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 51869
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-51869


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; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027.632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52280
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-52280
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Best Local Similarity 100.0%; Pred. No. 0;
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Qy 1 g 1
Db 2 G 2
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RESULT 3
US-10-027-632-52357/c
; Sequence 52357, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027.632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52357
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-52357
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Query Match 100.0%; Score 1; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
Qy 1 g 1
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```
Db 2 G 2
RESULT 4
US-10-027-632-53003/c
; Sequence 53003, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027.632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 53003
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-53003
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 g 1
Db 2 G 2
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RESULT 5
US-10-027-632-58305/c
; Sequence 58305, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027.632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 58305
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; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-58305

Query Match 100.0%; Score 1: DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
|
Db 1 G 1

RESULT 6

US-10-027-632-175312
; Sequence 175312, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027.632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 175312
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-175312

Query Match 100.0%; Score 1: DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
|
Db 1 G 1

RESULT 7

US-10-027-632-175337
; Sequence 175337, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027.632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29

; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 175337
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-175337

Query Match 100.0%; Score 1: DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
|
Db 1 G 1

RESULT 8

US-10-027-632-175354
; Sequence 175354, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027.632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 175354
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-175354

Query Match 100.0%; Score 1: DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
|
Db 1 G 1

RESULT 9

US-10-027-632-175401
; Sequence 175401, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.

; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027.632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 175401
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-175401

Query Match 100.0%; Score 1; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
|
Db 1 g 1

RESULT 10
US-10-027-632-175403
; Sequence 175403, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027.632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 175403
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-175403

Query Match 100.0%; Score 1; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
|
Db 1 g 1

RESULT 11
US-10-027-632-175415
; Sequence 175415, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027.632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 175415
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-175415

Query Match 100.0%; Score 1; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
|
Db 1 g 1

RESULT 12
US-10-027-632-175419
; Sequence 175419, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027.632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720

; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 175419
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-175419

Query Match 100.0%; Score 1; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
|
Db 1 g 1

RESULT 13
US-10-027-632-175426
; Sequence 175426, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 175426
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-175426

Query Match 100.0%; Score 1; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
|
Db 1 g 1

RESULT 14
US-10-027-632-175433
; Sequence 175433, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20

; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 175433
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-175433

Query Match 100.0%; Score 1; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
|
Db 1 g 1

RESULT 15
US-10-027-632-175849
; Sequence 175849, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 175849
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-175849

Query Match 100.0%; Score 1; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
|
Db 1 g 1

RESULT 16
US-10-027-632-176848
; Sequence 176848, Application US/10027632

Query Match 100.0%; Score 1; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
|
Db 1 g 1

RESULT 18
US-10-027-632-176880
; Sequence 176880, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; POLYMORPHISMS IN THE HUMAN GENOME
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 176848
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-176848

Query Match 100.0%; Score 1; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
|
Db 1 g 1

RESULT 17
US-10-027-632-176849
; Sequence 176849, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; POLYMORPHISMS IN THE HUMAN GENOME
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 176849
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-176849

Query Match 100.0%; Score 1; DB 6; Length 2;

Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
|
Db 1 g 1

RESULT 18
US-10-027-632-176880
; Sequence 176880, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; POLYMORPHISMS IN THE HUMAN GENOME
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 176880
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-176880

Query Match 100.0%; Score 1; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
|
Db 1 g 1

RESULT 19
US-10-027-632-178420
; Sequence 178420, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; POLYMORPHISMS IN THE HUMAN GENOME
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002

; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 178420
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-178420

Query Match 100.0%; Score 1; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1
|
Db 1 g 1

RESULT 20
US-10-027-632-178440
; Sequence 178440, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 178440
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-178440

Query Match 100.0%; Score 1; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1
|
Db 1 g 1

RESULT 21
US-10-027-632-178440/c
; Sequence 178440, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12

; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 178440
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-178440

Query Match 100.0%; Score 1; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1
|
Db 2 G 2

RESULT 22
US-10-027-632-178617
; Sequence 178617, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 178617
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-178617

Query Match 100.0%; Score 1; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1
|
Db 2 g 2

RESULT 23

US-10-027-632-178640
; Sequence 178640, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027.632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 178640
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-178640

Query Match 100.0% Score 1; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
|
Db 2 g 2

RESULT 24
PCT-US02-00351-20/c
; Sequence 20, Application PC/TUS0200351
; GENERAL INFORMATION:
; APPLICANT: Chet, Ilan
; APPLICANT: Viterbo, Ada
; TITLE OF INVENTION: RECOMBINANT FUNGAL CHITINASES, POLYNUCLEOTIDE SEQUENCES ENCODING
; FILE REFERENCE: 02/23682
; CURRENT APPLICATION NUMBER: PCT/US02/00351
; CURRENT FILING DATE: 2002-05-05
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 3
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: motif found in the URSs of both ech42 and prbl genes
PCT-US02-00351-20

Query Match 100.0% Score 1; DB 1; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
|
Db 3 G 3

RESULT 25

US-10-027-632-52136
; Sequence 52136, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027.632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52136
; LENGTH: 3
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-52136

Query Match 100.0% Score 1; DB 6; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
|
Db 3 g 3

RESULT 26
US-10-027-632-52402/c
; Sequence 52402, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027.632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52402
; LENGTH: 3
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-52402

Query Match 100.0%; Score 1; DB 6; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
|
Db 2 G 2

RESULT 27

US-10-027-632-52403/c
; Sequence 52403, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 52403
; LENGTH: 3
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-52403

Query Match 100.0%; Score 1; DB 6; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
|
Db 2 G 2

RESULT 28

US-10-027-632-52404/c
; Sequence 52404, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358

; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 52404
; LENGTH: 3
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-52404

Query Match 100.0%; Score 1; DB 6; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
|
Db 2 G 2

RESULT 29

US-10-027-632-52410/c
; Sequence 52410, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 52410
; LENGTH: 3
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-52410

Query Match 100.0%; Score 1; DB 6; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
|
Db 3 G 3

RESULT 30
US-10-027-632-52417/c
; Sequence 52417, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30

;
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52417
; LENGTH: 3
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-52417

Query Match 100.0%; Score 1; DB 6; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
|
Db 2 G 2

RESULT 31
US-10-027-632-52418/c
; Sequence 52418, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52418
; LENGTH: 3
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-52418

Query Match 100.0%; Score 1; DB 6; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
|
Db 2 G 2

RESULT 32
US-10-027-632-52419/c
; Sequence 52419, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52419
; LENGTH: 3
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-52419

Query Match 100.0%; Score 1; DB 6; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
|
Db 2 G 2

RESULT 33
US-10-027-632-52425/c
; Sequence 52425, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52425
; LENGTH: 3
; TYPE: DNA
; ORGANISM: Human

US-10-027-632-52425

Query Match 100.0%; Score 1; DB 6; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
|
Db 3 g 3

RESULT 34

US-10-027-632-52491
; Sequence 52491, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027.632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52491
; LENGTH: 3
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-52491

Query Match 100.0%; Score 1; DB 6; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
|
Db 2 g 2

RESULT 35

US-10-027-632-52495/c
; Sequence 52495, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027.632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363

; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52495
; LENGTH: 3
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-52495

Query Match 100.0%; Score 1; DB 6; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
|
Db 3 g 3

RESULT 36

US-10-027-632-52496
; Sequence 52496, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027.632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52496
; LENGTH: 3
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-52496

Query Match 100.0%; Score 1; DB 6; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
|
Db 2 g 2

RESULT 37

US-10-027-632-52508
; Sequence 52508, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129

; CURRENT APPLICATION NUMBER: US/10/027.632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52508
; LENGTH: 3
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-52508

Query Match 100.0%; Score 1; DB 6; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
|
Db 2 g 2

RESULT 38
US-10-027-632-52512/c
; Sequence 52512, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027.632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52512
; LENGTH: 3
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-52512

Query Match 100.0%; Score 1; DB 6; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
|

Db 3 G 3

RESULT 39
US-10-027-632-52513
; Sequence 52513, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027.632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52513
; LENGTH: 3
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-52513

Query Match 100.0%; Score 1; DB 6; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
|
Db 2 g 2

RESULT 40
US-10-027-632-52615
; Sequence 52615, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027.632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52615
; LENGTH: 3

; TYPE: DNA
; ORGANISM: Human
US-10-027-632-52615

Query Match 100.0%; Score 1; DB 6; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
|
Db 2 g 2

RESULT 41

US-10-027-632-52633
; Sequence 52633, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52633
; LENGTH: 3
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-52633

Query Match 100.0%; Score 1; DB 6; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
|
Db 2 g 2

RESULT 42

US-10-027-632-52651
; Sequence 52651, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218

; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52651
; LENGTH: 3
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-52651

Query Match 100.0%; Score 1; DB 6; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
|
Db 2 g 2

RESULT 43

US-10-027-632-52753
; Sequence 52753, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52753
; LENGTH: 3
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-52753

Query Match 100.0%; Score 1; DB 6; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
|
Db 2 g 2

RESULT 44

US-10-027-632-52758/c
; Sequence 52758, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027.632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52758
; LENGTH: 3
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-52758

Query Match 100.0%; Score 1; DB 6; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1
Db 1 g 1

RESULT 45
US-10-027-632-52761
; Sequence 52761, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027.632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52761
; LENGTH: 3
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-52761

Query Match 100.0%; Score 1; DB 6; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1
Db 1 g 1

Search completed: July 16, 2002, 02:57:00
Job time: 24558 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model
Run on: July 15, 2002, 20:07:36 ; Search time 7067.1 Seconds
(without alignments)
1.910 Million cell updates/sec

Title: US-09-375-248-1_COPY_2588_2588
Perfect score: 1
Sequence: 1 g 1

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 13736207 seqs, 6748477542 residues

Word size : 0

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estm:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_inv:*
15: em_gss_pln:*
16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	1	100.0	2	2 HSM003817	AL039341 Homo sapi
C 2	1	100.0	2	2 HSM007187	AL042337 Homo sapi
C 3	1	100.0	2	2 HSM008709	AL043859 Homo sapi
C 4	1	100.0	2	2 HSM011919	AL047069 Homo sapi
C 5	1	100.0	2	10 B1817789	B1817789 G3-G22 Ax
C 6	1	100.0	2	10 C55081	C55081 C55081 Yujl
C 7	1	100.0	2	10 BE351920	BE351920 894053D07
C 8	1	100.0	2	12 AZ463604	AZ463604 IM0272J05
C 9	1	100.0	3	9 AW672605	AW672605 2xA Expla
C 10	1	100.0	3	12 AZ438202	AZ438202 IM0228I08
C 11	1	100.0	3	12 CNS00KCV	AL077515 Drosophil
C 12	1	100.0	4	2 BG926576	BG926576 HNC56-1-A
C 13	1	100.0	4	2 BG926576	BG926576 HNC56-1-A
C 14	1	100.0	4	2 HSM003901	AL039425 Homo sapi
C 15	1	100.0	4	2 HSM010467	AL045617 Homo sapi
C 16	1	100.0	4	2 HSM010467	AL045617 Homo sapi
C 17	1	100.0	4	9 AW672622	AW672622 73C Expla

C 18	1	100.0	4	12 CNS004RB	AL054121 Drosophil
C 19	1	100.0	5	2 HSM007310	AL042460 Homo sapi
C 20	1	100.0	5	2 HSM007835	AL042985 Homo sapi
C 21	1	100.0	5	2 HSM011053	AL046203 Homo sapi
C 22	1	100.0	6	2 BG927410	Bg927410 HNC1-1-G7
C 23	1	100.0	6	2 HSM003844	AL039368 Homo sapi
C 24	1	100.0	6	2 HSM004423	AL039947 Homo sapi
C 25	1	100.0	6	2 HSM007334	AL042484 Homo sapi
C 26	1	100.0	6	2 HSM007683	AL042833 Homo sapi
C 27	1	100.0	6	2 HSM008014	AL043184 Homo sapi
C 28	1	100.0	6	2 HSM010918	AL046068 Homo sapi
C 29	1	100.0	6	2 HSM010918	AL046068 Homo sapi
C 30	1	100.0	6	10 BE726686	BE726686 894095D11
C 31	1	100.0	6	10 BE726686	BE726686 894095D11
C 32	1	100.0	7	2 BG97546	Bg97546 HOA14-1-H
C 33	1	100.0	7	2 BG97546	Bg97546 HOA14-1-H
C 34	1	100.0	7	2 HSM007412	AL042562 Homo sapi
C 35	1	100.0	7	2 HSM007412	AL042562 Homo sapi
C 36	1	100.0	7	2 HSM007502	AL042652 Homo sapi
C 37	1	100.0	7	2 HSM007502	AL042652 Homo sapi
C 38	1	100.0	7	10 C58888	C58888 C58888 Yujl
C 39	1	100.0	8	2 HSM001420	AL037095 Homo sapi
C 40	1	100.0	8	2 HSM001743	AL037413 Homo sapi
C 41	1	100.0	8	2 HSM004451	AL039975 Homo sapi
C 42	1	100.0	8	2 HSM004451	AL039975 Homo sapi
C 43	1	100.0	8	2 HSM007277	AL042427 Homo sapi
C 44	1	100.0	8	2 HSM007277	AL042427 Homo sapi
C 45	1	100.0	8	2 HSM007323	AL042473 Homo sapi

ALIGNMENTS

RESULT 1

HSM003817/C standard; RNA; EST; 2 BP.

AC AL039341;

SV AL039341.1

DT 12-MAR-1999 (Rel. 59, Created)

DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)

DE Homo sapiens mRNA; EST DKFZp434F2010_r1 (from clone DKFZp434F2010)

XX EST; expressed sequence tag.

XX Homo sapiens (human)

OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;

OC Eutheria; Primates; Catarrhini; Homnidae; Homo.

XX [1]

RN 1-2

RA Duesterhoeft A., Lauber J., Mewes W., Gassenhuber J., Wiemann S.;

RT Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.

RL MIPS, Am Klopferspitze 18a D-82152 Martinsried, GERMANY

XX Cloned from S. Wiemann, sequenced by Qiagen within the cDNA

CC sequencing consortium of the German Genome Project

CC No sl sequence available

CC This clone is available at the RZPD in Berlin

CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059

CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de

XX key Location/Qualifiers

FT source 1..2

FT /db_xref="taxon:9606"

FT /organism="Homo sapiens"

FT /clone="DKFZp434F2010"

FT /clone_lib="434 (synonym: htes3). Vector pSport1; host

FT DH10B; sites NotI + SalI"
 FT /dev_stage="adult"
 FT /tissue_type="testis"
 XX
 SQ Sequence 2 BP; 0 A; 1 C; 0 G; 1 T; 0 other;

Query Match 100.0%; Score 1; DB 2; Length 2;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1
 |
 Db 2 G 2

RESULT 2
 HSM007187/c
 ID HSM007187 standard; RNA; EST; 2 BP.
 XX
 AC AL042337;
 XX
 SV AL042337.1

XX 12-MAR-1999 (Rel. 59, Created)
 DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)
 XX

DE Homo sapiens mRNA; EST DKFZp43400820_r1 (from clone DKFZp43400820)
 XX
 KW EST; expressed sequence tag.

XX Homo sapiens (human)
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
 OC Eutheria; Primates; Catarrhini; Hominidae; Homo.

XX [1]
 RN 1-2
 RP Ottenwaelder B., Obermaier B., Mewes W., Gassenhuber J., Wiemann S.;
 RT Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
 RL MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY

XX Clone from S. Wiemann, sequenced by MediGenomix within the cDNA
 CC sequencing consortium of the German Genome Project
 CC No SI sequence available
 CC This clone is available at the RZPD in Berlin
 CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
 CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de

XX Key Location/Qualifiers

FT source 1..2
 FT /db_xref="taxon:9606"
 FT /organism="Homo sapiens"
 FT /clone="DKFZp43400820"
 FT /clone_lib="434 (synonym: htes3). Vector pSport1; host
 FT DH10B; sites NotI + SalI"
 FT /dev_stage="adult"
 FT /tissue_type="testis"

XX Sequence 2 BP; 0 A; 1 C; 0 G; 1 T; 0 other;

Query Match 100.0%; Score 1; DB 2; Length 2;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1
 |
 Db 2 G 2

RESULT 3

HSM008709/c
 ID HSM008709 standard; RNA; EST; 2 BP.
 XX
 AC AL043859;
 XX
 SV AL043859.1
 XX
 DT 12-MAR-1999 (Rel. 59, Created)
 DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)
 XX
 DE Homo sapiens mRNA; EST DKFZp434B2128_r1 (from clone DKFZp434B2128)
 XX
 KW EST; expressed sequence tag.

XX Homo sapiens (human)
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
 OC Eutheria; Primates; Catarrhini; Hominidae; Homo.

XX [1]
 RN 1-2
 RP Bloecker H., Boecher M., Brandt P., Mewes W., Gassenhuber J., Wiemann S.;
 RT Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
 RL MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY

XX Clone from S. Wiemann, sequenced by GBF within the cDNA
 CC sequencing consortium of the German Genome Project
 CC SI sequence also available
 CC This clone is available at the RZPD in Berlin
 CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
 CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de

XX Key Location/Qualifiers

FT source 1..2
 FT /db_xref="taxon:9606"
 FT /organism="Homo sapiens"
 FT /clone="DKFZp434B2128"
 FT /clone_lib="434 (synonym: htes3). Vector pSport1; host
 FT DH10B; sites NotI + SalI"
 FT /dev_stage="adult"
 FT /tissue_type="testis"

XX Sequence 2 BP; 0 A; 1 C; 0 G; 1 T; 0 other;

Query Match 100.0%; Score 1; DB 2; Length 2;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1
 |
 Db 2 G 2

RESULT 4

HSM011919/c
 ID HSM011919 standard; RNA; EST; 2 BP.
 XX
 AC AL047069;
 XX
 SV AL047069.1

XX 12-MAR-1999 (Rel. 59, Created)
 DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)
 XX

DE Homo sapiens mRNA; EST DKFZp586P0517_r1 (from clone DKFZp586P0517)
 XX
 KW EST; expressed sequence tag.

XX Homo sapiens (human)

OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
 OC Eutheria; Primates; Catarrhini; Hominidae; Homo.


```

XX RN [1]
XX RP 1-2
XX RA Koehrer K., Beyer A., Mewes W., Gassenhuber J., Wiemann S.;
XX RT :
XX RL Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
XX RM MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX XX
XX CC Clone from S. Wiemann, sequenced by BMFZ within the cDNA
XX CC sequencing consortium of the German Genome Project
XX CC No sl sequence available
XX CC This clone is available at the RZPD in Berlin
XX CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
XX CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX FH Key Location/Qualifiers
XX FT source
XX FT 1..2
XX FT /db_xref="taxon:9606"
XX FT /organism="Homo sapiens"
XX FT /clone="DKFZp586P0517"
XX FT /clone_lib="586 (synonym: hutel). Vector pSport1; host
XX FT DH10B; sites NotI + SalI/MluI"
XX FT /dev_stage="adult"
XX FT /tissue_type="uterus"
XX SQ Sequence 2 BP: 0 A; 1 C; 0 G; 1 T; 0 other;

Query Match 100.0%; Score 1; DB 2; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
Db 2 G 2

RESULT 5
Bi1817789/c
LOCUS Bi1817789 2 bp mRNA linear EST 04-OCT-2001
DEFINITION G3-C22 Axolotl Lambda Zap Library Ambystoma mexicanum cDNA similar
to putative ribosomal protein S2, mRNA sequence.
ACCESSION Bi1817789
VERSION Bi1817789.1 GI:15951401
KEYWORDS EST.
SOURCE axolotl.
ORGANISM Ambystoma mexicanum
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Caudata; Salamandroidea; Ambystomatidae;
Ambystoma.
REFERENCE 1 (bases 1 to 2)
AUTHORS Voss,S.R., King,D., Maness,N., Smith,J.J., Rondet,M., Bryant,S.V.,
Gardiner,D.M. and Parichy,D.M.
TITLE Expressed sequence tags from an axolotl limb regeneration library
JOURNAL Unpublished (2001)
COMMENT Contact: Voss SR
Department of Biology
Colorado State University
Fort Collins, CO 80523, USA
Tel.: 970 491 4869
Fax: 970 491 0649
Email: svross@lanar.colostate.edu
Single pass sequence from 5' end. Low quality sequence was trimmed
from the ends (PHRED error rate = 5%). Trace file available:
svross@lanar.colostate.edu.
FEATURES
Location/Qualifiers
source
1..2
/organism="Ambystoma mexicanum"
/db_xref="taxon:8296"
/clone_lib="Axolotl Lambda Zap Library"
/tissue_type="Regenerating forelimb"
/dev_stage="Medium-bud blastema"

Query Match 100.0%; Score 1; DB 2; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
Db 2 G 2

RESULT 5
Bi1817789/c
LOCUS Bi1817789 2 bp mRNA linear EST 04-OCT-2001
DEFINITION G3-C22 Axolotl Lambda Zap Library Ambystoma mexicanum cDNA similar
to putative ribosomal protein S2, mRNA sequence.
ACCESSION Bi1817789
VERSION Bi1817789.1 GI:15951401
KEYWORDS EST.
SOURCE axolotl.
ORGANISM Ambystoma mexicanum
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Caudata; Salamandroidea; Ambystomatidae;
Ambystoma.
REFERENCE 1 (bases 1 to 2)
AUTHORS Voss,S.R., King,D., Maness,N., Smith,J.J., Rondet,M., Bryant,S.V.,
Gardiner,D.M. and Parichy,D.M.
TITLE Expressed sequence tags from an axolotl limb regeneration library
JOURNAL Unpublished (2001)
COMMENT Contact: Voss SR
Department of Biology
Colorado State University
Fort Collins, CO 80523, USA
Tel.: 970 491 4869
Fax: 970 491 0649
Email: svross@lanar.colostate.edu
Single pass sequence from 5' end. Low quality sequence was trimmed
from the ends (PHRED error rate = 5%). Trace file available:
svross@lanar.colostate.edu.
FEATURES
Location/Qualifiers
source
1..2
/organism="Ambystoma mexicanum"
/db_xref="taxon:8296"
/clone_lib="Axolotl Lambda Zap Library"
/tissue_type="Regenerating forelimb"
/dev_stage="Medium-bud blastema"

Query Match 100.0%; Score 1; DB 10; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
Db 2 G 2

RESULT 7
BE351920
LOCUS BE351920 2 bp mRNA linear EST 18-JUL-2000
DEFINITION 894053D07.y1 C. reinhardtii CC-1690, normalized, Lambda Zap II
Chlamydomonas reinhardtii cDNA, mRNA sequence.
ACCESSION BE351920
VERSION BE351920.1 GI:9263773
KEYWORDS EST.
SOURCE Chlamydomonas reinhardtii.
ORGANISM Chlamydomonas reinhardtii
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadales; Chlamydomonas.
REFERENCE 1 (bases 1 to 2)

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BASE COUNT 0 a 1 c 0 g 1 t
ORIGIN

Query Match 100.0%; Score 1; DB 10; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
Db 1 G 1

RESULT 6
C55081/c
LOCUS C55081 2 bp mRNA linear EST 16-SEP-1997
DEFINITION C55081 Yuji Kohara unpublished cDNA Caenorhabditis elegans cDNA
clone yk350c9 3', mRNA sequence.
ACCESSION C55081
VERSION C55081.1 GI:2399682
KEYWORDS EST.
SOURCE Caenorhabditis elegans.
ORGANISM Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
; Rhabditidae; Peloderinae; Caenorhabditis.
REFERENCE 1 (bases 1 to 2)
AUTHORS Kohara,Y., Motohashi,T., Tabara,H., Watanabe,H., Sugimoto,A., Sano
,M., Miyata,A. and Nishigaki,A.
TITLE Expression map of the C.elegans genome
JOURNAL Unpublished (1996)
COMMENT Contact: Yuji Kohara
Genome Biology Lab.
National Institute of Genetics
Yata 111, Mishima, Shizuoka 411, Japan
Tel: 81-559-81-6854
Fax: 81-559-81-6855
Email: ykohara@lab.nig.ac.jp.
FEATURES
Location/Qualifiers
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1..2
/organism="Caenorhabditis elegans"
/strain="CBL489 him-8(e1489)"
/db_xref="taxon:6239"
/clone="yk350c9"
/clone_lib="Yuji Kohara unpublished cDNA"
/sex="hermaphrodite, male"
/tissue_type="whole animal"
/dev_stage="varied"

BASE COUNT 1 a 1 c 0 g 0 t
ORIGIN

Query Match 100.0%; Score 1; DB 10; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
Db 2 G 2

RESULT 7
BE351920
LOCUS BE351920 2 bp mRNA linear EST 18-JUL-2000
DEFINITION 894053D07.y1 C. reinhardtii CC-1690, normalized, Lambda Zap II
Chlamydomonas reinhardtii cDNA, mRNA sequence.
ACCESSION BE351920
VERSION BE351920.1 GI:9263773
KEYWORDS EST.
SOURCE Chlamydomonas reinhardtii.
ORGANISM Chlamydomonas reinhardtii
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadales; Chlamydomonas.
REFERENCE 1 (bases 1 to 2)

```

AUTHORS Grossman,A., Davies,J., Federspiel,N., Harris,E., Lefebvre,P.,
McDermott,J.P., Silflow,C., Stern,D. and Surzycki,R.
TITLE Analyses of the Chlamydomonas reinhardtii Genome: A Model,
Unicellular System for Analyzing Gene Function and Regulation in
Vascular Plants: project phase 2
JOURNAL Unpublished (2000)
COMMENT Contact: Elizabeth H. Harris
DCMB Box 91000
Duke University
Durham, NC 27708-1000, USA
Tel: 919 613 8164
Fax: 919 613 8177
Email: chlamy@duke.edu.

FEATURES source
1. .2
Location/Qualifiers
/organism="Chlamydomonas reinhardtii"
/strain="CC-1690 wild type mt+ 2lgr"
/db_xref="taxon:3055"
/clone_lib="C. reinhardtii CC-1690, normalized, Lambda Zap
II"
/note="Vector: pBluescript II SK-; Site_1: EcoRI; Site_2:
XhoI; This library, constructed by John Davies and Jeffrey
McDermott, combines cDNAs from CC-1690 cells grown to
mid-log phase in TAP (acetate-containing) medium in the
light, TAP medium in the dark, HS (minimal) medium in
ambient levels of CO₂ and HS medium bubbled with 5% CO₂.
PolyA mRNA was purified from each sample, pooled and cDNA
synthesized. The cDNA was directionally cloned into lambda
ZAP II (Stratagene) in the EcoRI (5') and XhoI (3') sites.
pBluescript II SK- plasmids were excised from the lambda
ZAP clones by superinfection with ExAssist (Stratagene)
phage. The library was normalized using method 4 described
in Bonaldo et al (1996) Genome Research 6: 791-806."

BASE COUNT 0 a 0 c 2 g 0 t
ORIGIN
Query Match 100.0%; Score 1; DB 10; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
|
Db 1 G 1

RESULT 8
AZ463604
LOCUS IM0272J05R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0272J05 R, DNA sequence.
DEFINITION
AZ463604
VERSION AZ463604.1 GI:10621729
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
1 (bases 1 to 2)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D., Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0272 row: J column: 05
Seq primer: CACACAGGAAACACGCTATGACC
Class: plasmid ends
High quality sequence stop: 451.
Location/Qualifiers
1. .2

FEATURES source
1. .2
Location/Qualifiers
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone_lib="UUGC1M0272J05"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gil4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

BASE COUNT 0 a 0 c 1 g 1 t
ORIGIN
Query Match 100.0%; Score 1; DB 12; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
|
Db 1 G 1

RESULT 9
AW672605
LOCUS AW672605 3 bp mRNA linear EST 26-SEP-2001
DEFINITION 2Xa Explanted metanephric mesenchyme induced to differentiate into
epithelial structures of the nephron ex vivo. Rattus norvegicus
cDNA similar to similar to: gb|AF022811.1|AF022811 Mus musculus
cornichon mRNA, mRNA sequence.

ACCESSION AW672605
VERSION AW672605.1 GI:7541085
KEYWORDS EST.
SOURCE Norway rat.
ORGANISM Rattus norvegicus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 3)

AUTHORS Plisov,S.Y., Ivanov,S.V., Yoshino,K., Dove,L.F., Plisova,T.M.,
Higginbotham,K.G., Karavanova,I., Lerman,M. and Perantonis,A.O.
TITLE Mesenchymal-epithelial transition in the developing metanephric
kidney: gene expression study by differential display
JOURNAL Genesis 27 (1), 22-31 (2000)
MEDLINE 20321327
COMMENT Contact: Plisov S.Y.
Laboratory of Comparative Carcinogenesis
National Cancer Institute
FCRDC, Bldg.538, Room 205, Frederick, MD 21702, USA

Tel: 301 846 1242
Fax: 301 846 4956
Email: plisov@mail.ncifcrf.gov

PCR Primers

FORWARD: ctgagctccctc

BACKWARD: ttaagcttttttttc

Insert Length: 350 Std Error: 0.00

Seq primer: SP6

High quality sequence stop: 261.

Location/Qualifiers

FEATURES

source

1. .3
/organism="Rattus norvegicus"
/db_xref="taxon:10116"
/clone_lib="Explanted metanephric mesenchyme induced to differentiate into epithelial structures of the nephron ex vivo."
/tissue_type="Metanephric mesenchyme"
/cell_type="Mesenchymal/Epithelial"
/dev_stage="13 dpc-16dpc"
/lab_host="JMI09"
/note="Organ: Kidney; Vector: pGEM-T-Easy (Promega); Restriction Enzymes: 1: ApaI, AatII, SphI, NcoI, BstZI, NotI, SacII, and EcoRI; SpeI, EcoRI, NotI, BstZI, PstI, SalI, NdeI, SacI, BstXI, and NsiI cDNA fragment PCR-amplified in mRNA differential display analysis; cloned in pGEM-T-Easy (Promega); its expression is developmentally regulated during mesenchymal-epithelial conversion in the metanephric kidney."
1 a 0 c 2 g 0 t

BASE COUNT

ORIGIN

Query Match 100.0%; Score 1; DB 9; Length 3;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1

|

Db 1 G 1

RESULT 10

AZ438202/c

LOCUS

DEFINITION AZ438202 3 bp DNA linear GSS 03-OCT-2000

clone UUGC1M0228108 F, DNA sequence.

ACCESSION AZ438202

VERSION AZ438202.1 GI:10562215

KEYWORDS GSS.

SOURCE house mouse.

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 3)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly

,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.

and Wright,D., Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112 USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0228 row: 1 column: 08

Seq primer: CGTTGTAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 302.

Location/Qualifiers

source

1. .3
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0228108"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
1 a 1 c 0 g 1 t

BASE COUNT

ORIGIN

Query Match 100.0%; Score 1; DB 12; Length 3;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1

|

Db 1 G 1

RESULT 11

CNS00KCV

LOCUS

DEFINITION CNS00KCV 3 bp DNA linear GSS 03-JUN-1999

Drosophila melanogaster genome survey sequence TET3 end of BAC:

BAC17D19 of RPCI-98 library from Drosophila melanogaster (fruit

fly), genomic survey sequence.

AL077515

AL077515.1 GI:4956992

KEYWORDS GSS.

SOURCE fruit fly.

ORGANISM Drosophila melanogaster

Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;

Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 3)

Genoscope.

Direct Submission

Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :

BP 191 91006 EVRY cedex - FRANCE (E-mail : secref@genoscope.cns.fr)

- Web : www.genoscope.cns.fr

Determination of this BAC-end sequence was carried out as part of a

collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila

melanogaster genome using these BACs. For further information

please see <http://www.fruitfly.org> The BDGP Drosophila

melanogaster BAC library was prepared by Kazutoyo Osoegawa and

Aaron Mammose in Pieter de Jong's laboratory in the Department of

Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,

NY. The library is named RPCI-98 and was constructed by partial

ECORI digestion of Drosophila DNA provided by the BDGP from the

isogenic strain y2: cn bw sp, the same strain used for the BDGP's

Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.hum.

FEATURES

source
1..3
/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone_lib="RPCI-98"
/clone="BACR17D19"
/note="end : TET3"

BASE COUNT 0 a 0 c 3 g 0 t
ORIGIN

Query Match 100.0%; Score 1; DB 12; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1
Db 1 G 1

RESULT 12

BG926576 standard; RNA; EST; 4 BP.

XX AC BG926576;

XX SV BG926576.1

XX 09-JUN-2001 (Rel. 68, Created)

DT 14-NOV-2001 (Rel. 69, Last updated, Version 2)

XX HNC56-1-A10.R HNC (Human Normal Cartilage) Homo sapiens cDNA, mRNA
DE sequence.

XX EST.

XX Homo sapiens (human)

OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia;

OC Eutheria; Primates; Catarrhini; Hominidae; Homo.

XX [1]

XX MEDLINE; 21482651.

XX PUBMED; 11597177.

RA Kumar S., Connor J.R., Dodds R.A., Halsey W., Van Horn M., Mao J.,
Sathé G.M., Mui P., Agarwal P., Badger A.M., Lee J.C., Gowen M., Lark M.W.;

RT "Identification and initial characterization of 5000 expressed sequenced
tags (ESTs) each from adult human normal and osteoarthritic cartilage cDNA
libraries";

RL Osteoarthritis Cartilage 9(7):641-653(2001).

XX Contact: Sanjay Kumar

CC UW2109

CC GlaxoSmithKline

CC 709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA

CC Tel: 610-270-7245

CC Fax: 610-270-5598

CC Email: sanjay.kumar-1@gsk.com

CC Seq primer: T7.

XX Key

XX Location/Qualifiers

XX source

1..4

/db_xref="taxon:9606"

/note="Vector: pSPORT 1; Site_1: SalI; Site_2: NotI;

Directional"

/organism="Homo sapiens"

/clone_lib="HNC (Human Normal Cartilage)"

/tissue_type="cartilage"

FT

FT

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FT

FT /lab_host="E.coli DH10 B"

XX Sequence 4 BP; 1 A; 1 C; 1 G; 1 T; 0 other;

SQ

Query Match 100.0%; Score 1; DB 2; Length 4;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1

Db 4 G 4

RESULT 13

BG926576/c

ID BG926576 standard; RNA; EST; 4 BP.

XX AC BG926576;

XX SV BG926576.1

XX 09-JUN-2001 (Rel. 68, Created)

DT 14-NOV-2001 (Rel. 69, Last updated, Version 2)

XX HNC56-1-A10.R HNC (Human Normal Cartilage) Homo sapiens cDNA, mRNA
DE sequence.

XX EST.

XX Homo sapiens (human)

OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia;

OC Eutheria; Primates; Catarrhini; Hominidae; Homo.

XX [1]

XX MEDLINE; 21482651.

XX PUBMED; 11597177.

RA Kumar S., Connor J.R., Dodds R.A., Halsey W., Van Horn M., Mao J.,
Sathé G.M., Mui P., Agarwal P., Badger A.M., Lee J.C., Gowen M., Lark M.W.;

RT "Identification and initial characterization of 5000 expressed sequenced
tags (ESTs) each from adult human normal and osteoarthritic cartilage cDNA
libraries";

RL Osteoarthritis Cartilage 9(7):641-653(2001).

XX Contact: Sanjay Kumar

CC UW2109

CC GlaxoSmithKline

CC 709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA

CC Tel: 610-270-7245

CC Fax: 610-270-5598

CC Email: sanjay.kumar-1@gsk.com

CC Seq primer: T7.

XX Key

XX Location/Qualifiers

XX source

1..4

/db_xref="taxon:9606"

/note="Vector: pSPORT 1; Site_1: SalI; Site_2: NotI;

Directional"

/organism="Homo sapiens"

/clone_lib="HNC (Human Normal Cartilage)"

/tissue_type="cartilage"

/lab_host="E.coli DH10 B"

XX

XX

XX

XX

XX

XX

Query Match 100.0%; Score 1; DB 2; Length 4;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1

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Db          1
            3 G 3

RESULT 14
HSM003901
ID HSM003901 standard; RNA; EST; 4 BP.
XX
AC AL039425;
XX
SV AL039425.1
XX
DT 12-MAR-1999 (Rel. 59, Created)
DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX
DE Homo sapiens mRNA; EST DKFZp434L0810_s1 (from clone DKFZp434L0810)
XX
KW EST; expressed sequence tag.
XX
OS Homo sapiens (human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
XX
RN [1]
RP 1-4
RA Dueterhoeft A., Lauber J., Mewes W., Gassenhuber J., Wiemann S.;
RT ; Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
RL MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX
CC Clone from S. Wiemann, sequenced by Qiagen within the cDNA
CC sequencing consortium of the German Genome Project
CC No sl sequence available
CC This clone is available at the RZPD in Berlin
CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
FH Key Location/Qualifiers
FH source 1..4
FT /db_xref="taxon:9606"
FT /organism="Homo sapiens"
FT /clone="DKFZp434O245"
FT /clone_lib="434 (synonym: htes3). Vector pSport1; host
FT DH10B; sites NotI + SalI"
FT /dev_stage="adult"
FT /tissue_type="testis"
XX
SQ Sequence 4 BP; 2 A; 0 C; 1 G; 0 T; 1 other;

Query Match 100.0%; Score 1; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
Db 4 G 4

RESULT 15
HSM010467
ID HSM010467 standard; RNA; EST; 4 BP.
XX
AC AL045617;
XX
SV AL045617.1
XX
DT 12-MAR-1999 (Rel. 59, Created)
DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX
DE Homo sapiens mRNA; EST DKFZp434O245_r1 (from clone DKFZp434O245)
XX
KW EST; expressed sequence tag.
XX
OS Homo sapiens (human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
XX
RN [1]
RP 1-4
RA Dueterhoeft A., Lauber J., Mewes W., Gassenhuber J., Wiemann S.;
RT ; Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
RL MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX
CC Clone from S. Wiemann, sequenced by Qiagen within the cDNA
CC sequencing consortium of the German Genome Project
CC No sl sequence available
CC This clone is available at the RZPD in Berlin
CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
FH Key Location/Qualifiers
FH source 1..4
FT /db_xref="taxon:9606"
FT /organism="Homo sapiens"
FT /clone="DKFZp434L0810"
FT /clone_lib="434 (synonym: htes3). Vector pSport1; host
FT DH10B; sites NotI + SalI"
FT /dev_stage="adult"
FT /tissue_type="testis"
XX
SQ Sequence 4 BP; 2 A; 0 C; 1 G; 0 T; 1 other;

Query Match 100.0%; Score 1; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
Db 4 G 4

RESULT 15
HSM010467
ID HSM010467 standard; RNA; EST; 4 BP.
XX
AC AL045617;
XX
SV AL045617.1
XX
DT 12-MAR-1999 (Rel. 59, Created)
DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX
DE Homo sapiens mRNA; EST DKFZp434O245_r1 (from clone DKFZp434O245)
XX
KW EST; expressed sequence tag.
XX
OS Homo sapiens (human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
XX
RN [1]
RP 1-4
RA Dueterhoeft A., Lauber J., Mewes W., Gassenhuber J., Wiemann S.;
RT ; Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
RL MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX
CC Clone from S. Wiemann, sequenced by Qiagen within the cDNA
CC sequencing consortium of the German Genome Project
CC No sl sequence available
CC This clone is available at the RZPD in Berlin

```

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CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
FH Key Location/Qualifiers
FH source 1..4
FH /db_xref="taxon:9606"
FH /organism="Homo sapiens"
FH /clone_lib="DKFZp4340245"
FH /clone_lib="434 (synonym: htes3)}. Vector pSport1; host
FH DH10B; sites NotI + SalI"
FH /dev_stage="adult"
FH /tissue_type="testis"
XX
XX Sequence 4 BP; 0 A; 2 C; 1 G; 1 T; 0 other;

Query Match 100.0%; Score 1; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
Db 2 G 2

RESULT 17
LOCUS AW672622
DEFINITION 73C Explanted metanephric mesenchyme induced to differentiate into
epithelial structures of the nephron ex vivo. Rattus norvegicus
cDNA similar to similar to: embIAL049970.1|HSM800317 Homo sapiens
mRNA: cDNA DKFZp564B102 (from clone DKFZp564B102);, mRNA sequence.
ACCESSION AW672622
VERSION AW672622.1 GI:7541102
KEYWORDS EST.
SOURCE Norway rat.
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 4)
Plisov,S.Y., Ivanov,S.V., Yoshino,K., Dove,L.F., Plisova,T.M.,
Higinbotham,K.G., Karavanova,I., Lerman,M. and Perantoni,A.O.
Mesenchymal-epithelial transition in the developing metanephric
kidney: gene expression study by differential display
Genesis 27 (1), 22-31 (2000)
20321327
Contact: Plisov S.Y.
Laboratory of Comparative Carcinogenesis
National Cancer Institute
FCRDC, Bldg. 538, Room 205, Frederick, MD 21702, USA
Tel: 301 846 1242
Fax: 301 846 4956
Email: plisov@mail.ncicfcr.gov
PCR Primers
FORWARD: ctccagctccgcgc
BACKWARD: ttaagctttttttttg
Insert Length: 262 Std Error: 0.00
Seq primer: Sp6
High quality sequence stop: 262
POLYA=Yes.
FEATURES
Source Location/Qualifiers
1..4
/organism="Rattus norvegicus"
/db_xref="taxon:10116"
/clone_lib="Explanted metanephric mesenchyme induced to
differentiate into epithelial structures of the nephron ex
vivo."
/tissue_type="Metanephric mesenchyme"
/cell_type="Mesenchymal/Epithelial"
/dev_stage="13 dpc-16dpc"
/lab_host="JMI09"

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/note="Organ: Kidney; Vector: pGEM-Teasy (Promega).;
Restriction Enzymes 1; ApaI, AatII, SphI, NcoI, BstZI,
NotI, SacII, and EcoRI SpeI, EcoRI, NotI, BstZI, PstII,
SalI, NdeI, SacI, BstXI, and NsiI cDNA fragment
PCR-amplified in mRNA differential display analysis;
cloned in pGEM-Teasy (Promega); its expression is
developmentally regulated during mesenchymal-epithelial
conversion in the metanephric kidney."
BASE COUNT 1 a 0 c 3 g 0 t
ORIGIN

Query Match 100.0%; Score 1; DB 9; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
Db 1 G 1

RESULT 18
LOCUS CNS004RB/c
DEFINITION Drosophila melanogaster genome survey sequence TET3 end of BAC #
BACR10A06 of RPCI-98 library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
ACCESSION AL054121
VERSION AL054121.1 GI:4931932
KEYWORDS GSS.
SOURCE fruit fly.
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 4)
Genoscope.
Direct Submission
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
COMMENT Determination of this BAC-end sequence was carried out as part of a
collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila
melanogaster genome using these BACs. For further information
please see http://www.fruitfly.org The BDGP Drosophila
melanogaster BAC library was prepared by Kazutoyo Osoegawa and
Aaron Mammosier in Pieter de Jong's laboratory in the Department of
Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
NY. The library is named RPCI-98 and was constructed by partial
EcoRI digestion of Drosophila DNA provided by the BDGP from the
isogenic strain Y2; cn bw sp, the same strain used for the BDGP's
PI and EST libraries. A more detailed description of the library
and how to order individual BAC clones, the entire library, or
filters for hybridization from the BACPAC Resource Center can be
found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
FEATURES
Source Location/Qualifiers
1..4
/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone_lib="RPCI-98"
/clone="BACR10A06"
/note="end : TET3"
BASE COUNT 1 a 1 c 0 g 2 t
ORIGIN

Query Match 100.0%; Score 1; DB 12; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1

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Db          4 G 4

RESULT 19
HSM007310
ID HSM007310 standard; RNA; EST: 5 BP.
XX
AC AL042460;
XX
SV AL042460.1
XX
DT 12-MAR-1999 (Rel. 59, Created)
DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX
DE Homo sapiens mRNA; EST DKFZp434E1821_r1 (from clone DKFZp434E1821)
XX
KW EST; expressed sequence tag.
XX
OS Homo sapiens (human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
XX
RN [1]
RP 1-5
RA Blum H., Bauersachs S., Mewes W., Gassenhuber J., Wiemann S.;
RT Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
RL MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX
CC Clone from S. Wiemann, sequenced by LMU within the cDNA
CC sequencing consortium of the German Genome Project
CC No.s1 sequence available
CC This clone is available at the RZPD in Berlin
CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
FH Key Location/Qualifiers
FH source 1..5
FT /db_xref="taxon:9606"
FT /organism="Homo sapiens"
FT /clone="DKFZp434E1821"
FT /clone_lib="434 (synonym: htes3). Vector pSport1; host
FT DH10B; sites NotI + SalI"
FT /dev_stage="adult"
FT /tissue_type="testis"
XX
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Query Match 100.0%; Score 1; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 g 1
Db 1 G 1

RESULT 20
HSM007835/c
ID HSM007835 standard; RNA; EST: 5 BP.
XX
AC AL042985;
XX
SV AL042985.1
XX
DT 12-MAR-1999 (Rel. 59, Created)
DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX
DE Homo sapiens mRNA; EST DKFZp434N1522_r1 (from clone DKFZp434N1522)
XX
KW EST; expressed sequence tag.

```

```

XX Homo sapiens (human)
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
XX
RN [1]
RP 1-5
RA Blum H., Bauersachs S., Mewes W., Gassenhuber J., Wiemann S.;
RT Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
RL MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX
CC Clone from S. Wiemann, sequenced by LMU within the cDNA
CC sequencing consortium of the German Genome Project
CC No.s1 sequence available
CC This clone is available at the RZPD in Berlin
CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
FH Key Location/Qualifiers
FH source 1..5
FT /db_xref="taxon:9606"
FT /organism="Homo sapiens"
FT /clone="DKFZp434N1522"
FT /clone_lib="434 (synonym: htes3). Vector pSport1; host
FT DH10B; sites NotI + SalI"
FT /dev_stage="adult"
FT /tissue_type="testis"
XX
SQ Sequence 5 BP; 2 A; 1 C; 0 G; 0 T; 2 other;

Query Match 100.0%; Score 1; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 g 1
Db 5 G 5

RESULT 21
HSM011053
ID HSM011053 standard; RNA; EST: 5 BP.
XX
AC AL046203;
XX
SV AL046203.1
XX
DT 12-MAR-1999 (Rel. 59, Created)
DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX
DE Homo sapiens mRNA; EST DKFZp434D137_r1 (from clone DKFZp434D137)
XX
KW EST; expressed sequence tag.
XX
OS Homo sapiens (human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
XX
RN [1]
RP 1-5
RA Koehrer K., Beyer A., Mewes W., Gassenhuber J., Wiemann S.;
RT Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
RL MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX
CC Clone from S. Wiemann, sequenced by BMFZ within the cDNA
CC sequencing consortium of the German Genome Project
CC No.s1 sequence available
CC This clone is available at the RZPD in Berlin
CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059

```

```

CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
FH Key Location/Qualifiers
FH source 1..5
FT /db_xref="taxon:9606"
FT /organism="Homo sapiens"
FT /clone="DKFZp434Dl37"
FT /clone_lib="434 (synonym: htes3). Vector pSport1; host
FT DH10B; sites NotI + SalI"
FT /dev_stage="adult"
FT /tissue_type="testis"
XX
XX Sequence 5 BP; 2 A; 0 C; 1 G; 2 T; 0 other;

Query Match 100.0%; Score 1; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
Db 1 G 1

RESULT 22
BG927410/G standard; RNA; EST; 6 BP.
ID BG927410
AC BG927410;
XX
XX BG927410.1
SV
XX
XX 09-JUN-2001 (Rel. 68, Created)
DT 14-NOV-2001 (Rel. 69, Last updated, Version 2)
XX
XX HNC1-1-G7-R HNC (Human Normal Cartilage) Homo sapiens cDNA, mRNA sequence.
XX EST.
XX Homo sapiens (human)
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
XX
XX [1]
RN 1-6
RP MEDLINE; 21482651.
RX PUBMED; 11597177.
RA Kumar S., Connor J.R., Dodds R.A., Halsey W., Van Horn M., Mao J.,
RA Sathe G.M., Mui P., Agarwal P., Badger A.M., Lee J.C., Cowen M., Lark M.W.;
RT "Identification and initial characterization of 5000 expressed sequenced
RT tags (ESTs) each from adult human normal and osteoarthritic cartilage cDNA
RT libraries";
RL Osteoarthritis Cartilage 9(7):641-653(2001).
XX
XX Contact: Sanjay Kumar
CC UW2109
CC GlaxoSmithKline
CC 709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA
CC Tel: 610-270-7245
CC Fax: 610-270-5598
CC Email: sanjay_kumar-legsk.com
CC Seq primer: T7.
XX
XX Key Location/Qualifiers
FH source 1..6
FT /db_xref="taxon:9606"
FT /note="Vector: pSPORT 1; Site_1: SalI; Site_2: NotI;
FT Directional"
FT /organism="Homo sapiens"
FT /clone_lib="HNC (Human Normal Cartilage)"
FT /tissue_type="cartilage"

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FT /lab_host="E.coli DH10 B"
XX
XX Sequence 6 BP; 0 A; 5 C; 0 G; 1 T; 0 other;

Query Match 100.0%; Score 1; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
Db 6 G 6

RESULT 23
HSM003844 standard; RNA; EST; 6 BP.
ID HSM003844
XX
XX AC AL039368;
XX
XX SV AL039368.1
XX
XX 12-MAR-1999 (Rel. 59, Created)
DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX
XX Homo sapiens mRNA; EST DKFZp434I0110_r1 (from clone DKFZp434I0110)
XX
XX KW EST; expressed sequence tag.
XX
XX Homo sapiens (human)
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
XX
XX [1]
RN 1-6
RP Dueterhoeft A., Lauber J., Newes W., Gassenhuber J., Wiemann S.;
RT Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
RL MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX
XX Clone from S. Wiemann, sequenced by Qiagen within the cDNA
XX sequencing consortium of the German Genome Project
CC No sl sequence available
CC This clone is available at the RZPD in Berlin
CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
XX Key Location/Qualifiers
FH source 1..6
FT /db_xref="taxon:9606"
FT /organism="Homo sapiens"
FT /clone="DKFZp434I0110"
FT /clone_lib="434 (synonym: htes3). Vector pSport1; host
FT DH10B; sites NotI + SalI"
FT /dev_stage="adult"
FT /tissue_type="testis"
XX
XX Sequence 6 BP; 2 A; 0 C; 2 G; 2 T; 0 other;

Query Match 100.0%; Score 1; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
Db 1 G 1

RESULT 24
HSM004423 standard; RNA; EST; 6 BP.
ID HSM004423

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XX AC AL039947;
XX SV
XX DT 12-MAR-1999 (Rel. 59, Created)
XX DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX DT
XX DE Homo sapiens mRNA; EST DKFZp434J0112_r1 (from clone DKFZp434J0112)
XX KW EST; expressed sequence tag.
XX OS Homo sapiens (human)
XX OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
XX OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
XX RN [1]
XX RA Duisterhoef A., Lauber J., Mewes W., Gassenhuber J., Wiemann S.;
XX RT Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
XX RL MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX CC Clone from S. Wiemann, sequenced by Qiagen within the cDNA
XX CC sequencing consortium of the German Genome Project
XX CC No s1 sequence available
XX CC This clone is available at the RZPD in Berlin
XX CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
XX CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX FH Key Location/Qualifiers
XX FT source
XX FT 1..6
XX FT /db_xref="taxon:9606"
XX FT /organism="Homo sapiens"
XX FT /clone="DKFZp434J0112"
XX FT /clone_lib="434 (synonym: htes3). Vector pSport1; host
XX FT DH10B; sites NotI + SalI"
XX FT /dev_stage="adult"
XX FT /tissue_type="testis"
XX SQ Sequence 6 BP; 2 A; 0 C; 2 G; 2 T; 0 other;

Query Match 100.0%; Score 1; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 g 1
DB 1 G 1

RESULT 25
HSM007334
ID HSM007334 standard; RNA; EST; 6 BP.
AC AL042484;
SV AL042484.1
XX DT 12-MAR-1999 (Rel. 59, Created)
XX DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX DE Homo sapiens mRNA; EST DKFZp434F0321_r1 (from clone DKFZp434F0321)
XX KW EST; expressed sequence tag.
XX OS Homo sapiens (human)
XX OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
XX OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
XX RN [1]

```

```

RP 1-6
RA Blum H., Bauersachs S., Mewes W., Gassenhuber J., Wiemann S.;
RT Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
RL MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX CC Clone from S. Wiemann, sequenced by LMU within the cDNA
XX CC sequencing consortium of the German Genome Project
XX CC No s1 sequence available
XX CC This clone is available at the RZPD in Berlin
XX CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
XX CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX FH Key Location/Qualifiers
XX FT source
XX FT 1..6
XX FT /db_xref="taxon:9606"
XX FT /organism="Homo sapiens"
XX FT /clone="DKFZp434F0321"
XX FT /clone_lib="434 (synonym: htes3). Vector pSport1; host
XX FT DH10B; sites NotI + SalI"
XX FT /dev_stage="adult"
XX FT /tissue_type="testis"
XX SQ Sequence 6 BP; 2 A; 0 C; 2 G; 2 T; 0 other;

Query Match 100.0%; Score 1; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 g 1
DB 1 G 1

RESULT 26
HSM007683/c
ID HSM007683 standard; RNA; EST; 6 BP.
AC AL042833;
XX SV AL042833.1
XX DT 12-MAR-1999 (Rel. 59, Created)
XX DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX DE Homo sapiens mRNA; EST DKFZp434G1622_r1 (from clone DKFZp434G1622)
XX KW EST; expressed sequence tag.
XX OS Homo sapiens (human)
XX OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
XX OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
XX RN [1]
XX RA Blum H., Bauersachs S., Mewes W., Gassenhuber J., Wiemann S.;
XX RT Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
XX RL MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX CC Clone from S. Wiemann, sequenced by LMU within the cDNA
XX CC sequencing consortium of the German Genome Project
XX CC No s1 sequence available
XX CC This clone is available at the RZPD in Berlin
XX CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
XX CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX FH Key Location/Qualifiers
XX FT source
XX FT 1..6
XX FT /db_xref="taxon:9606"

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FT      /organism="Homo sapiens"
FT      /clone="DKF2p434G1622"
FT      /clone_lib="434 (synonym: htes3)}. Vector pSport1; host
FT      DH10B; sites Noti + SalI"
FT      /dev_stage="adult"
FT      /tissue_type="testis"
XX
SQ      Sequence 6 BP; 2 A; 2 C; 0 G; 2 T; 0 other;

Query Match      100.0%; Score 1; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 g 1
Db      6 G 6

RESULT 27
HSM008014/c
ID      HSM008014 standard; RNA; EST; 6 BP.
XX
AC      AL043164;
XX
SV      AL043164.1
XX
12-MAR-1999 (Rel. 59, Created)
DT      12-MAR-1999 (Rel. 59, Last updated, Version 1)
DE      Homo sapiens mRNA; EST DKF2p434F1123_s1 (from clone DKF2p434F1123)
XX
KW      EST; expressed sequence tag.
XX
OS      Homo sapiens (human)
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC      Eutheria; Primates; Catarrhini; Hominidae; Homo.
XX
RN      [1]
RP      1-6
RA      Poustka A., Klein M., Mewes W., Gassenhuber J., Wiemann S.;
RT      Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
RL      MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX
CC      Clone from S. Wiemann, sequenced by LMU within the cDNA
CC      sequencing consortium of the German Genome Project
CC      r1 sequence also available
CC      This clone is available at the RZPD in Berlin
CC      Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC      Berlin-Charlottenburg, GERMANY; Email: clone@rzd.de
XX
FH      Key      Location/Qualifiers
FH      source      1. .6
FT      /db_xref="taxon:9606"
FT      /organism="Homo sapiens"
FT      /clone="DKF2p434F1123"
FT      /clone_lib="434 (synonym: htes3)}. Vector pSport1; host
FT      DH10B; sites Noti + SalI"
FT      /dev_stage="adult"
FT      /tissue_type="testis"
XX
SQ      Sequence 6 BP; 2 A; 2 C; 0 G; 2 T; 0 other;

Query Match      100.0%; Score 1; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 g 1
Db      6 G 6

RESULT 28
HSM010918
ID      HSM010918 standard; RNA; EST; 6 BP.
XX
AC      AL046068;
XX
SV      AL046068.1
XX
12-MAR-1999 (Rel. 59, Created)
DT      12-MAR-1999 (Rel. 59, Last updated, Version 1)
DE      Homo sapiens mRNA; EST DKF2p434F1672_r1 (from clone DKF2p434F1672)
XX
KW      EST; expressed sequence tag.
XX
OS      Homo sapiens (human)
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC      Eutheria; Primates; Catarrhini; Hominidae; Homo.
XX
RN      [1]
RP      1-6
RA      Poustka A., Klein M., Mewes W., Gassenhuber J., Wiemann S.;
RT      Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
RL      MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX
CC      Clone from S. Wiemann, sequenced by DKF2 within the cDNA
CC      sequencing consortium of the German Genome Project
CC      No s1 sequence available
CC      This clone is available at the RZPD in Berlin
CC      Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC      Berlin-Charlottenburg, GERMANY; Email: clone@rzd.de
XX
FH      Key      Location/Qualifiers
FH      source      1. .6
FT      /db_xref="taxon:9606"
FT      /organism="Homo sapiens"
FT      /clone="DKF2p434F1672"
FT      /clone_lib="434 (synonym: htes3)}. Vector pSport1; host
FT      DH10B; sites Noti + SalI"
FT      /dev_stage="adult"
FT      /tissue_type="testis"
XX
SQ      Sequence 6 BP; 0 A; 2 C; 2 G; 0 T; 2 other;

Query Match      100.0%; Score 1; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 g 1
Db      1 G 1

RESULT 29
HSM010918/c
ID      HSM010918 standard; RNA; EST; 6 BP.
XX
AC      AL046068;
XX
SV      AL046068.1
XX
12-MAR-1999 (Rel. 59, Created)
DT      12-MAR-1999 (Rel. 59, Last updated, Version 1)
DE      Homo sapiens mRNA; EST DKF2p434F1672_r1 (from clone DKF2p434F1672)
XX
KW      EST; expressed sequence tag.
XX

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```

OS Homo sapiens (human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
XX Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP 1-6
RA Poustka A., Klein M., Mewes W., Gassenhuber J., Wiemann S.;
RT ; Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
RL M1PS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX
CC Clone from S. Wiemann, sequenced by DKFZ within the cDNA
CC sequencing consortium of the German Genome Project
CC No sl sequence available
CC This clone is available at the RZPD in Berlin
CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
FH Key Location/Qualifiers
FH
FT 1..6
FT /db_xref="taxon:9606"
FT /organism="Homo sapiens"
FT /clone="DKFZp434F1672"
FT /clone_lib="434 (synonym: htes3). Vector pSport1; host
FT DH10B; sites NotI + SalI"
FT /dev_stage="adult"
FT /tissue_type="testis"
XX
SQ Sequence 6 BP; 0 A; 2 C; 2 G; 0 T; 2 other;

      Query Match      100.0%; Score 1; DB 2; Length 6;
      Best Local Similarity 100.0%; Pred. No. 0;
      Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
   |
Db 5 G 5

RESULT 30
BE726686
LOCUS      6 bp mRNA linear EST 14-SEP-2000
DEFINITION Chlamydomonas reinhardtii cDNA, mRNA sequence.
ACCESSION BE726686
VERSION BE726686.1 GI:10128110
KEYWORDS EST.
SOURCE Chlamydomonas reinhardtii.
ORGANISM Chlamydomonas reinhardtii.
REFERENCE 1 (bases 1 to 6)
AUTHORS Grossman,A., Davies,J., Federspiel,N., Harris,E., Lefebvre,P.,
McDermott,J.P., Silflow,C., Stern,D. and Surzycki,R.
TITLE Analyses of the Chlamydomonas reinhardtii Genome: A Model,
Unicellular System for Analyzing Gene Function and Regulation in
Vascular Plants; project phase 2
JOURNAL Unpublished (2000)
COMMENT Contact: Charles Hauser
DCMB Box 91000
Duke University
Durham, NC 27708-1000
Tel: 919 613 8159
Fax: 919 613 8177
Email: chauser@duke.edu.
Location/Qualifiers
1..6
/organism="Chlamydomonas reinhardtii"
/strain="CC-1690 wild type mt+ 2lgr"
/db_xref="taxon:3055"
/clone_lib="C. reinhardtii CC-1690, normalized, Lambda Zap
II"

FEATURES
source
1..6
/organism="Chlamydomonas reinhardtii"
/strain="CC-1690 wild type mt+ 2lgr"
/db_xref="taxon:3055"
/clone_lib="C. reinhardtii CC-1690, normalized, Lambda Zap
II"

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II"
/Note="Vector: pBluescript II SK-; Site.1: EcoRI; Site.2:
XhoI; This library, constructed by John Davies and Jeffrey
McDermott, combines cDNAs from CC-1690 cells grown to
mid-log phase in TAP (acetate-containing) medium in the
light, TAP medium in the dark, HS (minimal) medium in
ambient levels of CO2 and HS medium bubbled with 5% CO2.
polyA mRNA was purified from each sample, pooled and cDNA
synthesized. The cDNA was directionally cloned into lambda
ZAP II (Stratagene) in the EcoRI (5') and XhoI (3') sites.
pBluescript II SK- plasmids were excised from the lambda
ZAP clones by superinfection with ExAssist (Stratagene)
phage. The library was normalized using method 4 described
in Bonaldo et al (1996) Genome Research 6: 791-806."
BASE COUNT      0 a      1 c      5 g      0 t
ORIGIN

      Query Match      100.0%; Score 1; DB 10; Length 6;
      Best Local Similarity 100.0%; Pred. No. 0;
      Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
   |
Db 1 G 1

RESULT 31
BE726686/c
LOCUS      6 bp mRNA linear EST 14-SEP-2000
DEFINITION Chlamydomonas reinhardtii cDNA, mRNA sequence.
ACCESSION BE726686
VERSION BE726686.1 GI:10128110
KEYWORDS EST.
SOURCE Chlamydomonas reinhardtii.
ORGANISM Chlamydomonas reinhardtii.
REFERENCE 1 (bases 1 to 6)
AUTHORS Grossman,A., Davies,J., Federspiel,N., Harris,E., Lefebvre,P.,
McDermott,J.P., Silflow,C., Stern,D. and Surzycki,R.
TITLE Analyses of the Chlamydomonas reinhardtii Genome: A Model,
Unicellular System for Analyzing Gene Function and Regulation in
Vascular Plants; project phase 2
JOURNAL Unpublished (2000)
COMMENT Contact: Charles Hauser
DCMB Box 91000
Duke University
Durham, NC 27708-1000
Tel: 919 613 8159
Fax: 919 613 8177
Email: chauser@duke.edu.
Location/Qualifiers
1..6
/organism="Chlamydomonas reinhardtii"
/strain="CC-1690 wild type mt+ 2lgr"
/db_xref="taxon:3055"
/clone_lib="C. reinhardtii CC-1690, normalized, Lambda Zap
II"

FEATURES
source
1..6
/organism="Chlamydomonas reinhardtii"
/strain="CC-1690 wild type mt+ 2lgr"
/db_xref="taxon:3055"
/clone_lib="C. reinhardtii CC-1690, normalized, Lambda Zap
II"

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BASE COUNT      0 a      1 c      5 g      0 t
ORIGIN

Query Match      100.0%; Score 1; DB 10; Length 6;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 g 1
      |
DB      2 G 2

RESULT 32
BG897546      standard; RNA; EST; 7 BP.
ID BG897546
XX
AC BG897546;
XX
SV BG897546.1
XX
DT 09-JUN-2001 (Rel. 68, Created)
DT 14-NOV-2001 (Rel. 69, Last updated, Version 2)
XX
DE HOA14-1-H11 HOA (Human Osteoarthritic Cartilage) Homo sapiens cDNA, mRNA
DE sequence.
DE EST.
XX
KW Homo sapiens (human)
XX
OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
XX
RN [1]
RP MEDLINE: 21482651.
RP PUBMED: 11597177.
RA Kumar S., Connor J.R., Dodds R.A., Halsey W., Van Horn M., Mao J.,
RA Sathe G.M., Mui P., Agarwal P., Badger A.M., Lee J.C., Gowen M., Lark M.W.;
RA "Identification and initial characterization of 5000 expressed sequenced
RT tags (ESTs) each from adult human normal and osteoarthritic cartilage cDNA
RT libraries";
RL Osteoarthritiis Cartilage 9(7):641-653(2001).
XX
CC Contact: Sanjay Kumar
CC UW2109
CC GlaxoSmithKline
CC 709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA
CC Tel: 610-270-7245
CC Fax: 610-270-5598
CC Email: sanjay_kumar-legsk.com
CC Seq primer: T7.
XX
FH Key      Location/Qualifiers
FH source      1..7
FH      /db_xref="taxon:9606"
FH      /note="Vector: pSPORT 1; Site_1: SalI; Site_2: NotI;
FH      Directional"
FH      /organism="Homo sapiens"
FH      /clone_lib="HOA (Human Osteoarthritic Cartilage)"
FH      /tissue_type="cartilage"
FH      /lab_host="E.coli DH10 B"
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SQ      Sequence 7 BP; 1 A; 3 C; 1 G; 2 T; 0 other;

Query Match      100.0%; Score 1; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 g 1
      |
DB      7 G 7

RESULT 34
HSM007412
ID HSM007412      standard; RNA; EST; 7 BP.
XX
AC AL042562;
XX
SV AL042562.1
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XX 12-MAR-1999 (Rel. 59, Created)
DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX Homo sapiens mRNA; EST DKF2p434J1721_r1 (from clone DKF2p434J1721)
XX EST; expressed sequence tag.
XX Homo sapiens (human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
XX [1]
XX 1-7
RA Blum H., Bauersachs S., Mewes W., Gassenhuber J., Wiemann S.;
RT Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
RL MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX Clone from S. Wiemann, sequenced by LMU within the cDNA
CC sequencing consortium of the German Genome Project
CC No sl sequence available
CC This clone is available at the RZPD in Berlin
CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX Key Location/Qualifiers
FH source 1..7
FT /db_xref="taxon:9606"
FT /organism="Homo sapiens"
FT /clone="DKF2p434J1721"
FT /clone_lib="434 (synonym: htes3). Vector pSport1; host
FT DH10B; sites NotI + SalI"
FT /dev_stage="adult"
FT /tissue_type="testis"
XX Sequence 7 BP; 2 A; 1 C; 2 G; 2 T; 0 other;
SQ
Query Match 100.0%; Score 1; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. NO. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 g 1
Db 2 G 2
RESULT 35
HSM007412/c
ID HSM007412 standard; RNA; EST; 7 BP.
XX AL042562;
XX AL042562.1
SV AL042562.1
XX 12-MAR-1999 (Rel. 59, Created)
DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX Homo sapiens mRNA; EST DKF2p434J1721_r1 (from clone DKF2p434J1721)
XX EST; expressed sequence tag.
XX Homo sapiens (human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
XX [1]
XX 1-7
RA Blum H., Bauersachs S., Mewes W., Gassenhuber J., Wiemann S.;
RT Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
RL MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX Clone from S. Wiemann, sequenced by LMU within the cDNA
CC sequencing consortium of the German Genome Project
CC No sl sequence available
CC This clone is available at the RZPD in Berlin
CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX Key Location/Qualifiers
FH source 1..7
FT /db_xref="taxon:9606"
FT /organism="Homo sapiens"
FT /clone="DKF2p434J1721"
FT /clone_lib="434 (synonym: htes3). Vector pSport1; host
FT DH10B; sites NotI + SalI"
FT /dev_stage="adult"
FT /tissue_type="testis"
XX Sequence 7 BP; 2 A; 1 C; 2 G; 2 T; 0 other;
SQ
Query Match 100.0%; Score 1; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. NO. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 g 1
Db 2 G 2
RESULT 35
HSM007412/c
ID HSM007412 standard; RNA; EST; 7 BP.
XX AL042562;
XX AL042562.1
SV AL042562.1
XX 12-MAR-1999 (Rel. 59, Created)
DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX Homo sapiens mRNA; EST DKF2p434J1721_r1 (from clone DKF2p434J1721)
XX EST; expressed sequence tag.
XX Homo sapiens (human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
XX [1]
XX 1-7
RA Blum H., Bauersachs S., Mewes W., Gassenhuber J., Wiemann S.;
RT Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
RL MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX Clone from S. Wiemann, sequenced by LMU within the cDNA
CC sequencing consortium of the German Genome Project
CC No sl sequence available
CC This clone is available at the RZPD in Berlin
CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX Key Location/Qualifiers
FH source 1..7
FT /db_xref="taxon:9606"
FT /organism="Homo sapiens"
FT /clone="DKF2p434J1721"
FT /clone_lib="434 (synonym: htes3). Vector pSport1; host
FT DH10B; sites NotI + SalI"
FT /dev_stage="adult"
FT /tissue_type="testis"
XX Sequence 7 BP; 2 A; 1 C; 2 G; 2 T; 0 other;
SQ
Query Match 100.0%; Score 1; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. NO. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 g 1
Db 1 G 1
RESULT 36
HSM007502
ID HSM007502 standard; RNA; EST; 7 BP.
XX AL042652;
XX AL042652.1
SV AL042652.1
XX 12-MAR-1999 (Rel. 59, Created)
DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX Homo sapiens mRNA; EST DKF2p434N1921_r1 (from clone DKF2p434N1921)
XX EST; expressed sequence tag.
XX Homo sapiens (human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
XX [1]
XX 1-7
RA Blum H., Bauersachs S., Mewes W., Gassenhuber J., Wiemann S.;
RT Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
RL MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX Clone from S. Wiemann, sequenced by LMU within the cDNA
CC sequencing consortium of the German Genome Project
CC No sl sequence available
CC This clone is available at the RZPD in Berlin
CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX Key Location/Qualifiers
FH source 1..7
FT /db_xref="taxon:9606"
FT /organism="Homo sapiens"
FT /clone="DKF2p434N1921"
FT /clone_lib="434 (synonym: htes3). Vector pSport1; host
FT DH10B; sites NotI + SalI"

```

```

RL MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX Clone from S. Wiemann, sequenced by LMU within the cDNA
CC sequencing consortium of the German Genome Project
CC No sl sequence available
CC This clone is available at the RZPD in Berlin
CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX Key Location/Qualifiers
FH source 1..7
FT /db_xref="taxon:9606"
FT /organism="Homo sapiens"
FT /clone="DKF2p434J1721"
FT /clone_lib="434 (synonym: htes3). Vector pSport1; host
FT DH10B; sites NotI + SalI"
FT /dev_stage="adult"
FT /tissue_type="testis"
XX Sequence 7 BP; 2 A; 1 C; 2 G; 2 T; 0 other;
SQ
Query Match 100.0%; Score 1; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. NO. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 g 1
Db 1 G 1
RESULT 36
HSM007502
ID HSM007502 standard; RNA; EST; 7 BP.
XX AL042652;
XX AL042652.1
SV AL042652.1
XX 12-MAR-1999 (Rel. 59, Created)
DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX Homo sapiens mRNA; EST DKF2p434N1921_r1 (from clone DKF2p434N1921)
XX EST; expressed sequence tag.
XX Homo sapiens (human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
XX [1]
XX 1-7
RA Blum H., Bauersachs S., Mewes W., Gassenhuber J., Wiemann S.;
RT Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
RL MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX Clone from S. Wiemann, sequenced by LMU within the cDNA
CC sequencing consortium of the German Genome Project
CC No sl sequence available
CC This clone is available at the RZPD in Berlin
CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX Key Location/Qualifiers
FH source 1..7
FT /db_xref="taxon:9606"
FT /organism="Homo sapiens"
FT /clone="DKF2p434N1921"
FT /clone_lib="434 (synonym: htes3). Vector pSport1; host
FT DH10B; sites NotI + SalI"

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FT      /dev_stage="adult"
XX      /tissue_type="testis"
SQ      Sequence 7 BP; 0 A; 1 C; 3 G; 3 T; 0 other;

Query Match      100.0%; Score 1; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1 g 1
DB      2 G 2

RESULT 37
HSM007502/C
ID      HSM007502 standard; RNA; EST; 7 BP.
AC      AL042652;
XX
SV      AL042652.1
XX
DT      12-MAR-1999 (Rel. 59, Created)
DT      12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX
DE      Homo sapiens mRNA; EST DKFZp434N1921_r1 (from clone DKFZp434N1921)
XX
KW      EST; expressed sequence tag.
XX
OS      Homo sapiens (human)
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC      Eutheria; Primates; Catarrhini; Hominidae; Homo.
XX
[1]
RP      Blum H., Bauersachs S., Mewes W., Gassenhuber J., Wiemann S.;
RT      ;
RL      Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
RL      MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX
CC      Clone from S. Wiemann, sequenced by LMU within the cDNA
CC      sequencing consortium of the German Genome Project
CC      No sl sequence available
CC      This clone is available at the RZPD in Berlin
CC      Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC      Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
FH      Key      Location/Qualifiers
FT      source
FT      1..7
FT      /db_xref="taxon:9606"
FT      /organism="Homo sapiens"
FT      /clone="DKFZp434N1921"
FT      /clone_lib="434 (synonym: htes3). Vector pSport1; host
FT      DH10B; sites NotI + SalI"
FT      /dev_stage="adult"
FT      /tissue_type="testis"
XX
SQ      Sequence 7 BP; 0 A; 1 C; 3 G; 3 T; 0 other;

Query Match      100.0%; Score 1; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1 g 1
DB      1 G 1

RESULT 38
C58888
LOCUS      C58888      7 bp      mRNA      linear      EST 22-SEP-1997
DEFINITION      clone yk383a7 3', mRNA sequence.
ACCESSION      C58888
VERSION      C58888.1 GI:2417593
KEYWORDS      EST.
SOURCE      Caenorhabditis elegans.
ORGANISM      Caenorhabditis elegans.
REFERENCE      1 (bases 1 to 7)
AUTHORS      Kohara,Y., Motohashi,T., Tabara,H., Watanabe,H., Sugimoto,A., Sano
            ,M., Miyata,A. and Nishigaki,A.
TITLE      Expression map of the C.elegans genome
JOURNAL      Unpublished (1996)
COMMENT      Contact: Yuji Kohara
            Genome Biology Lab.
            National Institute of Genetics
            Yata 1111, Mishima, Shizuoka 411, Japan
            Tel: 81-559-81-6854
            Fax: 81-559-81-6855
            Email: ykohara@lab.nig.ac.jp.
FEATURES
            Location/Qualifiers
            1..7
            /organism="Caenorhabditis elegans"
            /strain="CB1489 him-8(e1489)"
            /db_xref="taxon:6239"
            /clone="yk383a7"
            /clone_lib="Yuji Kohara unpublished cDNA"
            /sex="hermaphrodite, male"
            /tissue_type="whole animal"
            /dev_stage="varied"
BASE COUNT      2 a      0 c      1 g      3 t      1 others
ORIGIN

Query Match      100.0%; Score 1; DB 10; Length 7;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1 g 1
DB      7 G 7

RESULT 39
HSM001420/C
ID      HSM001420 standard; RNA; EST; 8 BP.
XX
AC      AL037095;
XX
SV      AL037095.1
XX
DT      12-MAR-1999 (Rel. 59, Created)
DT      12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX
DE      Homo sapiens mRNA; EST DKFZp564L2064_r1 (from clone DKFZp564L2064)
XX
KW      EST; expressed sequence tag.
XX
OS      Homo sapiens (human)
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC      Eutheria; Primates; Catarrhini; Hominidae; Homo.
XX
[1]
RP      Duesterhoeft A., Lauber J., Mewes W., Gassenhuber J., Wiemann S.;
RT      ;
RL      Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
RL      MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX
CC      Clone from S. Wiemann, sequenced by Qiagen within the cDNA
CC      sequencing consortium of the German Genome Project

```

CC No sl sequence available
CC This clone is available at the RZPD in Berlin
CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de

XX Key Location/Qualifiers

FH source

FT 1. .8
FT /db_xref="taxon:9606"
FT /organism="Homo sapiens"
FT /clone="DKFZp564L2064"
FT /clone_lib="564 (synonym: hfbr2). Vector pAMP1; host
FT X1-2blue; sites NotI + SalI"
FT /dev_stage="fetal"
FT /tissue_type="brain"

XX Sequence 8 BP; 2 A; 3 C; 0 G; 3 T; 0 other;

Query Match 100.0%; Score 1; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1

Db 7 G 7

RESULT 40

HS0001743/C
ID HSM001743 standard; RNA; EST; 8 BP.

XX AC AL037413;

XX SV AL037413.1

XX DT 12-MAR-1999 (Rel. 59, Created)

XX DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)

XX DE Homo sapiens mRNA; EST DKFZp564L0771_s1 (from clone DKFZp564L0771)

XX KW EST; expressed sequence tag.

XX OS Homo sapiens (human)

XX OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;

XX OC Euthera; Primates; Catarrhini; Hominidae; Homo.

XX RN [1]

XX RA Bloeker H., Boescher M., Brandt P., Mewes W., Gassenhuber J., Wiemann S.;

XX RL Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.

XX RL MIPS, Am Klopferspitze 18a D-82152 Martinsried, GERMANY

XX XX Clone from S. Wiemann, sequenced by GBF within the cDNA

CC sequencing consortium of the German Genome Project

CC No sl sequence available

CC This clone is available at the RZPD in Berlin

CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059

CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de

XX Key Location/Qualifiers

FH source

FT 1. .8
FT /db_xref="taxon:9606"
FT /organism="Homo sapiens"
FT /clone="DKFZp564L0771"
FT /clone_lib="564 (synonym: hfbr2). Vector pAMP1; host
FT X1-2blue; sites NotI + SalI"
FT /dev_stage="fetal"
FT /tissue_type="brain"

XX Sequence 8 BP; 1 A; 7 C; 0 G; 0 T; 0 other;

Query Match 100.0%; Score 1; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1

Db 7 G 7

RESULT 41

HS0004451
ID HSM004451 standard; RNA; EST; 8 BP.

XX AC AL039975;

XX SV AL039975.1

XX DT 12-MAR-1999 (Rel. 59, Created)

XX DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)

XX DE Homo sapiens mRNA; EST DKFZp434K0712_r1 (from clone DKFZp434K0712)

XX KW EST; expressed sequence tag.

XX OS Homo sapiens (human)

XX OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;

XX OC Euthera; Primates; Catarrhini; Hominidae; Homo.

XX RN [1]

XX RA Duesterhoeft A., Lauber J., Mewes W., Gassenhuber J., Wiemann S.;

XX RL Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.

XX RL MIPS, Am Klopferspitze 18a D-82152 Martinsried, GERMANY

XX CC Clone from S. Wiemann, sequenced by Qiagen within the cDNA

CC sequencing consortium of the German Genome Project

CC No sl sequence available

CC This clone is available at the RZPD in Berlin

CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059

CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de

XX Key Location/Qualifiers

FH source

FT 1. .8
FT /db_xref="taxon:9606"
FT /organism="Homo sapiens"
FT /clone="DKFZp434K0712"
FT /clone_lib="434 (synonym: htes3). Vector pSport1; host
FT DH10B; sites NotI + SalI"
FT /dev_stage="adult"
FT /tissue_type="testis"

XX Sequence 8 BP; 2 A; 2 C; 2 G; 2 T; 0 other;

Query Match 100.0%; Score 1; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1

Db 1 G 1

RESULT 42

HS0004451/C

ID HSM004451 standard; RNA; EST; 8 BP.

XX AC AL039975;

XX

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SV AL039975.1
XX 12-MAR-1999 (Rel. 59, Created)
DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX
DE Homo sapiens mRNA; EST DKFZp434K0712_r1 (from clone DKFZp434K0712)
XX
KW EST; expressed sequence tag.
XX
OS Homo sapiens (human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
XX
RN [1]
RP 1-8
RA Dueterhoeft A., Lauber J., Mewes W., Gassenhuber J., Wiemann S.;
RT ;
RL Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
RI MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX
CC Clone from S. Wiemann, sequenced by Qiagen within the cDNA
CC sequencing consortium of the German Genome Project
CC No s1 sequence available
CC This clone is available at the RZPD in Berlin
CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
FH Key Location/Qualifiers
FT source
FT 1..8
FT /db_xref="taxon:9606"
FT /organism="Homo sapiens"
FT /clone="DKFZp434K0712"
FT /clone_lib="434 (synonym: htes3). Vector pSport1; host
FT DH10B; sites NotI + SalI"
FT /dev_stage="adult"
FT /tissue_type="testis"
XX
SQ Sequence 8 BP; 2 A; 2 C; 2 G; 2 T; 0 other;

Query Match 100.0%; Score 1; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
Db 8 G 8

RESULT 43
HSM007277
ID HSM007277 standard; RNA; EST; 8 BP.
XX
AC AL042427;
XX
SV AL042427.1
XX
DT 12-MAR-1999 (Rel. 59, Created)
DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX
DE Homo sapiens mRNA; EST DKFZp434C2421_r1 (from clone DKFZp434C2421)
XX
KW EST; expressed sequence tag.
XX
OS Homo sapiens (human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
XX
RN [1]
RP 1-8
RA Blum H., Bauersachs S., Mewes W., Gassenhuber J., Wiemann S.;
RT ;
RL Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
RI MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX
CC Clone from S. Wiemann, sequenced by LMU within the cDNA
CC sequencing consortium of the German Genome Project
CC No s1 sequence available
CC This clone is available at the RZPD in Berlin
CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
FH Key Location/Qualifiers
FT source
FT 1..8
FT /db_xref="taxon:9606"
FT /organism="Homo sapiens"
FT /clone="DKFZp434C2421"
FT /clone_lib="434 (synonym: htes3). Vector pSport1; host

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RL Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
RL MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX
CC Clone from S. Wiemann, sequenced by LMU within the cDNA
CC sequencing consortium of the German Genome Project
CC No s1 sequence available
CC This clone is available at the RZPD in Berlin
CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
FH Key Location/Qualifiers
FT source
FT 1..8
FT /db_xref="taxon:9606"
FT /organism="Homo sapiens"
FT /clone="DKFZp434C2421"
FT /clone_lib="434 (synonym: htes3). Vector pSport1; host
FT DH10B; sites NotI + SalI"
FT /dev_stage="adult"
FT /tissue_type="testis"
XX
SQ Sequence 8 BP; 2 A; 2 C; 2 G; 2 T; 0 other;

Query Match 100.0%; Score 1; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
Db 1 G 1

RESULT 44
HSM007277/c
ID HSM007277 standard; RNA; EST; 8 BP.
XX
AC AL042427;
XX
SV AL042427.1
XX
DT 12-MAR-1999 (Rel. 59, Created)
DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX
DE Homo sapiens mRNA; EST DKFZp434C2421_r1 (from clone DKFZp434C2421)
XX
KW EST; expressed sequence tag.
XX
OS Homo sapiens (human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
XX
RN [1]
RP 1-8
RA Blum H., Bauersachs S., Mewes W., Gassenhuber J., Wiemann S.;
RT ;
RL Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
RI MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX
CC Clone from S. Wiemann, sequenced by LMU within the cDNA
CC sequencing consortium of the German Genome Project
CC No s1 sequence available
CC This clone is available at the RZPD in Berlin
CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
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FT /organism="Homo sapiens"
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Search completed: July 15, 2002, 20:07:36
Job time: 14494 sec

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OS      Homo sapiens (human)
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC      Eutheria; Primates; Catarrhini; Hominidae; Homo.
XX
RN      [1]
RP      1-8
RT      ;
RL      Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
RL      MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX
CC      Clone from S. Wiemann, sequenced by LMU within the cDNA
CC      sequencing consortium of the German Genome Project
CC      No sl sequence available
CC      This clone is available at the RZPD in Berlin
CC      Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC      Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
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FH      Key      Location/Qualifiers
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FH      /organism="Homo sapiens"
FH      /clone="DKFZp434F012l"
FH      /clone_lib="434 (synonym: htes3). Vector pSport1; host
FH      DH10B; sites NotI + SalI"
FH      /dev_stage="adult"
FH      /tissue_type="testis"
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Query Match      100.0%; Score 1; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 g 1
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Db      1 G 1

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 16, 2002, 02:50:26 : Search time 12941.8 seconds
(without alignments)
1.672 Million cell updates/sec

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Sequence: 1 g 1

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 21979536 seqs, 10817449327 residues

Word size : 0

Total number of hits satisfying chosen parameters: 43959072

Minimum DB seq length: 0
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Post-processing: Listing first 45 summaries

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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	1	100.0	2	3	US-07-934-385-14
2	1	100.0	2	5	US-08-107-721-46
3	1	100.0	2	5	US-08-107-721B-46
4	1	100.0	2	15	US-09-172-828-15
5	1	100.0	2	16	US-09-284-725-201
6	1	100.0	2	17	US-09-306-333A-32
7	1	100.0	2	17	US-09-306-333A-32
8	1	100.0	2	17	US-09-387-777-2
9	1	100.0	2	17	US-09-387-777-3
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11	1	100.0	2	17	US-09-387-777-6
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13	1	100.0	2	17	US-09-387-777-7
14	1	100.0	2	17	US-09-387-777-8
15	1	100.0	2	17	US-09-387-777-9
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17	1	100.0	2	17	US-09-387-777-10
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19	1	100.0	2	17	US-09-387-777-12
20	1	100.0	2	17	US-09-387-777-14
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ALIGNMENTS

RESULT 1
US-07-934-385-14
: Sequence 14, Application US/07934385
: GENERAL INFORMATION:
: APPLICANT: LATHAM, JOHN
: APPLICANT: LEUNG, LAWRENCE
: TITLE OF INVENTION: APTAMERS SPECIFIC FOR BIOMOLECULES
: TITLE OF INVENTION: CONTAINING MODIFIED NUCLEOTIDE RESIDUES
: NUMBER OF SEQUENCES: 177
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: MORRISON & FOERSTER
: STREET: 755 Page Mill Road
: CITY: Palo Alto
: STATE: California
: COUNTRY: USA
: ZIP: 94304-1018
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/07/934,385
: FILING DATE: 19920821
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: GRACEY, NANCY J.
: REGISTRATION NUMBER: 28,216
: REFERENCE/DOCKET NUMBER: 24610-20022.22
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (415)813-5600
: TELEFAX: (415) 494-0792
: TELEX: 706141
: INFORMATION FOR SEQ ID NO: 14:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 2 base pairs
: TYPE: NUCLEIC ACID
: STRANDEDNESS: single
: TOPOLOGY: linear
: FEATURE:
: NAME/KEY: misc_difference
: LOCATION: replace(1,*)
: OTHER INFORMATION: /note= "This position is a
: biotin-17 nucleotide stretch of random sequences."
US-07-934-385-14

Query Match 100.0%; Score 1; DB 3; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 g 1
Db 2 G 2

RESULT 2
US-08-107-721-46
: Sequence 46, Application US/08107721
: GENERAL INFORMATION:
: APPLICANT: TOOLE, JOHN J.
: APPLICANT: GRIFFIN, LINDA C.
: APPLICANT: BOCK, LOUIS C.
: APPLICANT: LATHAM, JOHN A.
: APPLICANT: MUENCHAU, DARYL D.
: APPLICANT: KRAWCZYK, STEVEN
: TITLE OF INVENTION: APTAMERS SPECIFIC FOR BIOMOLECULES AND
: TITLE OF INVENTION: METHODS OF MAKING
: NUMBER OF SEQUENCES: 109
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: GILEAD SCIENCES, INC.
: STREET: 344 LAKESIDE DRIVE
: CITY: FOSTER CITY
: STATE: CALIFORNIA
: COUNTRY: USA
: ZIP: 94404
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/107,721
: FILING DATE: 20-AUG-1993
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: GRACEY, NANCY J.
: REGISTRATION NUMBER: 28216
: REFERENCE/DOCKET NUMBER: 24610-20022.20
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (415)574-3000
: TELEFAX: (415)578-9264
: INFORMATION FOR SEQ ID NO: 46:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 2 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: 1
: OTHER INFORMATION: /note= "This is a biotin-17
: nucleotide stretch of abasic residues."
US-08-107-721-46
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 g 1
Db 2 G 2
RESULT 3
US-08-107-721B-46
: Sequence 46, Application US/08107721B
: GENERAL INFORMATION:
: APPLICANT: TOOLE, JOHN J.
: APPLICANT: GRIFFIN, LINDA C.
: APPLICANT: BOCK, LOUIS C.
: APPLICANT: LATHAM, JOHN A.
: APPLICANT: MUENCHAU, DARYL D.
: APPLICANT: KRAWCZYK, STEVEN
: TITLE OF INVENTION: APTAMERS SPECIFIC FOR BIOMOLECULES AND
: TITLE OF INVENTION: METHODS OF MAKING

NUMBER OF SEQUENCES: 109
CORRESPONDENCE ADDRESS:
ADDRESSEE: GILEAD SCIENCES, INC.
STREET: 344 LAKEVIEW DRIVE
CITY: FOSTER CITY
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/107,721B
FILING DATE: 20-AUG-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: GRACEY, NANCY J.
REGISTRATION NUMBER: 28216
REFERENCE/DOCKET NUMBER: 24610-20022.20
TELEPHONE: (415)574-3000
TELEFAX: (415)578-9264
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 2 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1
OTHER INFORMATION: /note= "This is a biotin-17
US-08-107-721B-46

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Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1
Db 2 G 2

RESULT 4
US-09-172-828-15
GENERAL INFORMATION:
APPLICANT: Children's Medical Center Corporation
APPLICANT: Klagsbrun, Michael
APPLICANT: Elenius, Klaus
APPLICANT: Corfas, Gabriel
TITLE OF INVENTION: Novel Human EGF Receptors and Use
FILE REFERENCE: 47758-PCT
CURRENT APPLICATION NUMBER: US/09/172,828
CURRENT FILING DATE: 1998-10-15
NUMBER OF SEQ ID NOS: 31
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 15
LENGTH: 2
TYPE: DNA
ORGANISM: mouse
US-09-172-828-15

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1
Db 1 g 1
RESULT 5
US-09-284-725-201/c
Sequence 201, Application US/09284725
GENERAL INFORMATION:
APPLICANT: Quint, Wilhelmus
APPLICANT: Van Doorn, Leendert
TITLE OF INVENTION: Probes, methods and kits for detection and
TITLE OF INVENTION: typing of Helicobacter pylori nucleic acids in biological
NUMBER OF SEQUENCES: 280
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson & Bear, LLP
STREET: 620 Newport Center Drive, 16th Floor
CITY: Newport Beach
STATE: CA
COUNTRY: USA
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/284,725
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP96/870131.8
FILING DATE: 16-OCT-1996
APPLICATION NUMBER: PCT/EP97/05614
FILING DATE: 10-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Altman, Daniel E.
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: INNOG2.001APC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (949) 760-0404
TELEFAX: (949) 760-9395
INFORMATION FOR SEQ ID NO: 201:
SEQUENCE CHARACTERISTICS:
LENGTH: 2 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-09-284-725-201

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1
Db 2 G 2

RESULT 6
US-09-306-333A-32
Sequence 32, Application US/09306333A
GENERAL INFORMATION:
APPLICANT: Academy of Applied Science
TITLE OF INVENTION: BRCA1 and hMLH1 Gene Primer Sequences and Method for
TITLE OF INVENTION: testing
FILE REFERENCE: BRCA1
CURRENT APPLICATION NUMBER: US/09/306,333A
CURRENT FILING DATE: 1999-05-06

;; PRIOR APPLICATION NUMBER: PCT/IB00/01607
;; PRIOR FILING DATE: 2000-11-06
;; NUMBER OF SEQ ID NOS: 122
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 32
;; LENGTH: 2
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-09-306-333A-32

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Caps 0;

Qy 1 q 1
Db 2 g 2

RESULT 7

US-09-306-333A-32/c
;; Sequence 32, Application US/09306333A
;; GENERAL INFORMATION:
;; APPLICANT: Academy of Applied Science
;; TITLE OF INVENTION: BRCA1 and hMLH1 Gene Primer Sequences and Method for
;; FILE REFERENCE: BRCA1
;; CURRENT APPLICATION NUMBER: US/09/306,333A
;; CURRENT FILING DATE: 1999-05-06
;; PRIOR APPLICATION NUMBER: PCT/IB00/01607
;; PRIOR FILING DATE: 2000-11-06
;; NUMBER OF SEQ ID NOS: 122
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 32
;; LENGTH: 2
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-09-306-333A-32

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Matches 1; Conservative 0; Mismatches 0; Indels 0; Caps 0;

Qy 1 q 1
Db 1 g 1

RESULT 8

US-09-387-777-2/c
;; Sequence 2, Application US/09387777
;; GENERAL INFORMATION:
;; APPLICANT: Hadar Kless
;; TITLE OF INVENTION: TEMPLATE-DEPENDENT NUCLEIC ACID
;; TITLE OF INVENTION: POLYMERIZATION USING OLIGONUCLEOTIDE
;; TITLE OF INVENTION: TRIPHOSPHATES BUILDING BLOCKS
;; NUMBER OF SEQUENCES: 88
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Mark M. Friedman c/o Anthony Castorina
;; STREET: 2001 Jefferson Davis Highway, Suite 207
;; CITY: Arlington
;; STATE: Virginia
;; COUNTRY: United States of America
;; ZIP: 22202
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk
;; COMPUTER: Twinhead* Slimnote-890TX
;; OPERATING SYSTEM: MS DOS version 6.2,
;; SOFTWARE: Word for Windows version 2.0 converted
;; to an ASCII file

;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/387,777
;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER:
;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Friedman, Mark M.
;; REGISTRATION NUMBER: 33,883
;; REFERENCE/DOCKET NUMBER: 34/40
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 972-3-5625553
;; TELEFAX: 972-3-5625554
;; TELEX:
;; INFORMATION FOR SEQ ID NO: 2:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 2
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
US-09-387-777-2

Query Match 100.0%; Score 1; DB 17; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Caps 0;

Qy 1 q 1
Db 2 g 2

RESULT 9

US-09-387-777-3
;; Sequence 3, Application US/09387777
;; GENERAL INFORMATION:
;; APPLICANT: Hadar Kless
;; TITLE OF INVENTION: TEMPLATE-DEPENDENT NUCLEIC ACID
;; TITLE OF INVENTION: POLYMERIZATION USING OLIGONUCLEOTIDE
;; TITLE OF INVENTION: TRIPHOSPHATES BUILDING BLOCKS
;; NUMBER OF SEQUENCES: 88
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Mark M. Friedman c/o Anthony Castorina
;; STREET: 2001 Jefferson Davis Highway, Suite 207
;; CITY: Arlington
;; STATE: Virginia
;; COUNTRY: United States of America
;; ZIP: 22202
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk
;; COMPUTER: Twinhead* Slimnote-890TX
;; OPERATING SYSTEM: MS DOS version 6.2,
;; OPERATING SYSTEM: Windows version 3.11
;; SOFTWARE: Word for Windows version 2.0 converted
;; to an ASCII file
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/387,777
;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER:
;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Friedman, Mark M.
;; REGISTRATION NUMBER: 33,883
;; REFERENCE/DOCKET NUMBER: 34/40
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 972-3-5625553
;; TELEFAX: 972-3-5625554
;; TELEX:
;; INFORMATION FOR SEQ ID NO: 3:
;; SEQUENCE CHARACTERISTICS:

```
:      LENGTH: 2
:      TYPE: nucleic acid
:      STRANDEDNESS: single
:      TOPOLOGY: linear
US-09-387-777-3

Query Match      100.0%; Score 1; DB 17; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 g 1
Db      2 G 2

RESULT 10
US-09-387-777-5/c
: Sequence 5, Application US/09387777
: GENERAL INFORMATION:
: APPLICANT: Hadar Kless
: TITLE OF INVENTION: TEMPLATE-DEPENDENT NUCLEIC ACID
: TITLE OF INVENTION: POLYMERIZATION USING OLIGONUCLEOTIDE
: NUMBER OF SEQUENCES: 88
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Mark M. Friedman c/o Anthony Castorina
: STREET: 2001 Jefferson Davis Highway, Suite 207
: CITY: Arlington
: STATE: Virginia
: COUNTRY: United States of America
: ZIP: 22202
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk
: COMPUTER: Twinhead* Slimnote-890TX
: OPERATING SYSTEM: MS DOS version 6.2,
: OPERATING SYSTEM: Windows version 3.11
: SOFTWARE: Word for Windows version 2.0 converted
: SOFTWARE: to an ASCII file
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/387,777
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER:
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: Friedman, Mark M.
: REGISTRATION NUMBER: 33,883
: REFERENCE/DOCKET NUMBER: 34/40
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 972-3-5625553
: TELEFAX: 972-3-5625554
: TELEX:
: INFORMATION FOR SEQ ID NO: 5:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 2
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
US-09-387-777-5

Query Match      100.0%; Score 1; DB 17; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 g 1
Db      1 G 1

RESULT 11
```

```
US-09-387-777-6/c
: Sequence 6, Application US/09387777
: GENERAL INFORMATION:
: APPLICANT: Hadar Kless
: TITLE OF INVENTION: TEMPLATE-DEPENDENT NUCLEIC ACID
: TITLE OF INVENTION: POLYMERIZATION USING OLIGONUCLEOTIDE
: NUMBER OF SEQUENCES: 88
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Mark M. Friedman c/o Anthony Castorina
: STREET: 2001 Jefferson Davis Highway, Suite 207
: CITY: Arlington
: STATE: Virginia
: COUNTRY: United States of America
: ZIP: 22202
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk
: COMPUTER: Twinhead* Slimnote-890TX
: OPERATING SYSTEM: MS DOS version 6.2,
: OPERATING SYSTEM: Windows version 3.11
: SOFTWARE: Word for Windows version 2.0 converted
: SOFTWARE: to an ASCII file
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/387,777
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER:
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: Friedman, Mark M.
: REGISTRATION NUMBER: 33,883
: REFERENCE/DOCKET NUMBER: 34/40
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 972-3-5625553
: TELEFAX: 972-3-5625554
: TELEX:
: INFORMATION FOR SEQ ID NO: 6:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 2
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
US-09-387-777-6

Query Match      100.0%; Score 1; DB 17; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 g 1
Db      2 G 2

RESULT 12
US-09-387-777-7
: Sequence 7, Application US/09387777
: GENERAL INFORMATION:
: APPLICANT: Hadar Kless
: TITLE OF INVENTION: TEMPLATE-DEPENDENT NUCLEIC ACID
: TITLE OF INVENTION: POLYMERIZATION USING OLIGONUCLEOTIDE
: NUMBER OF SEQUENCES: 88
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Mark M. Friedman c/o Anthony Castorina
: STREET: 2001 Jefferson Davis Highway, Suite 207
: CITY: Arlington
: STATE: Virginia
: COUNTRY: United States of America
: ZIP: 22202
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk
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COMPUTER: Twinhead* Slimnote-890TX
OPERATING SYSTEM: MS DOS version 6.2,
SOFTWARE: Windows version 3.11
SOFTWARE: Word for Windows version 2.0 converted
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/387,777
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Friedmam, Mark M.
REGISTRATION NUMBER: 33,883
REFERENCE/DOCKET NUMBER: 34/40
TELECOMMUNICATION INFORMATION:
TELEPHONE: 972-3-5625553
TELEFAX: 972-3-5625554
TELEX:
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 2
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-387-777-7

Query Match 100.0%; Score 1; DB 17; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
Db 2 G 2

RESULT 13
US-09-387-777-7/c
Sequence 7, Application US/09387777
GENERAL INFORMATION:
APPLICANT: Hadar Kless
TITLE OF INVENTION: TEMPLATE-DEPENDENT NUCLEIC ACID
POLYMERIZATION USING OLIGONUCLEOTIDE
TITLE OF INVENTION: TRIPHOSPHATES BUILDING BLOCKS
NUMBER OF SEQUENCES: 88
CORRESPONDENCE ADDRESS:
ADDRESSEE: Mark M. Friedman c/o Anthony Castorina
STREET: 2001 Jefferson Davis Highway, Suite 207
CITY: Arlington
STATE: Virginia
COUNTRY: United States of America
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk
COMPUTER: Twinhead* Slimnote-890TX
OPERATING SYSTEM: MS DOS version 6.2,
SOFTWARE: Windows version 3.11
SOFTWARE: Word for Windows version 2.0 converted
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/387,777
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Friedmam, Mark M.
REGISTRATION NUMBER: 33,883
REFERENCE/DOCKET NUMBER: 34/40
TELECOMMUNICATION INFORMATION:

TELEPHONE: 972-3-5625553
TELEFAX: 972-3-5625554
TELEX:
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 2
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-387-777-7

Query Match 100.0%; Score 1; DB 17; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 q 1
Db 1 G 1

RESULT 14
US-09-387-777-8/c
Sequence 8, Application US/09387777
GENERAL INFORMATION:
APPLICANT: Hadar Kless
TITLE OF INVENTION: TEMPLATE-DEPENDENT NUCLEIC ACID
POLYMERIZATION USING OLIGONUCLEOTIDE
TITLE OF INVENTION: TRIPHOSPHATES BUILDING BLOCKS
NUMBER OF SEQUENCES: 88
CORRESPONDENCE ADDRESS:
ADDRESSEE: Mark M. Friedman c/o Anthony Castorina
STREET: 2001 Jefferson Davis Highway, Suite 207
CITY: Arlington
STATE: Virginia
COUNTRY: United States of America
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk
COMPUTER: Twinhead* Slimnote-890TX
OPERATING SYSTEM: MS DOS version 6.2,
SOFTWARE: Windows version 3.11
SOFTWARE: Word for Windows version 2.0 converted
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/387,777
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Friedmam, Mark M.
REGISTRATION NUMBER: 33,883
REFERENCE/DOCKET NUMBER: 34/40
TELECOMMUNICATION INFORMATION:
TELEPHONE: 972-3-5625553
TELEFAX: 972-3-5625554
TELEX:
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 2
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-387-777-8

Query Match 100.0%; Score 1; DB 17; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1


```
Db      1 G 1

RESULT 15
US-09-387-777-9
; Sequence 9, Application US/09387777
; GENERAL INFORMATION:
; APPLICANT: Hadar Kless
; TITLE OF INVENTION: TEMPLATE-DEPENDENT NUCLEIC ACID
; TITLE OF INVENTION: POLYMERIZATION USING OLIGONUCLEOTIDE
; TITLE OF INVENTION: TRIPHOSPHATES BUILDING BLOCKS
; NUMBER OF SEQUENCES: 88
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Mark M. Friedman c/o Anthony Castorina
; STREET: 2001 Jefferson Davis Highway, Suite 207
; CITY: Arlington
; STATE: Virginia
; COUNTRY: United States of America
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk
; COMPUTER: Twinhead* Slimnote-890TX
; OPERATING SYSTEM: MS DOS version 6.2,
; SOFTWARE: Word for Windows version 2.0 converted
; CURRENT APPLICATION DATA:
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/387,777
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Friedman, Mark M.
; REGISTRATION NUMBER: 33,883
; REFERENCE/DOCKET NUMBER: 34/40
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 972-3-5625553
; TELEFAX: 972-3-5625554
; TELEX:
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-387-777-9

Query Match      100.0%; Score 1; DB 17; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 g 1
        |
Db      1 G 1

RESULT 17
US-09-387-777-10/c
; Sequence 10, Application US/09387777
; GENERAL INFORMATION:
; APPLICANT: Hadar Kless
; TITLE OF INVENTION: TEMPLATE-DEPENDENT NUCLEIC ACID
; TITLE OF INVENTION: POLYMERIZATION USING OLIGONUCLEOTIDE
; TITLE OF INVENTION: TRIPHOSPHATES BUILDING BLOCKS
; NUMBER OF SEQUENCES: 88
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Mark M. Friedman c/o Anthony Castorina
; STREET: 2001 Jefferson Davis Highway, Suite 207
; CITY: Arlington
; STATE: Virginia
; COUNTRY: United States of America
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk
; COMPUTER: Twinhead* Slimnote-890TX
; OPERATING SYSTEM: MS DOS version 6.2,
; SOFTWARE: Word for Windows version 2.0 converted
; CURRENT APPLICATION DATA:
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/387,777
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Friedman, Mark M.
; REGISTRATION NUMBER: 33,883
; REFERENCE/DOCKET NUMBER: 34/40
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 972-3-5625553
; TELEFAX: 972-3-5625554
; TELEX:
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-387-777-10

Query Match      100.0%; Score 1; DB 17; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 g 1
        |
Db      1 G 1

RESULT 16
US-09-387-777-10
; Sequence 10, Application US/09387777
; GENERAL INFORMATION:
; APPLICANT: Hadar Kless
; TITLE OF INVENTION: TEMPLATE-DEPENDENT NUCLEIC ACID
; TITLE OF INVENTION: POLYMERIZATION USING OLIGONUCLEOTIDE
; TITLE OF INVENTION: TRIPHOSPHATES BUILDING BLOCKS
; NUMBER OF SEQUENCES: 88
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Mark M. Friedman c/o Anthony Castorina
; STREET: 2001 Jefferson Davis Highway, Suite 207
; CITY: Arlington
; STATE: Virginia
; COUNTRY: United States of America
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk
; COMPUTER: Twinhead* Slimnote-890TX
; OPERATING SYSTEM: MS DOS version 6.2,
; SOFTWARE: Word for Windows version 2.0 converted
; CURRENT APPLICATION DATA:
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/387,777
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Friedman, Mark M.
; REGISTRATION NUMBER: 33,883
; REFERENCE/DOCKET NUMBER: 34/40
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 972-3-5625553
; TELEFAX: 972-3-5625554
; TELEX:
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-387-777-9

Query Match      100.0%; Score 1; DB 17; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 g 1
        |
Db      1 G 1

RESULT 16
US-09-387-777-10
; Sequence 10, Application US/09387777
; GENERAL INFORMATION:
; APPLICANT: Hadar Kless
; TITLE OF INVENTION: TEMPLATE-DEPENDENT NUCLEIC ACID
; TITLE OF INVENTION: POLYMERIZATION USING OLIGONUCLEOTIDE
; TITLE OF INVENTION: TRIPHOSPHATES BUILDING BLOCKS
; NUMBER OF SEQUENCES: 88
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Mark M. Friedman c/o Anthony Castorina
; STREET: 2001 Jefferson Davis Highway, Suite 207
; CITY: Arlington
; STATE: Virginia
; COUNTRY: United States of America
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk
; COMPUTER: Twinhead* Slimnote-890TX
; OPERATING SYSTEM: MS DOS version 6.2,
; SOFTWARE: Word for Windows version 2.0 converted
; CURRENT APPLICATION DATA:
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/387,777
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Friedman, Mark M.
; REGISTRATION NUMBER: 33,883
; REFERENCE/DOCKET NUMBER: 34/40
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 972-3-5625553
; TELEFAX: 972-3-5625554
; TELEX:
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-387-777-9

Query Match      100.0%; Score 1; DB 17; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 g 1
        |
Db      1 G 1
```

ATTORNEY/AGENT INFORMATION:
NAME: Friedman, Mark M.
REGISTRATION NUMBER: 33,883
REFERENCE/DOCKET NUMBER: 34/40
TELECOMMUNICATION INFORMATION:
TELEPHONE: 972-3-562553
TELEFAX: 972-3-562554
TELEX:
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 2
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-387-777-10

Query Match 100.0%; Score 1; DB 17; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
Db 2 G 2

RESULT 18
US-09-387-777-11
Sequence 11, Application US/0938777
GENERAL INFORMATION:
APPLICANT: Hadar Kless
TITLE OF INVENTION: TEMPLATE-DEPENDENT NUCLEIC ACID
TITLE OF INVENTION: POLYMERIZATION USING OLIGONUCLEOTIDE
TITLE OF INVENTION: TRIPHOSPHATES BUILDING BLOCKS
NUMBER OF SEQUENCES: 88
CORRESPONDENCE ADDRESS:
ADDRESSEE: Mark M. Friedman c/o Anthony Castorina
STREET: 2001 Jefferson Davis Highway, Suite 207
CITY: Arlington
STATE: Virginia
COUNTRY: United States of America
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk
COMPUTER: Twinhead* Slimnote-890TX
OPERATING SYSTEM: MS DOS version 6.2
OPERATING SYSTEM: Windows version 3.11
SOFTWARE: Word for Windows version 2.0 converted
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/387.777
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Friedman, Mark M.
REGISTRATION NUMBER: 33,883
REFERENCE/DOCKET NUMBER: 34/40
TELEPHONE: 972-3-562553
TELEFAX: 972-3-562554
TELEX:
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 2
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-387-777-11

Query Match 100.0%; Score 1; DB 17; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 g 1
Db 1 G 1
RESULT 19
US-09-387-777-12
Sequence 12, Application US/0938777
GENERAL INFORMATION:
APPLICANT: Hadar Kless
TITLE OF INVENTION: TEMPLATE-DEPENDENT NUCLEIC ACID
TITLE OF INVENTION: POLYMERIZATION USING OLIGONUCLEOTIDE
TITLE OF INVENTION: TRIPHOSPHATES BUILDING BLOCKS
NUMBER OF SEQUENCES: 88
CORRESPONDENCE ADDRESS:
ADDRESSEE: Mark M. Friedman c/o Anthony Castorina
STREET: 2001 Jefferson Davis Highway, Suite 207
CITY: Arlington
STATE: Virginia
COUNTRY: United States of America
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk
COMPUTER: Twinhead* Slimnote-890TX
OPERATING SYSTEM: MS DOS version 6.2
OPERATING SYSTEM: Windows version 3.11
SOFTWARE: Word for Windows version 2.0 converted
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/387,777
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Friedman, Mark M.
REGISTRATION NUMBER: 33,883
REFERENCE/DOCKET NUMBER: 34/40
TELEPHONE: 972-3-562553
TELEFAX: 972-3-562554
TELEX:
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 2
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-387-777-12

Query Match 100.0%; Score 1; DB 17; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
Db 1 G 1

RESULT 20
US-09-387-777-14/c
Sequence 14, Application US/0938777
GENERAL INFORMATION:
APPLICANT: Hadar Kless
TITLE OF INVENTION: TEMPLATE-DEPENDENT NUCLEIC ACID
TITLE OF INVENTION: POLYMERIZATION USING OLIGONUCLEOTIDE
TITLE OF INVENTION: TRIPHOSPHATES BUILDING BLOCKS

```

:
: NUMBER OF SEQUENCES: 88
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Mark M. Friedman c/o Anthony Castorina
: STREET: 2001 Jefferson Davis Highway, Suite 207
: CITY: Arlington
: STATE: Virginia
: COUNTRY: United States of America
: ZIP: 22202
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk
: COMPUTER: Twinhead* Slimnote-890TX
: OPERATING SYSTEM: MS DOS version 6.2,
: OPERATING SYSTEM: Windows version 3.11
: SOFTWARE: Word for Windows version 2.0 converted
: SOFTWARE: to an ASCII file
: CURRENT APPLICATION DATA: US/09/387,777
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER:
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: Friedman, Mark M.
: REGISTRATION NUMBER: 33,883
: REFERENCE/DOCKET NUMBER: 34/40
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 972-3-562553
: TELEFAX: 972-3-562554
: TELEX:
: INFORMATION FOR SEQ ID NO: 14:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 2
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: US-09-387-777-14

Query Match 100.0%; Score 1; DB 17; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
Db 2 G 2

RESULT 21
US-09-387-777-15
: Sequence 15, Application US/09387777
: GENERAL INFORMATION:
: APPLICANT: Hadar Kless
: TITLE OF INVENTION: TEMPLATE-DEPENDENT NUCLEIC ACID
: TITLE OF INVENTION: POLYMERIZATION USING OLIGONUCLEOTIDE
: TITLE OF INVENTION: TRIPHOSPHATES BUILDING BLOCKS
: NUMBER OF SEQUENCES: 88
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Mark M. Friedman c/o Anthony Castorina
: STREET: 2001 Jefferson Davis Highway, Suite 207
: CITY: Arlington
: STATE: Virginia
: COUNTRY: United States of America
: ZIP: 22202
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk
: COMPUTER: Twinhead* Slimnote-890TX
: OPERATING SYSTEM: MS DOS version 6.2,
: OPERATING SYSTEM: Windows version 3.11
: SOFTWARE: Word for Windows version 2.0 converted
: SOFTWARE: to an ASCII file
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/387,777
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER:
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: Friedman, Mark M.
: REGISTRATION NUMBER: 33,883
: REFERENCE/DOCKET NUMBER: 74/77
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 972-3-562553
: TELEFAX: 972-3-562554
: TELEX:
: INFORMATION FOR SEQ ID NO: 19:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 2
```

```

:
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER:
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: Friedman, Mark M.
: REGISTRATION NUMBER: 33,883
: REFERENCE/DOCKET NUMBER: 34/40
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 972-3-562553
: TELEFAX: 972-3-562554
: TELEX:
: INFORMATION FOR SEQ ID NO: 15:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 2
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: US-09-387-777-15

Query Match 100.0%; Score 1; DB 17; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
Db 2 G 2

RESULT 22
US-09-472-035A-19
: Sequence 19, Application US/09472035A
: GENERAL INFORMATION:
: APPLICANT: Yechezkel Kashi et al.
: TITLE OF INVENTION: ABUNDANT, WELL DISTRIBUTED AND
: TITLE OF INVENTION: HYPERPOLYMORPHIC SIMPLE SEQUENCE REPEATS
: TITLE OF INVENTION: IN PROKARYOTE GENOMES AND USE OF SAME FOR
: TITLE OF INVENTION: PROKARYOTE CLASSIFICATION AND TYPING
: NUMBER OF SEQUENCES: 42
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Mark M. Friedman c/o Anthony Castorina
: STREET: 2001 Jefferson Davis Highway, Suite 207
: CITY: Arlington
: STATE: Virginia
: COUNTRY: United States of America
: ZIP: 22202
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk
: COMPUTER: Twinhead* Slimnote-890TX
: OPERATING SYSTEM: MS DOS version 6.2,
: OPERATING SYSTEM: Windows version 3.11
: SOFTWARE: Word for Windows version 2.0 converted to
: SOFTWARE: an ASCII file
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/472,035A
: FILING DATE:
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER:
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: Friedman, Mark M.
: REGISTRATION NUMBER: 33,883
: REFERENCE/DOCKET NUMBER: 74/77
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 972-3-562553
: TELEFAX: 972-3-562554
: TELEX:
: INFORMATION FOR SEQ ID NO: 19:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 2
```

;
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-09-472-035A-19

Query Match 100.0%; Score 1; DB 18; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
|
Db 1 G 1

RESULT 23

US-09-472-035A-20/c
; Sequence 20, Application US/09472035A
; GENERAL INFORMATION:
; APPLICANT: Yechezkel kashi et al.
; TITLE OF INVENTION: ABUNDANT, WELL DISTRIBUTED AND
; TITLE OF INVENTION: HYPERPOLYMORPHIC SIMPLE SEQUENCE REPEATS
; TITLE OF INVENTION: IN PROKARYOTE GENOMES AND USE OF SAME FOR
; TITLE OF INVENTION: PROKARYOTE CLASSIFICATION AND TYPING
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Mark M. Friedman c/o Anthony Castorina
; STREET: 2001 Jefferson Davis Highway, Suite 207
; CITY: Arlington
; STATE: Virginia
; COUNTRY: United States of America
; ZIP: 22202

; COMPUTER READABLE FORM:
; MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk
; COMPUTER: Twinhead* Slimnote-890TX
; OPERATING SYSTEM: MS DOS version 6.2,
; OPERATING SYSTEM: Windows version 3.11
; SOFTWARE: Word for Windows version 2.0 converted to
; SOFTWARE: an ASCII file
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/472,035A
; FILING DATE:

; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Friedman, Mark M.
; REGISTRATION NUMBER: 33,883
; REFERENCE/DOCKET NUMBER: 74/77
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 972-3-5625553
; TELEFAX: 972-3-5625554
; TELEX:

; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-09-472-035A-20

Query Match 100.0%; Score 1; DB 18; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
|
Db 2 G 2

RESULT 24

US-09-634-306B-52280

US-09-634-306B-51869/c
; Sequence 51869, Application US/09634306B
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/09/634,306B
; CURRENT FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 51869
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-09-634-306B-51869

Query Match 100.0%; Score 1; DB 24; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
|
Db 2 G 2

RESULT 25

US-09-634-306B-52280/c
; Sequence 52280, Application US/09634306B
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/09/634,306B
; CURRENT FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 52280
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-09-634-306B-52280

Query Match 100.0%; Score 1; DB 24; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
|
Db 2 G 2

RESULT 26

US-09-634-306B-52357/c
; Sequence 52357, Application US/09634306B
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/09/634,306B
; CURRENT FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52357
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-09-634-306B-52357

Query Match 100.0%; Score 1; DB 24; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
|
Db 2 G 2

RESULT 27

US-09-634-306B-53003/c
; Sequence 53003, Application US/09634306B
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/09/634,306B
; CURRENT FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358

; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 53003
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-09-634-306B-53003

Query Match 100.0%; Score 1; DB 24; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
|
Db 2 G 2

RESULT 28

US-09-634-306B-58305/c
; Sequence 58305, Application US/09634306B
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/09/634,306B
; CURRENT FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 58305
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-09-634-306B-58305

Query Match 100.0%; Score 1; DB 24; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
|
Db 1 G 1

RESULT 29

US-09-634-306B-175312
; Sequence 175312, Application US/09634306B
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/09/634,306B
; CURRENT FILING DATE: 2002-02-21

; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 175312
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-09-634-306B-175312

Query Match 100.0%; Score 1; DB 24; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
|
Db 1 g 1

RESULT 30
US-09-634-306B-175337
; Sequence 175337, Application US/09634306B
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/09/634,306B
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 175337
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-09-634-306B-175337

Query Match 100.0%; Score 1; DB 24; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
|
Db 1 g 1

RESULT 31
US-09-634-306B-175354
; Sequence 175354, Application US/09634306B
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/09/634,306B
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 175354
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-09-634-306B-175354

Query Match 100.0%; Score 1; DB 24; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
|
Db 1 g 1

RESULT 32
US-09-634-306B-175401
; Sequence 175401, Application US/09634306B
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/09/634,306B
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 175401
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human

US-09-634-306B-175401

Query Match 100.0%; Score 1; DB 24; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
|
Db 1 g 1

RESULT 33

US-09-634-306B-175403
; Sequence 175403, Application US/09634306B
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/09/634,306B
; CURRENT FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 175403
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-09-634-306B-175403

Query Match 100.0%; Score 1; DB 24; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
|
Db 1 g 1

RESULT 34

US-09-634-306B-175415
; Sequence 175415, Application US/09634306B
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/09/634,306B
; CURRENT FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363

; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 175415
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-09-634-306B-175415

Query Match 100.0%; Score 1; DB 24; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
|
Db 1 g 1

RESULT 35

US-09-634-306B-175419
; Sequence 175419, Application US/09634306B
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/09/634,306B
; CURRENT FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 175419
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-09-634-306B-175419

Query Match 100.0%; Score 1; DB 24; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
|
Db 1 g 1

RESULT 36

US-09-634-306B-175426
; Sequence 175426, Application US/09634306B
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129

; CURRENT APPLICATION NUMBER: US/09/634,306B
; CURRENT FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 175426
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-09-634-306B-175426

Query Match 100.0%; Score 1; DB 24; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
|
Db 1 g 1

RESULT 37
US-09-634-306B-175433
; Sequence 175433, Application US/09634306B
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/09/634,306B
; CURRENT FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 175433
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-09-634-306B-175433

Query Match 100.0%; Score 1; DB 24; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
|

Db 1 g 1

RESULT 38
US-09-634-306B-175849
; Sequence 175849, Application US/09634306B
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/09/634,306B
; CURRENT FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 175849
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-09-634-306B-175849

Query Match 100.0%; Score 1; DB 24; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
|
Db 1 g 1

RESULT 39
US-09-634-306B-176848
; Sequence 176848, Application US/09634306B
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/09/634,306B
; CURRENT FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 176848
; LENGTH: 2

TYPE: DNA
ORGANISM: Human
US-09-634-306B-176848

Query Match 100.0%; Score 1; DB 24; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
|
Db 1 g 1

RESULT 40

US-09-634-306B-176849
Sequence 176849, Application US/09634306B
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/09/634.306B
CURRENT FILING DATE: 2002-02-21
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 176849
LENGTH: 2
TYPE: DNA
ORGANISM: Human
US-09-634-306B-176849

Query Match 100.0%; Score 1; DB 24; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
|
Db 1 g 1

RESULT 41

US-09-634-306B-176880
Sequence 176880, Application US/09634306B
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/09/634.306B
CURRENT FILING DATE: 2002-02-21
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218

PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 176880
LENGTH: 2
TYPE: DNA
ORGANISM: Human
US-09-634-306B-176880

Query Match 100.0%; Score 1; DB 24; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
|
Db 1 g 1

RESULT 42

US-09-634-306B-178420
Sequence 178420, Application US/09634306B
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/09/634.306B
CURRENT FILING DATE: 2002-02-21
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 178420
LENGTH: 2
TYPE: DNA
ORGANISM: Human
US-09-634-306B-178420

Query Match 100.0%; Score 1; DB 24; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
|
Db 1 g 1

RESULT 43

US-09-634-306B-178440
Sequence 178440, Application US/09634306B
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/09/634,306B
; CURRENT FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 178440
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-09-634-306B-178440

Query Match 100.0%; Score 1; DB 24; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1
|
Db 1 g 1

RESULT 44
US-09-634-306B-178440/c
; Sequence 178440, Application US/09634306B
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/09/634,306B
; CURRENT FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 178440
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-09-634-306B-178440

Query Match 100.0%; Score 1; DB 24; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1
|
Db 2 g 2

RESULT 45
US-09-634-306B-178617
; Sequence 178617, Application US/09634306B
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/09/634,306B
; CURRENT FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 178617
; LENGTH: 2
; TYPE: DNA
; ORGANISM: Human
US-09-634-306B-178617

Query Match 100.0%; Score 1; DB 24; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1
|
Db 2 g 2

Search completed: July 16, 2002, 02:50:26
Job time: 31279 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: July 15, 2002, 23:07:38 ; Search time 223.79 Seconds
(without alignments)
1.098 Million cell updates/sec

Title: US-09-375-248-1_COPY_2588_2588

Perfect score: 1

Sequence: 1 g 1

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 383533 seqs, 122816752 residues

Word size : 0

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued Patents NA.*
1: /cgn2_6/ptodata/2/ina/5A_COMB.seq.*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq.*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq.*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq.*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq.*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1	100.0	2	1	US-08-268-679B-8
2	1	100.0	2	1	US-08-484-192-16
3	1	100.0	2	4	US-08-361-024-3
C 4	1	100.0	2	4	US-08-361-024-3
5	1	100.0	3	1	US-07-791-213D-46
C 6	1	100.0	3	1	US-07-791-213D-46
7	1	100.0	3	1	US-07-791-213D-62
C 8	1	100.0	3	1	US-07-791-213D-62
9	1	100.0	3	1	US-08-268-679B-7
10	1	100.0	3	1	US-08-602-036A-2
C 11	1	100.0	3	1	US-08-602-036A-2
12	1	100.0	3	1	US-08-293-150A-46
C 13	1	100.0	3	1	US-08-293-150A-46
14	1	100.0	3	1	US-08-293-150A-62
C 15	1	100.0	3	1	US-08-293-150A-62
16	1	100.0	3	2	US-08-502-374A-2
C 17	1	100.0	3	2	US-08-502-374A-2
18	1	100.0	3	2	US-08-642-407A-2
C 19	1	100.0	3	2	US-08-642-407A-2
20	1	100.0	3	3	US-08-873-709-9
21	1	100.0	3	3	US-09-032-365A-36
22	1	100.0	3	4	US-08-793-634B-12
23	1	100.0	3	4	US-08-973-568-55
24	1	100.0	4	1	US-07-755-462-2
C 25	1	100.0	4	1	US-07-755-462-2
26	1	100.0	4	1	US-08-169-950-6
C 27	1	100.0	4	1	US-08-169-950-6

Sequence 7, Appli
Sequence 11, Appl
Sequence 11, Appl
Sequence 13, Appl
Sequence 14, Appl
Sequence 14, Appl
Sequence 34, Appl
Sequence 34, Appl
Sequence 34, Appl
Sequence 25, Appl
Sequence 25, Appl
Sequence 25, Appl
Sequence 1, Appl
Sequence 1, Appl
Sequence 2, Appl
Sequence 2, Appl
Sequence 25, Appl
Sequence 25, Appl
Sequence 2, Appl
Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-08-268-679B-8
: Sequence 8, Application US/08268679B
: Patent No. 5674729
: GENERAL INFORMATION:
: APPLICANT: WINNER, ECKARD; MOLLA,
: APPLICANT: AKHTERUZZAMAN; PAUL, ANIKO V.
: TITLE OF INVENTION: DE NOVO CELL-FREE
: TITLE OF INVENTION: SYNTHESIS PICORNAVIRUS
: NUMBER OF SEQUENCES: 8
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
: STREET: 345 PARK AVE.
: CITY: NEW YORK
: STATE: NEW YORK
: COUNTRY: USA
: ZIP: 10154
: COMPUTER READABLE FORM:
: MEDIUM TYPE: FLOPPY DISK
: COMPUTER: IBM PC COMPATIBLE
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: WORD PERFECT # 5.1
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/268, 679B
: FILING DATE: 30-JUN-1994
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 07/846,914
: FILING DATE: 06-MAR-1992
: CLASSIFICATION: 435
: APPLICATION NUMBER: 07/719,761
: FILING DATE: 24-JUN-1991
: ATTORNEY/AGENT INFORMATION:
: NAME: MARIA C.H. LIN
: REGISTRATION NUMBER: 29,323
: REFERENCE/DOCKET NUMBER: 0887-4095 US2
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (212) 758-4800
: TELEFAX: (212) 751-6849
: TELEX: 421792
: INFORMATION FOR SEQ ID NO: 8:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 2
: TYPE: NUCLEIC ACID
: STRANDEDNESS: SINGLE
: TOPOLOGY: UNKNOWN
: MOLECULE TYPE:
: DESCRIPTION: OLIGONUCLEOTIDE
: HYPOTHETICAL: NO
: ANTI-SENSE: YES
: ORIGINAL SOURCE: N.A.

;
US-08-268-679B-8

Db 2 G 2

Query Match 100.0%; Score 1; DB 1; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
Db 1 G 1

RESULT 2
US-08-484-192-16
; Sequence 16, Application US/08484192
; Patent No. 5756291
; GENERAL INFORMATION:
; APPLICANT: GRIFFIN, LINDA C.
; APPLICANT: ALBRECHT, GLENN
; APPLICANT: LATHAM, JOHN
; APPLICANT: LEUNG, LAWRENCE
; APPLICANT: VERMAAS, ERIC
; APPLICANT: TOOLE, JOHN J.
; TITLE OF INVENTION: METHODS SPECIFIC FOR BIOMOLECULES AND
; TITLE OF INVENTION: METHODS OF MAKING
; NUMBER OF SEQUENCES: 181
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,192
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/934,387
; FILING DATE: 21-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: GRACEY, NANCY J.
; REGISTRATION NUMBER: 28,216
; REFERENCE/DOCKET NUMBER: 246102002221
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-813-5600
; TELEFAX: 415-494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: misc_difference
; LOCATION: replace(1, "")
; OTHER INFORMATION: /note= "This is a biotin-17
; OTHER INFORMATION: nucleotide stretch of abasic residues."
US-08-484-192-16

Query Match 100.0%; Score 1; DB 1; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1

US-08-361-024-3
; Sequence 3, Application US/08361024
; Patent No. 6207368
; GENERAL INFORMATION:
; APPLICANT: Adams, Craig W.
; TITLE OF INVENTION: Method, Reagent and Kit
; TITLE OF INVENTION: for Detection and
; TITLE OF INVENTION: Amplification of
; TITLE OF INVENTION: Nucleic Acid Sequence
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Beckman Instruments, Inc.
; STREET: 2500 Harbor Boulevard
; CITY: Fullerton
; STATE: California
; COUNTRY: USA
; ZIP: 92634
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch,
; MEDIUM TYPE: 1.44 Mb
; COMPUTER: IBM
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/361,024
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/925,059
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Burgoon, Richard P.
; REGISTRATION NUMBER: 34,787
; REFERENCE/DOCKET NUMBER: 128D-126
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (714) 773-7610
; TELEFAX: (714) 773-7936
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: yes
; ANTI-SENSE: no
US-08-361-024-3

Query Match 100.0%; Score 1; DB 4; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
Db 1 G 1

RESULT 4
US-08-361-024-3/c
; Sequence 3, Application US/08361024
; Patent No. 6207368
; GENERAL INFORMATION:
; APPLICANT: Adams, Craig W.
; TITLE OF INVENTION: Method, Reagent and Kit
; TITLE OF INVENTION: for Detection and
; TITLE OF INVENTION: Amplification of
; TITLE OF INVENTION: Nucleic Acid Sequence
US-08-361-024-3

NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Beckman Instruments, Inc.
STREET: 2500 Harbor Boulevard
CITY: Fullerton
STATE: California
COUNTRY: USA
ZIP: 92634
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch,
MEDIUM TYPE: 1.44 Mb
COMPUTER: IBM
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/361,024
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/925,059
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Burgoon, Richard P.
REGISTRATION NUMBER: 34,787
REFERENCE/DOCKET NUMBER: 128D-126
TELEPHONE: (714) 773-7610
TELEFAX: (714) 773-7936
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2 bases
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: yes
ANTI-SENSE: no
US-08-361-024-3

Query Match 100.0%; Score 1; DB 4; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1
|
Db 2 G 2

RESULT 5
US-07-791-213D-46
; Sequence 46, Application US/07791213D
; Patent No. 5409895
; GENERAL INFORMATION:
; APPLICANT: MORISHITA, Hideaki
; APPLICANT: KANAMORI, Toshinori
; APPLICANT: NOBUHARA, Masahiro
; TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE
; TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME
; TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF
; TITLE OF INVENTION: TREATING USING THE SAME
; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/791,213D
FILING DATE: 13-NOV-1991
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 2-306745
FILING DATE: 13-NOV-1990
ATTORNEY/AGENT INFORMATION:
NAME: Meuth, Donna M
REGISTRATION NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 029650-032
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 3 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-07-791-213D-46

Query Match 100.0%; Score 1; DB 1; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1
|
Db 2 G 2

RESULT 6
US-07-791-213D-46/c
; Sequence 46, Application US/07791213D
; Patent No. 5409895
; GENERAL INFORMATION:
; APPLICANT: MORISHITA, Hideaki
; APPLICANT: KANAMORI, Toshinori
; APPLICANT: NOBUHARA, Masahiro
; TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE
; TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME
; TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF
; TITLE OF INVENTION: TREATING USING THE SAME
; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/791,213D
FILING DATE: 13-NOV-1991
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 2-306745
FILING DATE: 13-NOV-1990
ATTORNEY/AGENT INFORMATION:
NAME: Meuth, Donna M
REGISTRATION NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 029650-032
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021

; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-07-791-213D-46

Query Match 100.0%; Score 1; DB 1; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 g 1
|
DB 3 G 3

RESULT 7

US-07-791-213D-62
; Sequence 62, Application US/07791213D
; Patent No. 5409895
; GENERAL INFORMATION:
; APPLICANT: MORISHITA, Hideaki
; APPLICANT: KANAMORI, Toshinori
; APPLICANT: NOBUHARA, Masahiro
; TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE
; TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME
; TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF
; TITLE OF INVENTION: TREATING USING THE SAME
; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/791,213D
; FILING DATE: 13-NOV-1991
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 2-306745
; FILING DATE: 13-NOV-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Meuth, Donna M
; REGISTRATION NUMBER: 36,607
; REFERENCE/DOCKET NUMBER: 029650-032
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 62:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-07-791-213D-62

Query Match 100.0%; Score 1; DB 1; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 g 1

DB 2 G 2
|

RESULT 8

US-07-791-213D-62/c
; Sequence 62, Application US/07791213D
; Patent No. 5409895
; GENERAL INFORMATION:
; APPLICANT: MORISHITA, Hideaki
; APPLICANT: KANAMORI, Toshinori
; APPLICANT: NOBUHARA, Masahiro
; TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE
; TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME
; TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF
; TITLE OF INVENTION: TREATING USING THE SAME
; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/791,213D
; FILING DATE: 13-NOV-1991
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 2-306745
; FILING DATE: 13-NOV-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Meuth, Donna M
; REGISTRATION NUMBER: 36,607
; REFERENCE/DOCKET NUMBER: 029650-032
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 62:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-07-791-213D-62

Query Match 100.0%; Score 1; DB 1; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 g 1

DB 3 G 3

RESULT 9

US-08-268-679B-7
; Sequence 7, Application US/08268679B
; Patent No. 5674729
; GENERAL INFORMATION:
; APPLICANT: WIMMER, ECKARD; MOLLA,
; APPLICANT: AKHERUZAMAN; PAUL, ANIKO V.
; TITLE OF INVENTION: DE NOVO CELL-FREE
; TITLE OF INVENTION: SYNTHESIS PICORNAVIRUS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:

ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
STREET: 345 PARK AVE.
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORD PERFECT # 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/268.679B
FILING DATE: 30-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07A846.914
FILING DATE: 06-MAR-1992
CLASSIFICATION: 435
APPLICATION NUMBER: 07\719.761
FILING DATE: 24-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: MARIA C. H. LIN
REGISTRATION NUMBER: 29.323
REFERENCE/DOCKET NUMBER: 0887-4095 US2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 3
TYPE: NUCLEIC ACID
STRANDEDNESS: SINGLE
TOPOLOGY: UNKNOWN
MOLECULE TYPE: OLIGONUCLEOTIDE
DESCRIPTION: NO
HYPOTHETICAL: YES
ANTI-SENSE: YES
ORIGINAL SOURCE: N.A.
POSITION IN GENOME: N.A.
US-08-268-679B-7

Query Match 100.0%; Score 1; DB 1; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
Db 2 g 2

RESULT 10
US-08-602-036A-2
Sequence 2, Application US/08602036A
Patent No. 5789248
GENERAL INFORMATION:
APPLICANT: Oeystein, Fodstad
APPLICANT: Hovig, Eivind
APPLICANT: Engebraaten, Olav
APPLICANT: Maelandsmo, Gunhild H.
TITLE OF INVENTION: CAPL SPECIFIC OLIGONUCLEOTIDES AND
METHODS OF INHIBITING METASTATIC CANCER
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: HALE AND DORR LLP
STREET: 60 State Street
CITY: Boston
STATE: MA
COUNTRY: United States of America
ZIP: 02109
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/602.036A
FILING DATE: 16-FEB-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Kerner, Ann-Louise
REGISTRATION NUMBER: 33,523
REFERENCE/DOCKET NUMBER: HYZ-039CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 526-6000
TELEFAX: (617) 526-5000
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 3 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-602-036A-2

Query Match 100.0%; Score 1; DB 1; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
Db 1 g 1

RESULT 11
US-08-602-036A-2/c
Sequence 2, Application US/08602036A
Patent No. 5789248
GENERAL INFORMATION:
APPLICANT: Oeystein, Fodstad
APPLICANT: Hovig, Eivind
APPLICANT: Engebraaten, Olav
APPLICANT: Maelandsmo, Gunhild H.
APPLICANT: Agrawal, Sudhir
TITLE OF INVENTION: CAPL SPECIFIC OLIGONUCLEOTIDES AND
METHODS OF INHIBITING METASTATIC CANCER
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: HALE AND DORR LLP
STREET: 60 State Street
CITY: Boston
STATE: MA
COUNTRY: United States of America
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/602.036A
FILING DATE: 16-FEB-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Kerner, Ann-Louise
REGISTRATION NUMBER: 33,523
REFERENCE/DOCKET NUMBER: HYZ-039CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 526-6000
TELEFAX: (617) 526-5000
INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 3 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: RNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-602-036A-2

Query Match 100.0%; Score 1; DB 1; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
|
Db 3 G 3

RESULT 12

US-08-293-150A-46
; Sequence 46, Application US/08293150A
; Patent No. 5792629

; GENERAL INFORMATION:

; APPLICANT: MORISHITA, Hideaki
; APPLICANT: KANAMORI, Toshinori
; APPLICANT: NOBUHARA, Masahiro

; TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE

; TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME
; TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF
; TITLE OF INVENTION: TREATING USING THE SAME

; NUMBER OF SEQUENCES: 110

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS

; STREET: P.O. Box 1404

; CITY: Alexandria

; STATE: Virginia

; COUNTRY: United States

; ZIP: 22313-1404

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/293.150A

; FILING DATE: 19-AUG-1994

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/791,213

; FILING DATE: 13-NOV-1990

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: JP 2-306745

; FILING DATE: 13-NOV-1990

; ATTORNEY/AGENT INFORMATION:

; NAME: Meuth, Donna M.

; REGISTRATION NUMBER: 36,607

; REFERENCE/DOCKET NUMBER: 029650-049

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (703) 836-6620

; TELEFAX: (703) 836-2021

; INFORMATION FOR SEQ ID NO: 46:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 3 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)

US-08-293-150A-46

Query Match

100.0%; Score 1; DB 1; Length 3;

Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
|
Db 2 G 2

RESULT 13

US-08-293-150A-46/c
; Sequence 46, Application US/08293150A
; Patent No. 5792629

; GENERAL INFORMATION:

; APPLICANT: MORISHITA, Hideaki
; APPLICANT: KANAMORI, Toshinori
; APPLICANT: NOBUHARA, Masahiro

; TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE

; TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME

; TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF

; TITLE OF INVENTION: TREATING USING THE SAME

; NUMBER OF SEQUENCES: 110

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS

; STREET: P.O. Box 1404

; CITY: Alexandria

; STATE: Virginia

; COUNTRY: United States

; ZIP: 22313-1404

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/293.150A

; FILING DATE: 19-AUG-1994

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/791,213

; FILING DATE: 13-NOV-1990

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: JP 2-306745

; FILING DATE: 13-NOV-1990

; ATTORNEY/AGENT INFORMATION:

; NAME: Meuth, Donna M.

; REGISTRATION NUMBER: 36,607

; REFERENCE/DOCKET NUMBER: 029650-049

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (703) 836-6620

; TELEFAX: (703) 836-2021

; INFORMATION FOR SEQ ID NO: 46:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 3 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)

US-08-293-150A-46

Query Match

100.0%; Score 1; DB 1; Length 3;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
|
Db 3 G 3

RESULT 14

US-08-293-150A-62
; Sequence 62, Application US/08293150A
; Patent No. 5792629

;
; GENERAL INFORMATION:
; APPLICANT: MORISHITA, Hideaki
; APPLICANT: KANAMORI, Toshinori
; APPLICANT: NOBUHARA, Masahiro
; TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE
; TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME
; TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF
; TITLE OF INVENTION: TREATING USING THE SAME
; NUMBER OF SEQUENCES: 110
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/293,150A
; FILING DATE: 19-AUG-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/791,213
; FILING DATE: 13-NOV-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 2-306745
; FILING DATE: 13-NOV-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Meuth, Donna M.
; REGISTRATION NUMBER: 36,607
; REFERENCE/DOCKET NUMBER: 029650-049
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 62:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-293-150A-62

Query Match 100.0%; Score 1; DB 1; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
Db 2 G 2

RESULT 15
US-08-293-150A-62/c
; Sequence 62, Application US/08293150A
; Patent No. 5792629
; GENERAL INFORMATION:
; APPLICANT: MORISHITA, Hideaki
; APPLICANT: KANAMORI, Toshinori
; APPLICANT: NOBUHARA, Masahiro
; TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE
; TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME
; TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF
; TITLE OF INVENTION: TREATING USING THE SAME
; NUMBER OF SEQUENCES: 110
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: P.O. Box 1404

;
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/293,150A
; FILING DATE: 19-AUG-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/791,213
; FILING DATE: 13-NOV-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 2-306745
; FILING DATE: 13-NOV-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Meuth, Donna M.
; REGISTRATION NUMBER: 36,607
; REFERENCE/DOCKET NUMBER: 029650-049
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 62:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-293-150A-62

Query Match 100.0%; Score 1; DB 1; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
Db 3 G 3

RESULT 16
US-08-502-374A-2
; Sequence 2, Application US/08502374A
; Patent No. 5872007
; GENERAL INFORMATION:
; APPLICANT: Fodstad, Oeystein
; APPLICANT: Hovig, Elvind
; APPLICANT: Engebraaten, Olav
; APPLICANT: Maelandsmo, Gunhild H.
; APPLICANT: Agrawal, Sudhir
; TITLE OF INVENTION: CAPL-SPECIFIC OLIGONUCLEOTIDES AND
; TITLE OF INVENTION: METHODS OF INHIBITING METASTATIC CANCER
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hale and Dorr LLP
; STREET: 60 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/502,374A
; FILING DATE: 14-Jul-1995

```

; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Kerner, Ann-Louise
; REGISTRATION NUMBER: 33,523
; REFERENCE/DOCKET NUMBER: HY2-039DV2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-526-6000
; TELEFAX: 617-526-5000
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: RNA
; HYPOTHETICAL: NO
; ANTI-SENSE: YES
; US-08-502-374A-2

Query Match 100.0%; Score 1; DB 2; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
Db 1 g 1

RESULT 17
US-08-502-374A-2/c
; Sequence 2, Application US/08502374A
; Patent No. 5872007
; GENERAL INFORMATION:
; APPLICANT: Fodstad, Oeystein
; APPLICANT: Hovig, Eivind
; APPLICANT: Engebraaten, Olav
; APPLICANT: Maelandsmo, Gunhild H.
; APPLICANT: Agrawal, Sudhir
; TITLE OF INVENTION: CAPL-SPECIFIC OLIGONUCLEOTIDES AND
; TITLE OF INVENTION: METHODS OF INHIBITING METASTATIC CANCER
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hale and Dorr LLP
; STREET: 60 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/502.374A
; FILING DATE: 14-Jul-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Kerner, Ann-Louise
; REGISTRATION NUMBER: 33,523
; REFERENCE/DOCKET NUMBER: HY2-039DV2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-526-6000
; TELEFAX: 617-526-5000
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: RNA
; HYPOTHETICAL: NO

; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Kerner, Ann-Louise
; REGISTRATION NUMBER: 33,523
; REFERENCE/DOCKET NUMBER: HY2-039CPDV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 526-6000
; TELEFAX: (617) 526-5000
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: RNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-08-642-407A-2

Query Match 100.0%; Score 1; DB 2; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
Db 1 g 1

RESULT 18
US-08-642-407A-2
; Sequence 2, Application US/08642407A
; Patent No. 5877308
; GENERAL INFORMATION:
; APPLICANT: Oeystein, Fodstad
; APPLICANT: Hovig, Eivind
; APPLICANT: Engebraaten, Olav
; APPLICANT: Maelandsmo, Gunhild H.
; APPLICANT: Agrawal, Sudhir
; TITLE OF INVENTION: CAPL-SPECIFIC OLIGONUCLEOTIDES AND
; TITLE OF INVENTION: METHODS OF INHIBITING METASTATIC CANCER
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HALE AND DORR LLP
; STREET: 60 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: United States of America
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/642.407A
; FILING DATE: 03-May-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Kerner, Ann-Louise
; REGISTRATION NUMBER: 33,523
; REFERENCE/DOCKET NUMBER: HY2-039CPDV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 526-6000
; TELEFAX: (617) 526-5000
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: RNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-08-642-407A-2

Query Match 100.0%; Score 1; DB 2; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
Db 1 g 1

RESULT 19
US-08-642-407A-2/c
; Sequence 2, Application US/08642407A
```

; Patent No. 5877308
; GENERAL INFORMATION:
; APPLICANT: Oeystein, Fodstad
; APPLICANT: Hovig, Eivind
; APPLICANT: Engebraten, Olav
; APPLICANT: Maelandsmo, Gunhild H.
; APPLICANT: Agrawal, Sudhir
; TITLE OF INVENTION: CAPL SPECIFIC OLIGONUCLEOTIDES AND
; METHODS OF INHIBITING METASTATIC CANCER
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HALE AND DORR LLP
; STREET: 60 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: United States of America
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/642.407A
; FILING DATE: 03-May-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Kerner, Ann-Louise
; REGISTRATION NUMBER: 33,523
; REFERENCE/DOCKET NUMBER: HY2-039CPDV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 526-6000
; TELEFAX: (617) 526-5000
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: RNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-642-407A-2

Query Match 100.0%; Score 1; DB 2; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
Db 3 G 3

RESULT 20
US-08-873-709-9
; Sequence 9, Application US/08873709
; Patent No. 6037126
; GENERAL INFORMATION:
; APPLICANT: Grossman, Abraham
; TITLE OF INVENTION: COMPOSITIONS, METHODS, KITS AND
; APPARATUS FOR DETERMINING THE PRESENCE OR ABSENCE OF
; A PROTEIN COMPONENT OF TELOMERASE ENZYME
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abraham Grossman
; STREET: 666 Washington Avenue
; CITY: Pleasantville
; STATE: NY
; COUNTRY: USA
; ZIP: 10570
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/873.709
; FILING DATE: 12-JUN-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Janiuk, Anthony J.
; REGISTRATION NUMBER: 29,809
; REFERENCE/DOCKET NUMBER: Q001/002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 914-747-9108
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: RNA
US-08-873-709-9

Query Match 100.0%; Score 1; DB 3; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
Db 1 G 1

RESULT 21
US-09-032-365A-36
; Sequence 36, Application US/09032365A
; Patent No. 6114502
; GENERAL INFORMATION:
; APPLICANT: No. 6114502th, Michael
; APPLICANT: Nishina, Patsy
; APPLICANT: Naggart, Juergen
; APPLICANT: No. 6114502en-Trauth, Konrad
; TITLE OF INVENTION: GENE FAMILY ASSOCIATED WITH
; NEUROSENSORY DEFECTS
; NUMBER OF SEQUENCES: 67
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bozicevic & Reed, LLP
; STREET: 285 Hamilton Avenue, Suite 200
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/032,365A
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sherwood, Pamela J
; REGISTRATION NUMBER: 36,677
; REFERENCE/DOCKET NUMBER: SEQ-2CIP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-327-3400
; TELEFAX: 650 327-3231
; TELEX:
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:

;
; LENGTH: 3 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-09-032-365A-36

Query Match 100.0%; Score 1; DB 3; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
|
Db 1 G 1

RESULT 22
US-08-793-634B-12
; Sequence 12, Application US/08793634B
; Patent No. 6211431
; GENERAL INFORMATION:
; APPLICANT: Boevink, Petra C.
; APPLICANT: Surin, Brian P.
; APPLICANT: Keese, Paul K.
; APPLICANT: Chu, Paul W.G.
; APPLICANT: Waterhouse, Peter M.
; APPLICANT: Khan, Rafiqul I.
; APPLICANT: Larkin, Philip J.
; APPLICANT: Taylor, William C.
; APPLICANT: Marchall, Jerry S.
; TITLE OF INVENTION: NOVEL PLANT PROMOTERS AND USES
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; City: Garden City
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 11530

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/793.634B
; FILING DATE: June 9, 1997
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Digiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 10530
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 516-742-4343
; TELEFAX: 516-742-4366
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-793-634B-12

Query Match 100.0%; Score 1; DB 4; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
|
Db 2 G 2

RESULT 23
US-08-973-568-55
; Sequence 55, Application US/08973568B
; Patent No. 6277634
; GENERAL INFORMATION:
; APPLICANT: McCall, Maxine J.
; APPLICANT: Hendry, Philip
; APPLICANT: Lockett, Trevor
; TITLE OF INVENTION: OPTIMIZED MINIZYMES AND MINIRIBOZYMES AND USES THEREOF
; FILE REFERENCE: 47203bpcus
; CURRENT APPLICATION NUMBER: US/08/973.568B
; CURRENT FILING DATE: 1998-05-18
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 55
; LENGTH: 3
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Combined DNA/RNA Molecule:
; OTHER INFORMATION: Synthetic Ribozyme or portion thereof
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Ribozymes and
US-08-973-568-55

Query Match 100.0%; Score 1; DB 4; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
|
Db 1 g 1

RESULT 24
US-07-755-462-2
; Sequence 2, Application US/07755462
; Patent No. 5273881
; GENERAL INFORMATION:
; APPLICANT: Sena, Elissa P.
; APPLICANT: Calhoun, Cornelia J.
; APPLICANT: Zarling, David A.
; TITLE OF INVENTION: Diagnostic Applications of Double-D-Loop
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Peter Dehlinger
; STREET: 350 Cambridge Avenue, Suite 300
; City: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/755.462
; FILING DATE: 19910904
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/520,321
; FILING DATE: 07-MAY-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Fabian, Gary R.
; REGISTRATION NUMBER: 33,875
; REFERENCE/DOCKET NUMBER: 4255-0001.30
; TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Cleavage site for DpnI
US-07-755-462-2

Query Match 100.0%; Score 1; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
|
Db 1 G 1

RESULT 25
US-07-755-462-2/c
; Sequence 2, Application US/07755462
; Patent No. 5273881
; GENERAL INFORMATION:
; APPLICANT: Sena, Elissa P.
; APPLICANT: Calhoun, Cornelia J.
; APPLICANT: Zarling, David A.
; TITLE OF INVENTION: Diagnostic Applications of Double-D-Loop
; TITLE OF INVENTION: Formation
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Peter Dehlinger
; STREET: 350 Cambridge Avenue, Suite 300
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/755.462
; FILING DATE: 19910904
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/520.321
; FILING DATE: 07-MAY-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Fabian, Gary R.
; REGISTRATION NUMBER: 33,875
; REFERENCE/DOCKET NUMBER: 4255-0001.30
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Cleavage site for DpnI
US-07-755-462-2

Query Match 100.0%; Score 1; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 g 1
|
Db 4 G 4
RESULT 26
US-08-169-950-6
; Sequence 6, Application US/08169950
; Patent No. 5366882
; GENERAL INFORMATION:
; APPLICANT: LUNNEN, KEITH D.
; APPLICANT: WILSON, GEOFFREY G.
; TITLE OF INVENTION: METHOD FOR PRODUCING THE BgII
; TITLE OF INVENTION: RESTRICTION ENDONUCLEASE AND METHYLASE
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
; ADDRESSEE: CUSHMAN
; STREET: 130 WATER STREET
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/169,950
; FILING DATE: 17-DEC-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: RESNICK, DAVID S.
; REGISTRATION NUMBER: 34235
; REFERENCE/DOCKET NUMBER: 43959
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 523-3400
; TELEFAX: (617) 523-6440
; TELEX: 200291 STRE UR
; INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
US-08-169-950-6

Query Match 100.0%; Score 1; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
|
Db 1 G 1

RESULT 27
US-08-169-950-6/c
; Sequence 6, Application US/08169950
; Patent No. 5366882
; GENERAL INFORMATION:
; APPLICANT: LUNNEN, KEITH D.
; APPLICANT: WILSON, GEOFFREY G.
; TITLE OF INVENTION: METHOD FOR PRODUCING THE BgII
; TITLE OF INVENTION: RESTRICTION ENDONUCLEASE AND METHYLASE

NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
ADDRESSEE: CUSHMAN
STREET: 130 WATER STREET
CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/169,950
FILING DATE: 17-DEC-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: RESNICK, DAVID S.
REGISTRATION NUMBER: 34235
REFERENCE/DOCKET NUMBER: 43959
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 523-3400
TELEFAX: (617) 523-6440
TELEX: 200291 STRE UR
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
US-08-169-950-6

Query Match 100.0% Score 1; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 g 1
|
Db 4 G 4

RESULT 28
US-07-630-288A-7
Sequence 7, Application US/07630288A
Patent No. 5472840
GENERAL INFORMATION:
APPLICANT: Stefano, James E.
TITLE OF INVENTION: Nucleic Acid Structures with Catalytic
TITLE OF INVENTION: and Autocatalytic Replicating Features and Methods of Use
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Joanne M. Glesser
STREET: Amoco Corp., Suite 600, 55 Shuman Blvd.
CITY: Naperville
STATE: IL
COUNTRY: USA
ZIP: 60563
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/630,288A
FILING DATE: 17-DEC-1990
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/370,218
FILING DATE: 06-JUN-1989

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/252,243
FILING DATE: 30-SEP-1988
ATTORNEY/AGENT INFORMATION:
NAME: Glesser, Joanne M.
REGISTRATION NUMBER: 32,838
REFERENCE/DOCKET NUMBER: 58190 2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (708) 717-2443
TELEFAX: (708) 717-2430
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-07-630-288A-7

Query Match 100.0% Score 1; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 g 1
|
Db 1 G 1

RESULT 29
US-07-630-288A-11
Sequence 11, Application US/07630288A
Patent No. 5472840
GENERAL INFORMATION:
APPLICANT: Stefano, James E.
TITLE OF INVENTION: Nucleic Acid Structures with Catalytic
TITLE OF INVENTION: and Autocatalytic Replicating Features and Methods of Use
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Joanne M. Glesser
STREET: Amoco Corp., Suite 600, 55 Shuman Blvd.
CITY: Naperville
STATE: IL
COUNTRY: USA
ZIP: 60563
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/630,288A
FILING DATE: 17-DEC-1990
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/370,218
FILING DATE: 06-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/252,243
FILING DATE: 30-SEP-1988
ATTORNEY/AGENT INFORMATION:
NAME: Glesser, Joanne M.
REGISTRATION NUMBER: 32,838
REFERENCE/DOCKET NUMBER: 58190 2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (708) 717-2443
TELEFAX: (708) 717-2430
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 base pairs
TYPE: nucleic acid

; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-07-630-288A-11

Query Match 100.0%; Score 1; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 q 1
|
Db 1 G 1

RESULT 30
US-07-630-288A-11/c
; Sequence 11, Application US/07630288A
; Patent No. 5472840
; GENERAL INFORMATION:
; APPLICANT: Stefano, James E.
; TITLE OF INVENTION: Nucleic Acid Structures with Catalytic
; and Autocatalytic Replicating Features and Methods of Use
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Joanne M. Giesler
; STREET: Amoco Corp., Suite 600, 55 Shuman Blvd.
; CITY: Naperville
; STATE: IL
; COUNTRY: USA
; ZIP: 60563
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/630,288A
; FILING DATE: 17-DEC-1990
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/370,218
; FILING DATE: 06-JUN-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/252,243
; FILING DATE: 30-SEP-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Giesler, Joanne M.
; REGISTRATION NUMBER: 32,838
; REFERENCE/DOCKET NUMBER: 58190 2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (708) 717-2443
; TELEFAX: (708) 717-2430
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-07-630-288A-11

Query Match 100.0%; Score 1; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 q 1
|

Db 4 G 4

RESULT 31
US-07-630-288A-13
; Sequence 13, Application US/07630288A
; Patent No. 5472840
; GENERAL INFORMATION:
; APPLICANT: Stefano, James E.
; TITLE OF INVENTION: Nucleic Acid Structures with Catalytic
; and Autocatalytic Replicating Features and Methods of Use
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Joanne M. Giesler
; STREET: Amoco Corp., Suite 600, 55 Shuman Blvd.
; CITY: Naperville
; STATE: IL
; COUNTRY: USA
; ZIP: 60563
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/630,288A
; FILING DATE: 17-DEC-1990
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/370,218
; FILING DATE: 06-JUN-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/252,243
; FILING DATE: 30-SEP-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Giesler, Joanne M.
; REGISTRATION NUMBER: 32,838
; REFERENCE/DOCKET NUMBER: 58190 2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (708) 717-2443
; TELEFAX: (708) 717-2430
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-07-630-288A-13

Query Match 100.0%; Score 1; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 q 1
|
Db 1 G 1

RESULT 32
US-07-630-288A-14
; Sequence 14, Application US/07630288A
; Patent No. 5472840
; GENERAL INFORMATION:
; APPLICANT: Stefano, James E.
; TITLE OF INVENTION: Nucleic Acid Structures with Catalytic
; and Autocatalytic Replicating Features and Methods of Use
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Joanne M. Giesler

STREET: Amoco Corp., Suite 600, 55 Shuman Blvd.
CITY: Naperville
STATE: IL
COUNTRY: USA
ZIP: 60563
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/630,288A
FILING DATE: 17-DEC-1990
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/370,218
FILING DATE: 06-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/252,243
FILING DATE: 30-SEP-1988
ATTORNEY/AGENT INFORMATION:
NAME: Glesser, Joanne M.
REGISTRATION NUMBER: 32,838
REFERENCE/DOCKET NUMBER: 58190 2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (708) 717-2443
TELEFAX: (708) 717-2430
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-07-630-288A-14

Query Match 100.0%; Score 1; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
I
Db 1 G 1

RESULT 33
US-07-630-288A-14/c
Sequence 14, Application US/07630288A
Patent No. 5472840
GENERAL INFORMATION:
APPLICANT: Stefano, James E.
TITLE OF INVENTION: Nucleic Acid Structures with Catalytic
and Autocatalytic Replicating Features and Methods of Use
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Joanne M. Glesser
STREET: Amoco Corp., Suite 600, 55 Shuman Blvd.
CITY: Naperville
STATE: IL
COUNTRY: USA
ZIP: 60563
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/630,288A
FILING DATE: 17-DEC-1990
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/370,218
FILING DATE: 06-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/252,243
FILING DATE: 30-SEP-1988
ATTORNEY/AGENT INFORMATION:
NAME: Glesser, Joanne M.
REGISTRATION NUMBER: 32,838
REFERENCE/DOCKET NUMBER: 58190 2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (708) 717-2443
TELEFAX: (708) 717-2430
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-07-630-288A-14

Query Match 100.0%; Score 1; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
I
Db 4 G 4

RESULT 34
US-07-630-288A-34
Sequence 34, Application US/07630288A
Patent No. 5472840
GENERAL INFORMATION:
APPLICANT: Stefano, James E.
TITLE OF INVENTION: Nucleic Acid Structures with Catalytic
and Autocatalytic Replicating Features and Methods of Use
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Joanne M. Glesser
STREET: Amoco Corp., Suite 600, 55 Shuman Blvd.
CITY: Naperville
STATE: IL
COUNTRY: USA
ZIP: 60563
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/630,288A
FILING DATE: 17-DEC-1990
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/370,218
FILING DATE: 06-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/252,243
FILING DATE: 30-SEP-1988
ATTORNEY/AGENT INFORMATION:
NAME: Glesser, Joanne M.
REGISTRATION NUMBER: 32,838
REFERENCE/DOCKET NUMBER: 58190 2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (708) 717-2443
TELEFAX: (708) 717-2430
INFORMATION FOR SEQ ID NO: 34:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: RNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-07-630-288A-34

Query Match 100.0%; Score 1; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
Db 2 g 2

RESULT 35

US-07-630-288A-34/c
; Sequence 34, Application US/07630288A
; Patent No. 5472840
; GENERAL INFORMATION:
; APPLICANT: Stefano, James E.
; TITLE OF INVENTION: Nucleic Acid Structures with Catalytic
; AND Autocatalytic Replicating Features and Methods of Use
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Joanne M. Giesser
; STREET: Amoco Corp., Suite 600, 55 Shuman Blvd.
; CITY: Naperville
; STATE: IL
; COUNTRY: USA
; ZIP: 60563

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/630.288A
; FILING DATE: 17-DEC-1990
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/370.218
; FILING DATE: 06-JUN-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/252.243
; FILING DATE: 30-SEP-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Giesser, Joanne M.
; REGISTRATION NUMBER: 32,838
; REFERENCE/DOCKET NUMBER: 58190 2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (708) 717-2443
; TELEFAX: (708) 717-2430
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: RNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-07-630-288A-34

Query Match 100.0%; Score 1; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
Db 4 g 4

RESULT 36

US-08-126-594-25
; Sequence 25, Application US/08126594
; Patent No. 5482845
; GENERAL INFORMATION:
; APPLICANT: Soares, M. Bento
; APPLICANT: Efstratiadis, Algriris
; TITLE OF INVENTION: METHOD FOR CONSTRUCTION OF NORMALIZED
; TITLE OF INVENTION: CDNA LIBRARIES
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John P. White, c/o Cooper & Dunham
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/126.594
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 42840/JPW/AKC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 977-9550
; TELEFAX: (212) 664-0525
; TELEX: 422523 COOP UI
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-126-594-25

Query Match 100.0%; Score 1; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
Db 3 g 3

RESULT 37

US-08-126-594-25/c
; Sequence 25, Application US/08126594
; Patent No. 5482845
; GENERAL INFORMATION:
; APPLICANT: Soares, M. Bento
; APPLICANT: Efstratiadis, Algriris
; TITLE OF INVENTION: METHOD FOR CONSTRUCTION OF NORMALIZED
; TITLE OF INVENTION: CDNA LIBRARIES
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John P. White, c/o Cooper & Dunham

STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/126.594
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 42840/JPW/AKC
TELEPHONE: (212) 977-9550
TELEFAX: (212) 664-0525
TELEX: 422523 COOP UT
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-126-594-25

Query Match 100.0%; Score 1; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
Db 4 G 4

RESULT 38
US-08-188-943-1
Sequence 1, Application US/08188943
Patent No. 5635347
GENERAL INFORMATION:
APPLICANT: Link, John R.
APPLICANT: Gudibande, Satyanarayana R.
APPLICANT: Kenten, John H.
TITLE OF INVENTION: Rapid Assays for Amplification
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Curtis, Morris & Safford
STREET: 530 Fifth Avenue
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 28-JAN-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/792,602
FILING DATE: 15-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: Evans, Barry
REGISTRATION NUMBER: 22,802
REFERENCE/DOCKET NUMBER: 370068-3630
TELEPHONE: (212) 840-0712
TELEFAX: (212) 840-0712
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-188-943-1

ATTORNEY/AGENT INFORMATION:
NAME: Evans, Barry
REGISTRATION NUMBER: 22,802
REFERENCE/DOCKET NUMBER: 370068-3630
TELEPHONE: (212) 840-3333
TELEFAX: (212) 840-0712
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-188-943-1

Query Match 100.0%; Score 1; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
Db 3 G 3

RESULT 39
US-08-188-943-1/c
Sequence 1, Application US/08188943
Patent No. 5635347
GENERAL INFORMATION:
APPLICANT: Link, John R.
APPLICANT: Gudibande, Satyanarayana R.
APPLICANT: Kenten, John H.
TITLE OF INVENTION: Rapid Assays for Amplification
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Curtis, Morris & Safford
STREET: 530 Fifth Avenue
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 28-JAN-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/792,602
FILING DATE: 15-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: Evans, Barry
REGISTRATION NUMBER: 22,802
REFERENCE/DOCKET NUMBER: 370068-3630
TELEPHONE: (212) 840-3333
TELEFAX: (212) 840-0712
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-188-943-1

Query Match 100.0%; Score 1; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;

Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1

Db 4 G 4

RESULT 40

US-08-188-943-2
; Sequence 2, Application US/08188943
; Patent No. 5635347
; GENERAL INFORMATION:
; APPLICANT: Link, John R.
; APPLICANT: Gudibande, Satyanarayana R.
; APPLICANT: Kenten, John H.
; TITLE OF INVENTION: Rapid Assays for Amplification
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Curtis, Morris & Safford
; ADDRESSEE: C/O Barry Evans
; STREET: 530 Fifth Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/188,943
; FILING DATE: 28-JAN-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/792,602
; FILING DATE: 15-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Evans, Barry
; REGISTRATION NUMBER: 22,802
; REFERENCE/DOCKET NUMBER: 370068-3630
; TELEPHONE: (212) 840-3333
; TELEFAX: (212) 840-0712
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-188-943-2

Query Match 100.0%; Score 1; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;

Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1

Db 1 G 1

RESULT 41

US-08-188-943-2/c
; Sequence 2, Application US/08188943
; Patent No. 5635347
; GENERAL INFORMATION:
; APPLICANT: Link, John R.
; APPLICANT: Gudibande, Satyanarayana R.
; APPLICANT: Kenten, John H.
; TITLE OF INVENTION: Rapid Assays for Amplification
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Curtis, Morris & Safford
; ADDRESSEE: C/O Barry Evans
; STREET: 530 Fifth Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/188,943
; FILING DATE: 28-JAN-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/792,602
; FILING DATE: 15-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Evans, Barry
; REGISTRATION NUMBER: 22,802
; REFERENCE/DOCKET NUMBER: 370068-3630
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 840-3333
; TELEFAX: (212) 840-0712
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-188-943-2

Query Match 100.0%; Score 1; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;

Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1

Db 2 G 2

RESULT 42

US-08-465-811A-25
; Sequence 25, Application US/08465811A
; Patent No. 5637685
; GENERAL INFORMATION:
; APPLICANT: Soares, M. Bento
; APPLICANT: Efstratiadis, Argiris
; TITLE OF INVENTION: METHOD FOR CONSTRUCTION OF
; TITLE OF INVENTION: NORMALIZED CDNA LIBRARIES
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John P. White, c/o Cooper & Dunham
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/465,811A
; FILING DATE: June 6, 1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678

REFERENCE/DOCKET NUMBER: 42840/JPW/AKC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 977-9550
TELEFAX: (212) 664-0525
TELEX: 422523 COOP UI
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-465-811A-25

Query Match 100.0%; Score 1; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1
|
Db 3 G 3

RESULT 43
US-08-465-811A-25/c
Sequence 25, Application US/08465811A
Patent No. 5637685
GENERAL INFORMATION:
APPLICANT: Soares, M. Bento
APPLICANT: Efstratiadis, Argiris
TITLE OF INVENTION: METHOD FOR CONSTRUCTION OF
TITLE OF INVENTION: NORMALIZED CDNA LIBRARIES
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: John P. White, c/o Cooper & Dunham
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,811A
FILING DATE: June 6, 1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 42840/JPW/AKC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 977-9550
TELEFAX: (212) 664-0525
TELEX: 422523 COOP UI
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-465-811A-25

Query Match 100.0%; Score 1; DB 1; Length 4;

Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 g 1
|
Db 4 G 4
RESULT 44
US-08-199-317-2
Sequence 2, Application US/08199317
Patent No. 5670316
GENERAL INFORMATION:
APPLICANT: Sena, Elissa P.
APPLICANT: Calhoun, Cornelia J.
APPLICANT: Zarling, David A.
TITLE OF INVENTION: Diagnostic Applications of Double D-loop
TITLE OF INVENTION: Formation
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Ave., Suite 250
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/199,317
FILING DATE: 25-MAY-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/910,791
FILING DATE: 09-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/755,462
FILING DATE: 04-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/520,321
FILING DATE: 07-MAY-1990
ATTORNEY/AGENT INFORMATION:
NAME: Stratford, Carol A.
REGISTRATION NUMBER: 34,444
REFERENCE/DOCKET NUMBER: 9150-0004
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-324-0880
TELEFAX: 415-324-0960
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Cleavage site for Dpn I
US-08-199-317-2

Query Match 100.0%; Score 1; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 g 1
|
Db 1 G 1

RESULT 45
US-08-199-317-2/c
; Sequence 2, Application US/08199317
; Patent No. 5670316
; GENERAL INFORMATION:
; APPLICANT: Sena, Elissa P.
; APPLICANT: Calhoun, Cornelia J.
; APPLICANT: Zarling, David A.
; TITLE OF INVENTION: Diagnostic Applications of Double D-loop
; TITLE OF INVENTION: Formation
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Ave., Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/199,317
; FILING DATE: 25-MAY-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/910,791
; FILING DATE: 09-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/755,462
; FILING DATE: 04-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/520,321
; FILING DATE: 07-MAY-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Stratford, Carol A.
; REGISTRATION NUMBER: 34,444
; REFERENCE/DOCKET NUMBER: 9150-0004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-324-0880
; TELEFAX: 415-324-0960
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: Cleavage site for Dpn I
US-08-199-317-2

Query Match 100.0%; Score 1; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
|
Db 4 G 4

Search completed: July 15, 2002, 23:07:38
Job time: 22991 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: July 15, 2002, 23:10:11 ; Search time 932.4 Seconds
(without alignments)
1.841 Million cell updates/sec

Title: US-09-375-248-1_COPY_2588_2588

Perfect score: 1
Sequence: 1 g 1

Scoring table: OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 1736436 seqs, 858457221 residues

Word size : 0

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : N_Geneseq_032802.*

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- 19: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT.*
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- 21: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT.*
- 22: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT.*
- 23: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT.*
- 24: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT.*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	
1	1	100.0	3	17	AAT33326	
C	2	1	100.0	3	17	AAT33326
C	3	1	100.0	3	21	AAA94655
C	4	1	100.0	3	22	AA120244
C	5	1	100.0	4	16	AAQ81664
C	6	1	100.0	4	16	AAQ81664
C	7	1	100.0	4	16	AAQ81665
C	8	1	100.0	4	16	AAQ81665
C	9	1	100.0	4	18	AAT86385
						CAPL trinucleotide
						CAPL trinucleotide
						Human TUB gene pro
						Human breast cancer
						bFGF binding oligo
						bFGF binding oligo
						bFGF binding oligo
						bFGF binding oligo
						probe for target n

C	10	1	100.0	4	18	AAT86385	Probe for target n
C	11	1	100.0	4	18	AAT77252	Immunostimulatory
C	12	1	100.0	4	18	AAT77252	Immunostimulatory
C	13	1	100.0	4	22	AA17191	Human breast cancer
C	14	1	100.0	4	22	AA17191	Human breast cancer
C	15	1	100.0	4	22	AA17191	Human breast cancer
C	16	1	100.0	4	22	AA17191	Human breast cancer
C	17	1	100.0	4	22	AA17191	Cyclin binding ham
C	18	1	100.0	5	10	AAQ81665	Synthetic probe fo
C	19	1	100.0	5	15	AAQ81665	CHA255 heavy chain
C	20	1	100.0	5	16	AAQ81667	bFGF binding oligo
C	21	1	100.0	5	17	AAQ81667	Clearable replicab
C	22	1	100.0	5	19	AAQ81663	Fusarium sp. 18S r
C	23	1	100.0	5	19	AAQ81663	Fusarium sp. 18S r
C	24	1	100.0	5	19	AAQ81663	Fungal telomeric n
C	25	1	100.0	5	20	AAQ81665	Oligonucleotide se
C	26	1	100.0	5	20	AAQ81665	Oligonucleotide se
C	27	1	100.0	5	20	AAQ81665	DNA enhancer seque
C	28	1	100.0	5	20	AAQ81665	DNA enhancer seque
C	29	1	100.0	5	20	AAQ81665	US5908745 primer #
C	30	1	100.0	5	20	AAQ81665	US5908745 primer #
C	31	1	100.0	5	20	AAQ81665	US5908745 primer #
C	32	1	100.0	5	20	AAQ81665	US5908745 primer #
C	33	1	100.0	5	20	AAQ81665	US5908745 primer #
C	34	1	100.0	5	20	AAQ81665	Ras gene modulat
C	35	1	100.0	5	20	AAQ81665	Ras gene modulat
C	36	1	100.0	5	20	AAQ81665	Mutant H-ras speci
C	37	1	100.0	5	21	AAQ81665	Mutant H-ras speci
C	38	1	100.0	5	21	AAQ81665	Human colon cancer
C	39	1	100.0	5	21	AAQ81665	Human colon cancer
C	40	1	100.0	5	21	AAQ81665	Transcription fact
C	41	1	100.0	5	21	AAQ81665	Transcription fact
C	42	1	100.0	5	21	AAQ81665	Human UCP3 promote
C	43	1	100.0	5	21	AAQ81665	Human UCP3 promote
C	44	1	100.0	5	21	AAQ81665	Human UCP3 promote
C	45	1	100.0	5	21	AAQ81665	First DNA arm segm

ALIGNMENTS

RESULT 1
AAT33326 1
ID AAT33326 standard; RNA; 3 BP.

AC AAT33326;

DT 12-NOV-1996 (first entry)

DE CAPL trinucleotide.

KW CAPL; antisense oligonucleotide; ribozyme; cancer; metastasis;

KX osteosarcoma; therapy; ss.

OS Synthetic.

PN WO9625499-A1.

XX 22-AUG-1996.

PF 16-FEB-1996; 96WO-US02108.

XX 17-FEB-1995; 95US-0391375.

PR (HYBR-) HYBRIDON INC.

PA (NORA-) NORWEGIAN RADIUM HOSPITAL RES FOUND.

XX Agrawal S, Engebraaten O, Fodstad O, Hovig E, Maelandsmo GJ;

PI Von Hofe E;

XX WPI; 1996-393400/39.

DR Synthetic oligo:nucleotide(s) inhibiting CAPL gene expression -

XX

PT

PT useful to inhibit metastatic cancer, partic. osteosarcoma

PS Claim 2; Page 56; 70pp; English.

CC Novel antisense oligonucleotides capable of inhibiting CAPL gene
 CC expression may include the trinucleotide GUC (AAT33326, given in 5'
 CC to 3' direction) found in codon 14 of CAPL mRNA. These and
 CC other antisense oligonucleotides (AAT33327-36) complementary to
 CC specific regions of the CAPL gene (see also AAT33345), as well as
 CC CAPL-specific ribozymes (AAT33337-40) can be administered to a
 CC patient as a means of inhibiting metastatic cancer.

XX Sequence 3 BP; 0 A; 1 C; 1 G; 1 U; 0 other;

Query Match 100.0%; Score 1; DB 17; Length 3;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1

Db 3 g 3

RESULT 2

AAT33326/c

ID AAT33326 standard; RNA; 3 BP.

XX AAT33326;

XX AAT33326;

DT 12-NOV-1996 (first entry)

XX CAPL trinucleotide.

XX CAPL; antisense oligonucleotide; ribozyme; cancer; metastasis;
 KW osteosarcoma; therapy; ss.

XX Synthetic.

XX WO9625499-A1.

XX 22-AUG-1996.

PF 16-FEB-1996; 96WO-US02108.

XX 17-FEB-1995; 95US-0391375.

XX (HYBR-) HYBRIDON INC.

PA (NORA-) NORWEGIAN RADIUM HOSPITAL RES FOUND.

XX Agrawal S, Engebraaten O, Fodstad O, Hovig E, Maelandsmo GJ;
 PI Von Hofe E;

XX WPI; 1996-393400/39.

XX Synthetic oligo:nucleotide(s) inhibiting CAPL gene expression -
 PT useful to inhibit metastatic cancer, partic. osteosarcoma

PS Claim 2; Page 56; 70pp; English.

XX Novel antisense oligonucleotides capable of inhibiting CAPL gene
 CC expression may include the trinucleotide GUC (AAT33326, given in 5'
 CC to 3' direction) found in codon 14 of CAPL mRNA. These and
 CC other antisense oligonucleotides (AAT33327-36) complementary to
 CC specific regions of the CAPL gene (see also AAT33345), as well as
 CC CAPL-specific ribozymes (AAT33337-40) can be administered to a
 CC patient as a means of inhibiting metastatic cancer.

XX Sequence 3 BP; 0 A; 1 C; 1 G; 1 U; 0 other;

Query Match

Best Local Similarity 100.0%; Score 1; DB 17; Length 3;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1

Db 1 g 1

RESULT 3

AAA94655

ID AAA94655 standard; DNA; 3 BP.

XX AAA94655;

XX AAA94655;

DT 15-JAN-2001 (first entry)

XX Human TUB gene probe #2.

XX Human; TULP; neurosensory defect; retina; retinal dystrophy; probe;
 KW TUB; ss.

XX Homo sapiens.

XX US6114502-A.

XX 05-SEP-2000.

XX 27-FEB-1998; 98US-0032365.

XX 22-AUG-1996; 96US-0701380.

XX 04-SEP-1996; 96US-0706292.

XX 10-APR-1996; 96US-0630592.

XX 17-SEP-1996; 96US-0714991.

XX 30-APR-1997; 97US-0850218.

XX 01-AUG-1997; 97US-0904699.

XX 17-SEP-1997; 97US-0932306.

PA (AXYS-) AXYS PHARM INC.

XX North M, Nishina P, Noben-Trauth K, Naggert J;

XX WPI; 2000-586483/55.

XX Mammalian proteins expressed in retina and brain, useful for producing
 PT antibodies and for diagnosing neurosensory defects including cochlear
 PT degeneration, peripheral retinal degeneration and cone-rod retinal
 PT dystrophy.

XX Disclosure; Columns 81-82; 61pp; English.

XX The present invention relates to human and murine cDNAs from a
 CC neurosensory defect associated gene family. The novel cDNAs are mouse
 CC tub form I (see AAA94629), mouse tub form II (see AAA94630), human TUB
 CC form 6 (see AAA94632), human TUB form 1 (see AAA94633), human TULP1 (see
 CC AAA94635), human TULP2 (see AAA94636), human TULP3 (see AAA94637) and
 CC mouse TULP4 (see AAA94638). The novel coding sequences are useful as
 CC immunogens to raise antibodies that specifically identify TUB/TULP
 CC expressing cells and in drug screening assays directed at neurosensory
 CC defects. The novel proteins encoded by the present sequence can be used
 CC for the treatment of neurosensory degenerative conditions e.g. retinal
 CC dystrophies. The present sequence is a probe used to isolate the novel
 CC genes of the present invention.

XX Sequence 3 BP; 0 A; 0 C; 3 G; 0 U; 0 other;

Query Match 100.0%; Score 1; DB 21; Length 3;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1

Db 1 g 1

RESULT 4
 AAL20244/c
 ID AAL20244 standard; CDNA; 3 BP.
 XV
 AAL20244;
 XX
 DT 07-DEC-2001 (first entry)
 XX
 DE Human breast cancer expressed polynucleotide 12701.
 XX
 KW Human; breast cancer; cell marker; cytostatic; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200151628-A2.
 XX
 PD 19-JUL-2001.
 XX
 PF 10-JAN-2001; 2001WO-US00798.
 XX
 PR 14-JAN-2000; 2000US-0176077.
 PR 14-MAR-2000; 2000US-0189167.
 PR 24-MAR-2000; 2000US-0192099.
 PR 29-MAR-2000; 2000US-0193480.
 PR 15-MAY-2000; 2000US-0205230.
 PR 09-JUN-2000; 2000US-0211315.
 PR 25-JUL-2000; 2000US-0220534.
 XX
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 XX
 PI Lillie J, Xu Y, Wang Y, Steinmann K;
 XX
 DR WPI; 2001-451856/48.
 XX
 PT New peptide useful as a marker for the diagnosis of breast cancer
 XX
 PS Claim 1; Page 2245; 3695pp; English.
 XX
 CC The invention relates to human breast cancer expressed polynucleotides
 CC (AAL07544-AAL26789) and methods of assessing whether a patient is
 CC afflicted with breast cancer by examining the correlation between the
 CC expression of certain markers and the cancerous state of breast cells.
 CC The polynucleotides and encoded polypeptides are potential markers for
 CC detecting, diagnosing, monitoring, characterising treating and
 CC potentially preventing breast cancer. The polynucleotides and encoded
 CC polypeptides are also useful for isolating compounds with cytostatic
 CC activity.
 XX
 SQ Sequence 3 BP; 1 A; 1 C; 0 G; 1 T; 0 other;

 Query Match 100.0%; Score 1; DB 22; Length 3;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 1 g 1
 Db 2 G 2

 RESULT 5
 AAQ81664
 ID AAQ81664 standard; RNA; 4 BP.
 XX
 AC AAQ81664;
 XX
 DT 29-SEP-1995 (first entry)
 XX
 DE bFGF binding oligomer core sequence #1.
 XX
 KW Basic; fibroblast growth factor; bFGF; stem-loop structure;
 KW bubble structure; pseudoknot; receptor; heparin; competition;
 inhibition; enhance; neovascularisation; solid tumour; cancer;
 metastasis; diagnosis; gene therapy; ss.
 OS Synthetic.
 PN WO9500528-A.
 XX

inhibition; enhance; neovascularisation; solid tumour; cancer;
 metastasis; diagnosis; gene therapy; ss.
 OS Synthetic.
 PN WO9500528-A.
 XX
 PD 05-JAN-1995.
 XX
 PF 17-JUN-1994; 94WO-US06884.
 XX
 PR 18-JUN-1993; 93US-0079677.
 PR 07-JAN-1994; 94US-0179491.
 XX
 PA (PHAR-) PHARMAGENICS INC.
 XX
 PI Beutel BA, Joesten ME;
 XX
 DR WPI; 1995-051992/07.
 XX
 PT New oligo-nucleotide(s) that bind to basic fibroblast growth
 factor - modulating, esp. inhibiting, its activity, useful in
 PT treating cancer, preventing metastasis, and diagnosis.
 XX
 PS Claim 3; Page 25; 44pp; English.
 XX
 CC The sequences given in AAQ81642-95 are oligonucleotides which modulate
 CC the activity of basic fibroblast growth factor (bFGF) by binding
 CC to the bFGF protein. Most esp. the sequences given in AAQ81664-67
 CC represent core sequences of which at least one is present in each of
 CC the binding oligos. These oligonucleotides may form a single
 CC strand, double strand, a stem-loop structure, a bubble structure, a
 CC pseudoknot or a closed, circular structure. bFGF binds to high
 CC affinity receptor and low affinity heparin-like molecules on the
 CC cell surface. These oligonucleotides bind to bFGF in competition
 CC with its receptor and heparin. These oligonucleotides may inhibit
 CC or enhance the activity of bFGF. Particularly, they inhibit
 CC neovascularisation so they can be used to suppress growth of solid
 CC tumours and to reduce the risk of metastasis. They can be used as
 CC diagnostic reagents to determine the presence of thrombin, or used in
 CC gene therapy.
 XX
 SQ Sequence 4 BP; 0 A; 1 C; 2 G; 1 U; 0 other;

 Query Match 100.0%; Score 1; DB 16; Length 4;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 1 g 1
 Db 1 g 1

 RESULT 6
 AAQ81664/c
 ID AAQ81664 standard; RNA; 4 BP.
 XX
 AC AAQ81664;
 XX
 DT 29-SEP-1995 (first entry)
 XX
 DE bFGF binding oligomer core sequence #1.
 XX
 KW Basic; fibroblast growth factor; bFGF; stem-loop structure;
 KW bubble structure; pseudoknot; receptor; heparin; competition;
 KW inhibition; enhance; neovascularisation; solid tumour; cancer;
 KW metastasis; diagnosis; gene therapy; ss.
 XX
 OS Synthetic.
 PN WO9500528-A.
 XX

PD 05-JAN-1995.
 XX
 PF 17-JUN-1994; 94WO-US06884.
 XX
 PR 18-JUN-1993; 93US-0079677.
 PR 07-JAN-1994; 94US-0179491.
 XX
 PA (PHAR-) PHARMAGENICS INC.
 XX
 PI Beutel BA, Joesten ME;
 XX
 DR WPI; 1995-051992/07.
 XX
 PT New oligo-nucleotide(s) that bind to basic fibroblast growth
 factor - modulating, esp. inhibiting, its activity, useful in
 treating cancer, preventing metastasis, and diagnosis.
 XX
 PS Claim 3; Page 25; 44pp; English.
 XX
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 the activity of basic fibroblast growth factor (bFGF) by binding
 to the bFGF protein. Most esp. the sequences given in AAQ81664-67
 represent core sequences of which at least one is present in each of
 the binding oligos. These oligonucleotides may form a single
 strand, double strand, a stem-loop structure, a bubble structure, a
 pseudoknot or a closed, circular structure. bFGF binds to high
 affinity receptor and low affinity heparin-like molecules on the
 cell surface. These oligonucleotides bind to bFGF in competition
 with its receptor and heparin. These oligonucleotides may inhibit
 or enhance the activity of bFGF. Particularly, they inhibit
 neovascularisation so they can be used to suppress growth of solid
 tumours and to reduce the risk of metastasis. They can be used as
 diagnostic reagents to determine the presence of thrombin, or used in
 gene therapy.
 XX
 SQ Sequence 4 BP; 0 A; 1 C; 2 G; 1 U; 0 other;
 Query Match 100.0%; Score 1; DB 16; Length 4;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 g 1
 Db 4 G 4
 RESULT 7
 ID AAQ81665 standard; RNA; 4 BP.
 AC AAQ81665;
 XX
 DT 29-SEP-1995 (first entry)
 XX
 DE bFGF binding oligomer core sequence #2.
 KW Basic; fibroblast growth factor; bFGF; stem-loop structure;
 KW bubble structure; pseudoknot; receptor; heparin; competition;
 KW inhibition; enhance; neovascularisation; solid tumour; cancer;
 KW metastasis; diagnosis; gene therapy; ss.
 XX
 OS Synthetic.
 XX
 PN WO9500528-A.
 XX
 PD 05-JAN-1995.
 XX
 PF 17-JUN-1994; 94WO-US06884.
 XX
 PR 18-JUN-1993; 93US-0079677.
 PR 07-JAN-1994; 94US-0179491.
 XX
 PA (PHAR-) PHARMAGENICS INC.
 XX
 PI Beutel BA, Joesten ME;
 XX
 DR WPI; 1995-051992/07.
 XX
 PT New oligo-nucleotide(s) that bind to basic fibroblast growth

PA (PHAR-) PHARMAGENICS INC.
 XX
 PI Beutel BA, Joesten ME;
 XX
 DR WPI; 1995-051992/07.
 XX
 PT New oligo-nucleotide(s) that bind to basic fibroblast growth
 factor - modulating, esp. inhibiting, its activity, useful in
 treating cancer, preventing metastasis, and diagnosis.
 XX
 PS Claim 3; Page 25; 44pp; English.
 XX
 CC The sequences given in AAQ81642-95 are oligonucleotides which modulate
 the activity of basic fibroblast growth factor (bFGF) by binding
 to the bFGF protein. Most esp. the sequences given in AAQ81664-67
 represent core sequences of which at least one is present in each of
 the binding oligos. These oligonucleotides may form a single
 strand, double strand, a stem-loop structure, a bubble structure, a
 pseudoknot or a closed, circular structure. bFGF binds to high
 affinity receptor and low affinity heparin-like molecules on the
 cell surface. These oligonucleotides bind to bFGF in competition
 with its receptor and heparin. These oligonucleotides may inhibit
 or enhance the activity of bFGF. Particularly, they inhibit
 neovascularisation so they can be used to suppress growth of solid
 tumours and to reduce the risk of metastasis. They can be used as
 diagnostic reagents to determine the presence of thrombin, or used in
 gene therapy.
 XX
 SQ Sequence 4 BP; 0 A; 2 C; 1 G; 1 U; 0 other;
 Query Match 100.0%; Score 1; DB 16; Length 4;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 g 1
 Db 3 g 3
 RESULT 8
 ID AAQ81665/c
 ID AAQ81665 standard; RNA; 4 BP.
 XX
 AC AAQ81665;
 XX
 DT 29-SEP-1995 (first entry)
 XX
 DE bFGF binding oligomer core sequence #2.
 KW Basic; fibroblast growth factor; bFGF; stem-loop structure;
 KW bubble structure; pseudoknot; receptor; heparin; competition;
 KW inhibition; enhance; neovascularisation; solid tumour; cancer;
 KW metastasis; diagnosis; gene therapy; ss.
 XX
 OS Synthetic.
 XX
 PN WO9500528-A.
 XX
 PD 05-JAN-1995.
 XX
 PF 17-JUN-1994; 94WO-US06884.
 XX
 PR 18-JUN-1993; 93US-0079677.
 PR 07-JAN-1994; 94US-0179491.
 XX
 PA (PHAR-) PHARMAGENICS INC.
 XX
 PI Beutel BA, Joesten ME;
 XX
 DR WPI; 1995-051992/07.
 XX
 PT New oligo-nucleotide(s) that bind to basic fibroblast growth

PT factor - modulating, esp. inhibiting, its activity, useful in
PT treating cancer, preventing metastasis, and diagnosis.
XX
PS Claim 3; Page 25; 44pp; English.
XX
CC The sequences given in AAQ81642-95 are oligonucleotides which modulate
CC the activity of basic fibroblast growth factor (bFGF) by binding
CC to the bFGF protein. Most esp. the sequences given in AAQ81644-67
CC represent core sequences of which at least one is present in each of
CC the binding oligos. These oligonucleotides may form a single
CC strand, double strand, a stem-loop structure, a bubble structure, a
CC pseudoknot or a closed, circular structure. bFGF binds to high
CC affinity receptor and low affinity heparin-like molecules on the
CC cell surface. These oligonucleotides bind to bFGF in competition
CC with its receptor and heparin. These oligonucleotides may inhibit
CC or enhance the activity of bFGF. Particularly, they inhibit
CC neovascularisation so they can be used to suppress growth of solid
CC tumours and to reduce the risk of metastasis. They can be used as
CC diagnostic reagents to determine the presence of thrombin, or used in
XX gene therapy.
SQ Sequence 4 BP; 0 A; 2 C; 1 G; 1 U; 0 other;

Query Match 100.0%; Score 1; DB 16; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
Db 4 G 4

RESULT 9
AAT86385
ID AAT86385 standard; DNA; 4 BP.
XX
AC AAT86385;
XX
DT 23-APR-1998 (first entry)
XX
DE Probe for target nucleic acid sequence P0.
XX
KW Point mutation detection; nucleic acid sequence analysis; probe;
KW viral disease diagnosis; genetic disease diagnosis; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1
FT /*tag= a
FT /note= "C-5'phosphate"
XX
PN WO9738131-A1.
XX
PD 16-OCT-1997.
XX
PF 11-APR-1996; 96WO-RU00087.
XX
PR 11-APR-1996; 96WO-RU00087.
XX
PA (DYMS/) DYMSHITS G M.
PA (IVAN/) IVANOVA E M.
PA (KRIV/) KRIVENKO A A.
PA (KULI/) KULIKOVA V F.
PA (LOKH/) LOKHOV S G.
PA (PYSH/) PYSHNY D V.
XX
PI Dymshits GM, Ivanova EM, Krivenko AA, Kulikova VF;
PI Lohkov SG, Pyshtny DV;
XX
DR WPI; 1997-512737/47.
XX

PT Detection of target nucleic acid sequence - based on ligation of
PT hybridised short probe to flanking target-complementary sequences
XX
PS Example; Page 4; 15pp; Russian.
XX
CC This sequence represents a probe for the target sequence P0 (shown in
CC AAT86376). This sequence was used to test the method of the invention.
CC The method of the invention is for detecting a nucleic acid sequence to
CC be analysed, and comprises hybridisation of an oligonucleotide probe
CC complementary to the sequence to be analysed and bearing a reporter
CC group, the novelty is that detection of a sequence is based on the
CC ligation of a short oligonucleotide (with a length of 4-6 units) with
CC flanking oligonucleotide sequences (or their derivatives bearing
CC polycyclic aromatic groups). The method is especially useful for
CC detecting point mutations. Diagnosis of viral, genetic and other
XX diseases is also mentioned.
SQ Sequence 4 BP; 1 A; 2 C; 1 G; 0 U; 0 other;

Query Match 100.0%; Score 1; DB 18; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
Db 3 g 3

RESULT 10
AAT86385/C
ID AAT86385 standard; DNA; 4 BP.
XX
AC AAT86385;
XX
DT 23-APR-1998 (first entry)
XX
DE Probe for target nucleic acid sequence P0.
XX
KW Point mutation detection; nucleic acid sequence analysis; probe;
KW viral disease diagnosis; genetic disease diagnosis; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1
FT /*tag= a
FT /note= "C-5'phosphate"
XX
PN WO9738131-A1.
XX
PD 16-OCT-1997.
XX
PF 11-APR-1996; 96WO-RU00087.
XX
PR 11-APR-1996; 96WO-RU00087.
XX
PA (DYMS/) DYMSHITS G M.
PA (IVAN/) IVANOVA E M.
PA (KRIV/) KRIVENKO A A.
PA (KULI/) KULIKOVA V F.
PA (LOKH/) LOKHOV S G.
PA (PYSH/) PYSHNY D V.
XX
PI Dymshits GM, Ivanova EM, Krivenko AA, Kulikova VF;
PI Lohkov SG, Pyshtny DV;
XX
DR WPI; 1997-512737/47.
XX
PT Detection of target nucleic acid sequence - based on ligation of
PT hybridised short probe to flanking target-complementary sequences
XX
PS Example; Page 4; 15pp; Russian.
XX

XX This sequence represents a probe for the target sequence P0 (shown in
CC AA#86376). This sequence was used to test the method of the invention.
CC The method of the invention is for detecting a nucleic acid sequence to
CC be analysed, and comprises hybridisation of an oligonucleotide probe
CC complementary to the sequence to be analysed and bearing a reporter
CC group, the novelty is that detection of a sequence is based on the
CC ligation of a short oligonucleotide (with a length of 4-6 units) with
CC flanking oligonucleotide sequences (or their derivatives bearing
CC polycyclic aromatic groups). The method is especially useful for
CC detecting point mutations. Diagnosis of viral, genetic and other
CC diseases is also mentioned.
XX
XX Sequence 4 BP; 1 A; 2 C; 1 G; 0 U; 0 other;

Query Match 100.0%; Score 1; DB 18; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1
|
Db 4 G 4

RESULT 11
AAT77252
ID AAT77252 standard; DNA; 4 BP.
XX
AC AAT77252;
XX
DT 18-MAR-1998 (first entry)
XX
DE Immunostimulatory polynucleotide 11.
XX
KW Immunostimulatory polynucleotide; ISP; palindrome; vaccine;
KW immune response; antigen; naked gene expression vector; IgE;
KW antibody; immunotherapy; ss.
XX
OS Synthetic.
XX
PN WO9728259-A1.
XX
PD 07-AUG-1997.
XX
PF 28-JAN-1997; 97WO-US01277.
XX
PR 30-JAN-1996; 96US-0593554.
XX
PA (REGC) UNIV CALIFORNIA.
XX
PI Carson DA, Raz E;
XX
DR WPI; 1997-402613/37.
XX
PT Recombinant vector containing immunostimulatory palindromic
PT polynucleotide - useful for selectively enhancing the Th1 immune
PT response in a host, whilst reducing the risk of anaphylaxis
XX
PS Claim 16; Page 15; 102pp; English.
XX
CC This sequence represents a non-coding immunostimulatory polynucleotide
CC (ISP) comprised of at least one strand of a palindrome, which includes
CC at least one dinucleotide consisting of adjacent, unmethylated cytosine
CC and guanine residues. ISP's could be used in vaccination methods
CC for enhancing the immune response of a host to an antigen. Administration
CC of naked gene expression vectors which encode antigens or their
CC immunostimulatory fragments suppresses IgE antibody production
CC reducing the risk of anaphylaxis posed by conventional immunotherapy.
XX
XX Sequence 4 BP; 1 A; 1 C; 1 G; 1 T; 0 other;

Query Match 100.0%; Score 1; DB 18; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1
|
Db 2 G 2

RESULT 13
AAL17191
ID AAL17191 standard; cDNA; 4 BP.
XX
AC AAL17191;
XX
DT 07-DEC-2001 (first entry)

Query Match 100.0%; Score 1; DB 18; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1
|
Db 3 g 3

RESULT 12
AAT77252/c
ID AAT77252 standard; DNA; 4 BP.
XX
AC AAT77252;
XX
DT 18-MAR-1998 (first entry)
XX
DE Immunostimulatory polynucleotide 11.
XX
KW Immunostimulatory polynucleotide; ISP; palindrome; vaccine;
KW immune response; antigen; naked gene expression vector; IgE;
KW antibody; immunotherapy; ss.
XX
OS Synthetic.
XX
PN WO9728259-A1.
XX
PD 07-AUG-1997.
XX
PF 28-JAN-1997; 97WO-US01277.
XX
PR 30-JAN-1996; 96US-0593554.
XX
PA (REGC) UNIV CALIFORNIA.
XX
PI Carson DA, Raz E;
XX
DR WPI; 1997-402613/37.
XX
PT Recombinant vector containing immunostimulatory palindromic
PT polynucleotide - useful for selectively enhancing the Th1 immune
PT response in a host, whilst reducing the risk of anaphylaxis
XX
PS Claim 16; Page 15; 102pp; English.
XX
CC This sequence represents a non-coding immunostimulatory polynucleotide
CC (ISP) comprised of at least one strand of a palindrome, which includes
CC at least one dinucleotide consisting of adjacent, unmethylated cytosine
CC and guanine residues. ISP's could be used in vaccination methods
CC for enhancing the immune response of a host to an antigen. Administration
CC of naked gene expression vectors which encode antigens or their
CC immunostimulatory fragments suppresses IgE antibody production
CC reducing the risk of anaphylaxis posed by conventional immunotherapy.
XX
XX Sequence 4 BP; 1 A; 1 C; 1 G; 1 T; 0 other;

Query Match 100.0%; Score 1; DB 18; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1
|
Db 2 G 2

RESULT 13
AAL17191
ID AAL17191 standard; cDNA; 4 BP.
XX
AC AAL17191;
XX
DT 07-DEC-2001 (first entry)

```
XX DE Human breast cancer expressed polynucleotide 9648.
XX KW Human; breast cancer; cell marker; cytostatic; ss.
XX OS Homo sapiens.
XX PN WO200151628-A2.
XX PD 19-JUL-2001.
XX PF 10-JAN-2001; 2001WO-US00798.
XX PR 14-JAN-2000; 2000US-0176077.
XX PR 14-MAR-2000; 2000US-0189167.
XX PR 24-MAR-2000; 2000US-0192099.
XX PR 29-MAR-2000; 2000US-0193480.
XX PR 15-MAY-2000; 2000US-0205230.
XX PR 09-JUN-2000; 2000US-0211315.
XX PR 25-JUL-2000; 2000US-0220534.
XX PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX PI Lillie J, Xu Y, Wang Y, Steinmann K;
XX WPI; 2001-451856/48.
XX PT New peptide useful as a marker for the diagnosis of breast cancer -
XX PS Claim 1; Page 1720; 3695pp; English.
XX CC The invention relates to human breast cancer expressed polynucleotides
XX CC (AAL07544-AAL26789) and methods of assessing whether a patient is
XX CC afflicted with breast cancer by examining the correlation between the
XX CC expression of certain markers and the cancerous state of breast cells.
XX CC The polynucleotides and encoded polypeptides are potential markers for
XX CC detecting, diagnosing, monitoring, characterising treating and
XX CC potentially preventing breast cancer. The polynucleotides and encoded
XX CC polypeptides are also useful for isolating compounds with cytostatic
XX CC activity.
XX SQ Sequence 4 BP; 1 A; 1 C; 1 G; 1 T; 0 other;

Query Match 100.0%; Score 1; DB 22; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
Db 1 g 1

RESULT 14
AAL17191/c
ID AAL17191 standard; cDNA; 4 BP.
AC AAL17191;
XX DT 07-DEC-2001 (first entry)
XX DE Human breast cancer expressed polynucleotide 9648.
XX KW Human; breast cancer; cell marker; cytostatic; ss.
XX OS Homo sapiens.
XX PN WO200151628-A2.
XX PD 19-JUL-2001.
XX PF 10-JAN-2001; 2001WO-US00798.
XX PR 14-JAN-2000; 2000US-0176077.
XX PR 14-MAR-2000; 2000US-0189167.
XX PR 24-MAR-2000; 2000US-0192099.
XX PR 29-MAR-2000; 2000US-0193480.
XX PR 15-MAY-2000; 2000US-0205230.
XX PR 09-JUN-2000; 2000US-0211315.
XX PR 25-JUL-2000; 2000US-0220534.
XX PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX PI Lillie J, Xu Y, Wang Y, Steinmann K;
XX WPI; 2001-451856/48.
XX PT New peptide useful as a marker for the diagnosis of breast cancer -
XX PS Claim 1; Page 1720; 3695pp; English.
XX CC The invention relates to human breast cancer expressed polynucleotides
XX CC (AAL07544-AAL26789) and methods of assessing whether a patient is
XX CC afflicted with breast cancer by examining the correlation between the
XX CC expression of certain markers and the cancerous state of breast cells.
XX CC The polynucleotides and encoded polypeptides are potential markers for
XX CC detecting, diagnosing, monitoring, characterising treating and
XX CC potentially preventing breast cancer. The polynucleotides and encoded
XX CC polypeptides are also useful for isolating compounds with cytostatic
XX CC activity.
XX SQ Sequence 4 BP; 1 A; 1 C; 1 G; 1 T; 0 other;

Query Match 100.0%; Score 1; DB 22; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
Db 1 g 1

RESULT 15
AAL24357/c
ID AAL24357 standard; cDNA; 4 BP.
XX AC AAL24357;
XX DT 07-DEC-2001 (first entry)
XX DE Human breast cancer expressed polynucleotide 16814.
XX KW Human; breast cancer; cell marker; cytostatic; ss.
XX OS Homo sapiens.
XX PN WO200151628-A2.
XX PD 19-JUL-2001.
XX PF 10-JAN-2001; 2001WO-US00798.
XX PR 14-JAN-2000; 2000US-0176077.
XX PR 14-MAR-2000; 2000US-0189167.
XX PR 24-MAR-2000; 2000US-0192099.
XX PR 29-MAR-2000; 2000US-0193480.
XX PR 15-MAY-2000; 2000US-0205230.
XX PR 09-JUN-2000; 2000US-0211315.
XX PR 25-JUL-2000; 2000US-0220534.
XX PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX PI Lillie J, Xu Y, Wang Y, Steinmann K;
XX WPI; 2001-451856/48.
XX DR
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PR 14-JAN-2000; 2000US-0176077.
PR 14-MAR-2000; 2000US-0189167.
PR 24-MAR-2000; 2000US-0192099.
PR 29-MAR-2000; 2000US-0193480.
PR 15-MAY-2000; 2000US-0205230.
PR 09-JUN-2000; 2000US-0211315.
PR 25-JUL-2000; 2000US-0220534.
XX PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX PI Lillie J, Xu Y, Wang Y, Steinmann K;
XX WPI; 2001-451856/48.
XX DR New peptide useful as a marker for the diagnosis of breast cancer -
XX PT Claim 1; Page 1720; 3695pp; English.
XX PS Claim 1; Page 1720; 3695pp; English.
XX CC The invention relates to human breast cancer expressed polynucleotides
XX CC (AAL07544-AAL26789) and methods of assessing whether a patient is
XX CC afflicted with breast cancer by examining the correlation between the
XX CC expression of certain markers and the cancerous state of breast cells.
XX CC The polynucleotides and encoded polypeptides are potential markers for
XX CC detecting, diagnosing, monitoring, characterising treating and
XX CC potentially preventing breast cancer. The polynucleotides and encoded
XX CC polypeptides are also useful for isolating compounds with cytostatic
XX CC activity.
XX SQ Sequence 4 BP; 1 A; 1 C; 1 G; 1 T; 0 other;
```

```
Query Match 100.0%; Score 1; DB 22; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
Db 3 g 3

RESULT 15
AAL24357/c
ID AAL24357 standard; cDNA; 4 BP.
XX AC AAL24357;
XX DT 07-DEC-2001 (first entry)
XX DE Human breast cancer expressed polynucleotide 16814.
XX KW Human; breast cancer; cell marker; cytostatic; ss.
XX OS Homo sapiens.
XX PN WO200151628-A2.
XX PD 19-JUL-2001.
XX PF 10-JAN-2001; 2001WO-US00798.
XX PR 14-JAN-2000; 2000US-0176077.
XX PR 14-MAR-2000; 2000US-0189167.
XX PR 24-MAR-2000; 2000US-0192099.
XX PR 29-MAR-2000; 2000US-0193480.
XX PR 15-MAY-2000; 2000US-0205230.
XX PR 09-JUN-2000; 2000US-0211315.
XX PR 25-JUL-2000; 2000US-0220534.
XX PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX PI Lillie J, Xu Y, Wang Y, Steinmann K;
XX WPI; 2001-451856/48.
XX DR
```

XX New peptide useful as a marker for the diagnosis of breast cancer -
 PT Claim 1: Page 3087; 3695pp; English.
 PS
 XX The invention relates to human breast cancer expressed polynucleotides
 CC (AAL07544-AAL26789) and methods of assessing whether a patient is
 CC afflicted with breast cancer by examining the correlation between the
 CC expression of certain markers and the cancerous state of breast cells.
 CC The polynucleotides and encoded polypeptides are potential markers for
 CC detecting, diagnosing, monitoring, characterising treating and
 CC potentially preventing breast cancer. The polynucleotides and encoded
 CC polypeptides are also useful for isolating compounds with cytostatic
 CC activity.
 XX Sequence 4 BP; 0 A; 1 C; 0 G; 3 T; 0 other;
 SQ

Query Match 100.0%; Score 1; DB 22; Length 4;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1
 |
 Db 3 G 3

RESULT 16
 AAF61450
 ID AAF61450 standard; RNA; 4 BP.
 XX AC AAF61450;
 XX
 DT 18-JUN-2001 (first entry)
 XX
 DE Cyclin binding hammerhead ribozyme 3' catalytic fragment SEQ ID 19.
 XX
 KW Hammerhead ribozyme; cyclin E; restenosis; catalytic; angioplasty;
 KW cyclin E2F1; vasotropic; gene therapy; cell cycle arrest; ss.
 XX Synthetic.
 OS
 XX WO200121789-A1.
 XX
 PD 29-MAR-2001.
 XX
 PF 22-SEP-1999; 99WO-EP07049.
 XX
 PR 22-SEP-1999; 99WO-EP07049.
 XX
 PA (UYTU-) UNIV TUEBINGEN EBERHARD-KARLS.
 XX
 PI Grassi G, Kuhn AC, Kandolf R;
 XX
 DR WPI: 2001-257985/26.
 XX

New catalytically acting RNA molecule comprising hammerhead ribozyme
 PT directed against mRNA molecules encoding cyclin E or E2F1, useful for
 PT inhibiting vascular smooth muscle cell proliferation and restenosis -
 XX
 PS Claim 12: Page 28; 40pp; German.
 XX

This invention describes a novel catalytic RNA molecule which is directed
 CC against mRNA molecules (II) which encode the cell-relevant protein cyclin
 CC E or E2F1. The products of the invention have vasotropic activity and can
 CC be used for gene therapy. The use of (I), or a DNA molecule or a plasmid
 CC of the invention is claimed for obtaining a vector for gene therapy and
 CC for inhibiting restenosis of blood vessel after angioplasty; therapeutic
 CC compositions containing these components are also claimed. (I)
 CC efficiently induces cell cycle arrest by combined inactivation of cyclin
 CC E and E2F1.
 XX
 SQ Sequence 4 BP; 2 A; 0 C; 1 G; 0 U; 1 other;

Query Match 100.0%; Score 1; DB 22; Length 4;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1
 |
 Db 2 g 2

RESULT 17
 AAN93676/c
 ID AAN93676 standard; DNA; 5 BP.
 XX AC AAN93676;
 XX
 DT 24-JUN-1990 (first entry)
 XX
 DE Synthetic probe for hop growth retarding viroid (HSV), HSV cucumber
 DE variant (HSV-c) and HSV grape variant (HSV-g).
 XX
 KW Hop growth retarding viroid; cucumber variant; grape variant; probe; ss.
 XX Hop growth retarding viroid.
 OS
 XX JP01040000-A.
 PN
 XX 10-FEB-1989.
 PD
 XX 05-AUG-1987; 87JP-0194377.
 PF
 XX 05-AUG-1987; 87JP-0195377.
 PR
 XX (YUKI) YUKI GOSEI YAKUHIN.
 PA
 XX WPI: 1989-089715/12.
 DR
 XX Fractionating and detecting hop growth retarding viroids -
 PT using synthetic DNA probe contg. specific base sequence
 PT
 XX Disclosure; page 3; 5pp; Japanese.
 PS
 XX The synthetic probes is complementary to the RNA of HSV-g bases 53-59.
 CC HSV, HSV-c and HSV-g are fractionated and detected using the synthetic
 CC probe. The probe is 15-25mer. The probe can be used to diagnose HSV
 CC infections in plants.
 CC
 XX Sequence 5 BP; 1 A; 3 C; 0 G; 1 T; 0 other;

Query Match 100.0%; Score 1; DB 10; Length 5;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1
 |
 Db 5 G 5

RESULT 18
 AAQ68752
 ID AAQ68752 standard; DNA; 5 BP.
 XX AC AAQ68752;
 XX
 DT 22-FEB-1995 (first entry)
 XX
 DE CHA255 heavy chain CDRI clone 3.3.3. coding sequence.
 XX
 KW Polymerase chain reaction; primer; PCR; amplify; heavy; light;
 KW chain; complementarity determining region; CDR; variable; constant;
 KW region; monoclonal antibody; MAb; binding affinity; EDTA; DOTA;

KW tumour; cancer; colorectal; breast; metal chelate; haptens; ss.

OS Synthetic.

PN AU9350602-A.

XX 26-MAY-1994.

PF 10-NOV-1993; 93AU-0050602.

XX 12-NOV-1992; 92US-0975230.

PR (HYBR-) HYBRITECH INC.

XX Ahrweiler PM, Moore MD;

XX WPI; 1994-209063/26.

DR P-PSDB; AAR54150.

XX Polypeptide used in imaging and treatment of carcinomas and
tumours - comprising substd antibody CDR having binding affinity
for metal chelate of EDTA or DETA or analogues

PS Claim 25; Fig 3A; 61pp; English.

XX The sequences given in AAQ86747-57 encode the wild type and mutagenised
versions of the complementarity determining region 1 (CDR1) of the
antibody designated CHA255. CHA255 is a murine monoclonal antibody
(MAB) which is capable of binding complexes. Mutagenesis of these
CDRs, causes the production of polypeptides with a particularly
high binding affinity for EDTA or DOTA metal complexes. CDR1 and -3
of the heavy chain, and CDR2 and -3 of the light chain were targeted
for mutagenesis. Five residues of both CDR1 and -3 of the CHA255
heavy chain, five of seven residues of light chain CDR and six of
nine light chain CDR3 residues were specifically targeted for
codon-based mutagenesis. The mutagenised MAB's can be used in
compositions for in vivo imaging of malignant tissues or tumours. They
are also useful for the treatment of malignant tissues or tumours eg.
colorectal or breast cancer. Both methods involve the use of
radionuclides which bind to metal chelates or haptens which are
specifically delivered to the target site by a targeting molecule. CDR
derived peptides may be used to construct bi-functional antibodies
having dual specificities, or as donor or recipients of CDR sequences.

XX Sequence 5 BP; 0 A; 0 C; 1 G; 1 T; 3 other;

Query Match 100.0%; Score 1; DB 15; Length 5;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1

Db 1 g 1

RESULT 19

AAQ81667/C

ID AAQ81667 standard; RNA; 5 BP.

XX AAQ81667;

AC AAQ81667;

DT 29-SEP-1995 (first entry)

XX bFGF binding oligomer core sequence #4.

XX Basic: fibroblast growth factor; bFGF; stem-loop structure;
bubble structure; pseudoknot; receptor; heparin; competition;
inhibition; enhance; neovascularisation; solid tumour; cancer;
metastasis; diagnosis; gene therapy; ss.

OS Synthetic.

XX

PN WO9500528-A.

XX 05-JAN-1995.

XX 17-JUN-1994; 94WO-US06884.

XX 18-JUN-1993; 93US-0079677.

PR 07-JAN-1994; 94US-0179491.

XX (PHAR-) PHARMAGENICS INC.

XX Beutel BA, Joesten ME;

XX WPI; 1995-051992/07.

XX New oligo-nucleotide(s) that bind to basic fibroblast growth
factor - modulating, esp. inhibiting, its activity, useful in
treating cancer, preventing metastasis, and diagnosis.

PS Claim 3; Page 25; 44pp; English.

XX The sequences given in AAQ81642-95 are oligonucleotides which modulate
the activity of basic fibroblast growth factor (bFGF) by binding
to the bFGF protein. Most esp. the sequences given in AAQ81664-67
represent core sequences of which at least one is present in each of
the binding oligos. These oligonucleotides may form a single
strand, double strand, a stem-loop structure, a bubble structure, a
pseudoknot or a closed, circular structure. bFGF binds to high
affinity receptor and low affinity heparin-like molecules on the
cell surface. These oligonucleotides bind to bFGF in competition
with its receptor and heparin. These oligonucleotides may inhibit
or enhance the activity of bFGF. Particularly, they inhibit
neovascularisation so they can be used to suppress growth of solid
tumours and to reduce the risk of metastasis. They can be used as
diagnostic reagents to determine the presence of thrombin, or used in
gene therapy.

XX Sequence 5 BP; 2 A; 2 C; 0 G; 1 U; 0 other;

Query Match 100.0%; Score 1; DB 16; Length 5;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1

Db 5 G 5

RESULT 20

AAT12043/C

ID AAT12043 standard; RNA; 5 BP.

XX AAT12043;

AC AAT12043;

XX 17-JUL-1996 (first entry)

XX Cleavable replicable-inhibiting sequence.

XX Ribozyme; hairpin; hammerhead; probe; MDV-1; midvariant-1;

XX replication; cleavage; ss.

OS Synthetic.

XX US5472840-A.

PN 05-DEC-1995.

XX 30-SEP-1988; 88US-0252243.

XX 17-DEC-1990; 90US-0630288.

PR 30-SEP-1988; 88US-0252243.

PR 22-JUN-1989; 89US-0370218.

XX (STAD) AMOCO CORP.
 XX Stefano JE;
 XX WPI; 1996-029807/03.
 XX Ribozyme-forming nucleic acid probes - contg. MDV-1 sequence and
 XX cleavable replicable-inhibiting sequence.
 XX Claim 4; Column 62; 43pp; English.
 XX A composition comprises RNA of formula P4-P1-P2-P3 (Ia), a nucleic
 XX acid of formula R1-R2 (III), where (Ia) and (III) bind to a target
 XX nucleic acid of formula X2-X1-X3 (II) to form a hammerhead ribozyme,
 XX where P1 is a MDV-1 sequence capable of autocatalytic replication in
 XX the absence of P3; P2 is a sequence (AAT12042 or AAT12044) that binds
 XX to (II) and forms a cleavage site between P1 and P3; P3 (AAT12043)
 XX is an inhibitory element that binds to X2 and interacts with a
 XX region of P1 corresp. to nucleotides 81-126 of MDV-1; P4 contributes
 XX nucleotides to form the ribozyme with X1 and P2, or is the terminal
 XX nucleotide of P1; X1 is a target region of (II); X2 and X3 are
 XX terminal nucleotides or second or third target regions of (II); R1
 XX is a ribozyme-forming area of (III); and R2 is a terminal nucleotide
 XX of R1 or an area of (III) that binds to (II). X1 and R1 are
 XX mutually exclusive and are represented by the sequences of AAT12040 and
 XX AAT12041. For hairpin ribozymes, P2 is AAT12045 and R1 is AAT12046.
 XX Probes bearing ribozymes are produced in a single step by transcription
 XX of DNA of appropriate sequence, thereby reducing costs. The ribozymes
 XX produce specific cleavage events, leading to a product RNA with
 XX defined replication properties.
 XX Sequence 5 BP; 0 A; 1 C; 0 G; 2 U; 2 other;

Query Match 100.0%; Score 1; DB 17; Length 5;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
 Db 5 G 5

RESULT 21
 AAV61663
 ID AAV61663 standard; DNA; 5 BP.
 XX AAV61663;
 XX 03-DEC-1998 (first entry)
 XX Fusarium sp. 18S rRNA DNA fragment #7.
 XX 18S rRNA; detection; identification; fungus; ss.
 XX Fusarium sp.
 XX JPI0234380-A.
 XX 08-SEP-1998.
 XX 28-FEB-1997; 97JP-0062104.
 XX 28-FEB-1997; 97JP-0062104.
 XX (SHIN-) SHINKINRUI KINO KAIHATSU KENKYUSHO KK.
 XX WPI; 1998-535034/46.
 XX Use of oligo:nucleotide for detecting and identification of fungus
 XX of Fusarium genus - as primer or probe to detect or identify
 XX microbes rapidly and exactly

Query Match 100.0%; Score 1; DB 17; Length 5;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
 Db 5 G 5

RESULT 23
 AAT96299
 ID AAT96299 standard; DNA; 5 BP.
 XX AAT96299
 XX Use of oligo:nucleotide for detecting and identification of fungus
 XX of Fusarium genus - as primer or probe to detect or identify
 XX microbes rapidly and exactly

XX Claim 1; Page 7; 20pp; Japanese.
 XX AAV61657-V61664 are fragments of a Fusarium sp. 18S rRNA gene which are
 XX used in a method for the detection and identification of a fungus of
 XX Fusarium genus. The process can be used to detect or identify microbes
 XX rapidly and exactly.
 XX Sequence 5 BP; 1 A; 2 C; 1 G; 1 T; 0 other;

Query Match 100.0%; Score 1; DB 19; Length 5;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
 Db 4 g 4

RESULT 22
 AAV61663/c
 ID AAV61663 standard; DNA; 5 BP.
 XX AAV61663;
 XX 03-DEC-1998 (first entry)
 XX Fusarium sp. 18S rRNA DNA fragment #7.
 XX 18S rRNA; detection; identification; fungus; ss.
 XX Fusarium sp.
 XX JPI0234380-A.
 XX 08-SEP-1998.
 XX 28-FEB-1997; 97JP-0062104.
 XX 28-FEB-1997; 97JP-0062104.
 XX (SHIN-) SHINKINRUI KINO KAIHATSU KENKYUSHO KK.
 XX WPI; 1998-535034/46.
 XX Use of oligo:nucleotide for detecting and identification of fungus
 XX of Fusarium genus - as primer or probe to detect or identify
 XX microbes rapidly and exactly

Query Match 100.0%; Score 1; DB 19; Length 5;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
 Db 5 G 5

RESULT 23
 AAT96299
 ID AAT96299 standard; DNA; 5 BP.
 XX AAT96299
 XX Use of oligo:nucleotide for detecting and identification of fungus
 XX of Fusarium genus - as primer or probe to detect or identify
 XX microbes rapidly and exactly


```

AC AAT96299;
XX
DT 08-APR-1998 (first entry)
XX
DE Fungal telomeric nucleic acid sequence.
XX
KW Detection; eukaryotic pathogen; telomeric nucleic acid sequence;
KW telomerase activity; diagnosis; fungal infection; fungus; fungi;
KW malarial infection; malaria; ss.
XX
OS Saccharomyces cerevisiae.
XX
PN US5695932-A.
XX
PD 09-DEC-1997.
XX
PF 13-MAY-1993; 93US-0060952.
XX
PR 13-MAY-1993; 93US-0060952.
PR 13-MAY-1992; 92US-0882438.
PR 24-MAR-1993; 93US-0038766.
XX
PA (REGC ) UNIV CALIFORNIA.
PA (TEXA ) UNIV TEXAS SYSTEM.
XX
PI Blackburn EH, McEachern MJ, Shay J, West MD, Wright W;
XX WPI; 1998-041292/04.
XX
DR Detection of eukaryotic pathogens, especially fungal or Plasmodium
PT spp. - by detecting telomerase activity
XX
PS Claim 5; Columns 81-82; 82pp; English.
XX
CC The present sequence can be used in a novel method for detecting a
CC eukaryotic pathogen in a patient. The method comprises obtaining a
CC sample of somatic tissue or cells from the patient, determining if
CC telomerase activity is present and correlating this with the
CC presence of the pathogen. The method is useful for diagnosis of
CC fungal infections, especially a fungus of the genus Candida,
CC Kluyveromyces, Saccharomyces, Sporothrix, Coccidioides,
CC Histoplasma, Blastomyces, Paracoccidioides, Cryptococcus,
CC Aspergillus, Mucor or Rhizopus, or malarial infections, especially
CC Plasmodium vivax, P. ovale, P. malariae or P. falciparum.
XX
SQ Sequence 5 BP; 0 A; 0 C; 3 G; 2 T; 0 other;

Query Match 100.0%; Score 1; DB 19; Length 5;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 g 1
Db 2 g 2

RESULT 24
AAZ10695
ID AAZ10695 standard; DNA; 5 BP.
XX
AC AAZ10695;
XX
DT 23-NOV-1999 (first entry)
XX
DE Oligonucleotide sequence that increases p53 activity in a cell.
XX
KW p53 activity; UV mimetic; UV-irradiation; UV-induced dermatosis;
KW UV-induced hyperproliferative disease; psoriasis; vitiligo;
KW atopic dermatitis; allergic rhinitis; conjunctivitis; photoaging;
KW skin cancer; ss.
XX
OS Synthetic.
XX
PN AAZ10695
XX
PD 13-OCT-1999.
XX
PF 24-MAR-1999; 99GB-0006758.
XX
PR 26-MAR-1998; 98US-0048927.
XX
PA (UYBO-) UNIV BOSTON.
XX
PI Gilchrist BA, Yaar M, Eller M;
XX WPI; 1999-543520/46.
XX
DR DNA fragments useful for increasing p53 activity in a cell and reducing
PT
```

```

XX GB2336157-A.
XX
PD 13-OCT-1999.
XX
PF 24-MAR-1999; 99GB-0006758.
XX
PR 26-MAR-1998; 98US-0048927.
XX
PA (UYBO-) UNIV BOSTON.
XX
PI Gilchrist BA, Yaar M, Eller M;
XX WPI; 1999-543520/46.
XX
DR DNA fragments useful for increasing p53 activity in a cell and reducing
PT susceptibility to UV-induced hyperproliferative diseases -

Claim 11; Page 30; 44pp; English.
XX
CC AAZ10692-97 represent DNA fragments that are used for increasing p53
CC activity in a cell. The oligonucleotides are UV mimetics and
CC protect cells against subsequent exposure to UV-irradiation or
CC chemicals. The oligonucleotides are useful for increasing p53 activity
CC in a cell, reducing the susceptibility to UV-induced hyperproliferative
CC diseases, treating psoriasis, vitiligo, atopic dermatitis, allergic
CC rhinitis, conjunctivitis, and UV-induced dermatoses, reducing photoaging
CC and reducing susceptibility to skin cancer.
XX
SQ Sequence 5 BP; 1 A; 0 C; 2 G; 2 T; 0 other;

Query Match 100.0%; Score 1; DB 20; Length 5;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 g 1
Db 1 g 1

RESULT 25
AAZ10696/c
ID AAZ10696 standard; DNA; 5 BP.
XX
AC AAZ10696;
XX
DT 23-NOV-1999 (first entry)
XX
DE Oligonucleotide sequence that increases p53 activity in a cell.
XX
KW p53 activity; UV mimetic; UV-irradiation; UV-induced dermatosis;
KW UV-induced hyperproliferative disease; psoriasis; vitiligo;
KW atopic dermatitis; allergic rhinitis; conjunctivitis; photoaging;
KW skin cancer; ss.
XX
OS Synthetic.
XX
PN GB2336157-A.
XX
PD 13-OCT-1999.
XX
PF 24-MAR-1999; 99GB-0006758.
XX
PR 26-MAR-1998; 98US-0048927.
XX
PA (UYBO-) UNIV BOSTON.
XX
PI Gilchrist BA, Yaar M, Eller M;
XX WPI; 1999-543520/46.
XX
DR DNA fragments useful for increasing p53 activity in a cell and reducing
PT
```

PT susceptibility to UV-induced hyperproliferative diseases -
PS Claim 11; Page 30; 44pp; English.
XX
CC AAZ10692-97 represent DNA fragments that are used for increasing p53
CC activity in a cell. The oligonucleotides are are UV mimetics and
CC protect cells against subsequent exposure to UV-irradiation or
CC chemicals. The oligonucleotides are useful for increasing p53 activity
CC in a cell, reducing the susceptibility to UV-induced hyperproliferative
CC diseases, treating psoriasis, vitiligo, atopic dermatitis, allergic
CC rhinitis, conjunctivitis, and UV-induced dermatoses, reducing photoaging
CC and reducing susceptibility to skin cancer.
XX
SQ Sequence 5 BP; 2 A; 2 C; 0 G; 1 T; 0 other;

Query Match 100.0%; Score 1; DB 20; Length 5;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 q 1
Db 5 G 5

RESULT 26
AAZ11611
ID AAZ11611 standard; DNA; 5 BP.
XX
AC AAZ11611;
XX
DT 16-NOV-1999 (first entry)
XX
DE DNA enhancer sequence present in an upstream element.
XX
KW Plant promoter; TATA motif; transcription start site; upstream element;
KW gene expression; oxalate oxidase; plant resistance; pathogen; maize;
KW Ubi-1 promoter; Syn II core promoter; ss.
XX
OS Synthetic.
XX
PN WO9943838-A1.
XX
PD 02-SEP-1999.
XX
PF 23-FEB-1999; 99WO-US03863.
XX
PR 24-FEB-1998; 98US-0028819.
XX
PA (PION-) PIONEER HT-BRED INT INC.
XX
PI Bowen BA, Bruce WB, Lu G, Sims LE, Tagliani LA;
XX
DR WPI; 1999-540601/45.
XX
PT New synthetic promoter functional in plants to provide non-tissue
PT specific, constitutive expression, particularly of oxalate oxidase for
PT increased resistance to pathogens -
XX
PS Claim 39; Page 47; 61pp; English.
XX
CC The invention provides a new synthetic plant promoter that comprises a
CC TATA motif; a transcription start site (TSS) and a region between TATA
CC and TSS containing at least 64 percent GC content. The synthetic core
CC promoter, optionally containing additional upstream elements are used to
CC increase expression, provides non-tissue specific, constitutive
CC transcription of heterologous genes in any sort of plant, especially the
CC gene for oxalate oxidase for increasing plant resistance to pathogens.
CC The upstream activating elements can be used to increase transcription
CC from any promoter. A combination of the synthetic core promoter with
CC synthetic upstream elements can induce expression 10 times greater than
CC that provided by the maize Ubi-1 promoter. The present sequence
CC represents a DNA enhancer OSC-like motif present in an upstream element

CC sequence.
XX
SQ Sequence 5 BP; 1 A; 1 C; 2 G; 1 T; 0 other;

Query Match 100.0%; Score 1; DB 20; Length 5;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 q 1
Db 2 g 2

RESULT 27
AAZ11611/c
ID AAZ11611 standard; DNA; 5 BP.
XX
AC AAZ11611;
XX
DT 16-NOV-1999 (first entry)
XX
DE DNA enhancer sequence present in an upstream element.
XX
KW Plant promoter; TATA motif; transcription start site; upstream element;
KW gene expression; oxalate oxidase; plant resistance; pathogen; maize;
KW Ubi-1 promoter; Syn II core promoter; ss.
XX
OS Synthetic.
XX
PN WO9943838-A1.
XX
PD 02-SEP-1999.
XX
PF 23-FEB-1999; 99WO-US03863.
XX
PR 24-FEB-1998; 98US-0028819.
XX
PA (PION-) PIONEER HI-BRED INT INC.
XX
PI Bowen BA, Bruce WB, Lu G, Sims LE, Tagliani LA;
XX
DR WPI; 1999-540601/45.
XX
PT New synthetic promoter functional in plants to provide non-tissue
PT specific, constitutive expression, particularly of oxalate oxidase for
PT increased resistance to pathogens -
XX
PS Claim 39; Page 47; 61pp; English.
XX
CC The invention provides a new synthetic plant promoter that comprises a
CC TATA motif; a transcription start site (TSS) and a region between TATA
CC and TSS containing at least 64 percent GC content. The synthetic core
CC promoter, optionally containing additional upstream elements are used to
CC increase expression, provides non-tissue specific, constitutive
CC transcription of heterologous genes in any sort of plant, especially the
CC gene for oxalate oxidase for increasing plant resistance to pathogens.
CC The upstream activating elements can be used to increase transcription
CC from any promoter. A combination of the synthetic core promoter with
CC synthetic upstream elements can induce expression 10 times greater than
CC that provided by the maize Ubi-1 promoter. The present sequence
CC represents a DNA enhancer OSC-like motif present in an upstream element
XX
SQ Sequence 5 BP; 1 A; 1 C; 2 G; 1 T; 0 other;

Query Match 100.0%; Score 1; DB 20; Length 5;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 q 1
Db 1

The present sequence

DE	US5908745 primer #5.
XX	DNA sequencing; disease-associated allele; polyacrylamide matrix;
KW	continuous/contiguous stacking hybridization technique; detection;
KW	mutation; diagnosis; primer; ss.
XX	Synthetic.
OS	
XX	US5908745-A.
PN	
XX	01-JUN-1999.
PD	
XX	16-JAN-1996; 96US-0587332.
XX	16-JAN-1996; 96US-0587332.
XX	(UYCH-) UNIV CHICAGO.
PA	
XX	Barski VE, Kirillov EV, Lysov YP, Mirzabekov AD;
XX	Parinov SV, Yershov GM;
PI	
XX	WPI: 1999-347002/29.
DR	
XX	Detecting disease-associated alleles using continuous/contiguous
PT	stacking hybridization as a diagnostic tool
PT	
XX	Example 1; Column 9; 16pp; English.
PS	
XX	This invention describes novel methods for sequencing and analysing DNA
CC	samples to detect disease-associated alleles, by continuous/contiguous
CC	stacking hybridization techniques (utilizing universal bases) with
CC	oligonucleotides immobilized on polyacrylamide matrices. The methods may
CC	be used to detect multiple DNA base mutations which are specific for
CC	certain diseases. The methods of the invention provide accurate and
CC	efficient and sensitive methods for diagnosing disease by detecting
CC	multiple mutation sequences in patient DNA. The method require the
CC	minimum number of oligonucleotides and few stacking hybridization steps
CC	than prior art methods. The methods are also efficient enough to
CC	discriminate between perfect and imperfect duplexes. The methods also
CC	obviate the need for the fabrication and array placement of large numbers
CC	of immobilized oligomers.
XX	
SQ	Sequence 5 BP; 2 A; 2 C; 1 G; 0 U; 0 other;
Query Match	100.0%; Score 1; DB 20; Length 5;
Best Local Similarity	100.0%; Pred. No. 0;
Matches	1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 g 1
Db	2 g 2
RESULT	30
AAV72347/c	
ID	AAV72348 standard; DNA; 5 BP.
XX	
AC	AAV72348;
XX	
DT	28-JUL-1999 (first entry)
XX	
DE	US5908745 primer #5.
XX	DNA sequencing; disease-associated allele; polyacrylamide matrix;
KW	continuous/contiguous stacking hybridization technique; detection;
KW	mutation; diagnosis; primer; ss.
XX	Synthetic.
OS	
XX	US5908745-A.
PN	
XX	01-JUN-1999.
PD	
XX	16-JAN-1996; 96US-0587332.
XX	16-JAN-1996; 96US-0587332.
XX	(UYCH-) UNIV CHICAGO.
PA	
XX	Barski VE, Kirillov EV, Lysov YP, Mirzabekov AD;
XX	Parinov SV, Yershov GM;
PI	
XX	WPI: 1999-347002/29.
DR	
XX	Detecting disease-associated alleles using continuous/contiguous
PT	stacking hybridization as a diagnostic tool
PT	
XX	Example 1; Column 9; 16pp; English.
PS	
XX	This invention describes novel methods for sequencing and analysing DNA
CC	samples to detect disease-associated alleles, by continuous/contiguous
CC	stacking hybridization techniques (utilizing universal bases) with
CC	oligonucleotides immobilized on polyacrylamide matrices. The methods may
CC	be used to detect multiple DNA base mutations which are specific for
CC	certain diseases. The methods of the invention provide accurate and
CC	efficient and sensitive methods for diagnosing disease by detecting
CC	multiple mutation sequences in patient DNA. The method require the
CC	minimum number of oligonucleotides and few stacking hybridization steps
CC	than prior art methods. The methods are also efficient enough to
CC	discriminate between perfect and imperfect duplexes. The methods also
CC	obviate the need for the fabrication and array placement of large numbers
CC	of immobilized oligomers.
XX	
SQ	Sequence 5 BP; 2 A; 3 C; 0 G; 0 U; 0 other;
Query Match	100.0%; Score 1; DB 20; Length 5;
Best Local Similarity	100.0%; Pred. No. 0;
Matches	1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 g 1
Db	5 G 5
RESULT	29
AAV72348	
ID	AAV72348 standard; DNA; 5 BP.
XX	
AC	AAV72348;
XX	
DT	28-JUL-1999 (first entry)
XX	
DE	US5908745 primer #5.
XX	DNA sequencing; disease-associated allele; polyacrylamide matrix;
KW	continuous/contiguous stacking hybridization technique; detection;
KW	mutation; diagnosis; primer; ss.
XX	Synthetic.
OS	
XX	US5908745-A.
PN	
XX	01-JUN-1999.
PD	
XX	16-JAN-1996; 96US-0587332.
XX	16-JAN-1996; 96US-0587332.
XX	(UYCH-) UNIV CHICAGO.
PA	
XX	Barski VE, Kirillov EV, Lysov YP, Mirzabekov AD;
XX	Parinov SV, Yershov GM;
PI	
XX	WPI: 1999-347002/29.
DR	
XX	Detecting disease-associated alleles using continuous/contiguous
PT	stacking hybridization as a diagnostic tool
PT	
XX	Example 1; Column 9; 16pp; English.
PS	
XX	This invention describes novel methods for sequencing and analysing DNA
CC	samples to detect disease-associated alleles, by continuous/contiguous
CC	stacking hybridization techniques (utilizing universal bases) with
CC	oligonucleotides immobilized on polyacrylamide matrices. The methods may
CC	be used to detect multiple DNA base mutations which are specific for
CC	certain diseases. The methods of the invention provide accurate and
CC	efficient and sensitive methods for diagnosing disease by detecting
CC	multiple mutation sequences in patient DNA. The method require the
CC	minimum number of oligonucleotides and few stacking hybridization steps
CC	than prior art methods. The methods are also efficient enough to
CC	discriminate between perfect and imperfect duplexes. The methods also
CC	obviate the need for the fabrication and array placement of large numbers
CC	of immobilized oligomers.
XX	
SQ	Sequence 5 BP; 2 A; 3 C; 0 G; 0 U; 0 other;
Query Match	100.0%; Score 1; DB 20; Length 5;
Best Local Similarity	100.0%; Pred. No. 0;
Matches	1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 g 1
Db	5 G 5
RESULT	29
AAV72348	
ID	AAV72348 standard; DNA; 5 BP.
XX	
AC	AAV72348;
XX	
DT	28-JUL-1999 (first entry)
XX	
DE	US5908745 primer #5.
XX	DNA sequencing; disease-associated allele; polyacrylamide matrix;
KW	continuous/contiguous stacking hybridization technique; detection;
KW	mutation; diagnosis; primer; ss.
XX	Synthetic.
OS	
XX	US5908745-A.
PN	
XX	01-JUN-1999.
PD	
XX	16-JAN-1996; 96US-0587332.
XX	16-JAN-1996; 96US-0587332.
XX	(UYCH-) UNIV CHICAGO.
PA	
XX	Barski VE, Kirillov EV, Lysov YP, Mirzabekov AD;
XX	Parinov SV, Yershov GM;</

```
XX 16-JAN-1996; 96US-0587332.
XX 16-JAN-1996; 96US-0587332.
XX (UYCH-) UNIV CHICAGO.
XX Barski VE, Kirillov EV, Lysov YP, Mirzabekov AD;
XX Parinov SV, Yerшов GM;
XX WPI; 1999-347002/29.
XX Detecting disease-associated alleles using continuous/contiguous
XX stacking hybridization as a diagnostic tool
XX Example 1; Column 9; 16pp; English.
XX This invention describes novel methods for sequencing and analysing DNA
XX samples to detect disease-associated alleles, by continuous/contiguous
XX stacking hybridization techniques (utilizing universal bases) with
XX oligonucleotides immobilized on polyacrylamide matrices. The methods may
XX be used to detect multiple DNA base mutations which are specific for
XX certain diseases. The methods of the invention provide accurate and
XX efficient and sensitive methods for diagnosing disease by detecting
XX multiple mutation sequences in patient DNA. The method require the
XX minimum number of oligonucleotides and few stacking hybridization steps
XX than prior art methods. The methods are also efficient enough to
XX discriminate between perfect and imperfect duplexes. The methods also
XX obviate the need for the fabrication and array placement of large numbers
XX of immobilized oligomers.
XX Sequence 5 BP; 2 A; 2 C; 1 G; 0 U; 0 other;
```

```
Query Match 100.0%; Score 1; DB 20; Length 5;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1 g 1
Db 5 G 5
```

```
RESULT 31
AAV72349/c
ID AAV72349 standard; DNA; 5 BP.
AC AAV72349;
XX 28-JUL-1999 (first entry)
XX US5908745 primer #6.
XX DNA sequencing; disease-associated allele; polyacrylamide matrix;
XX continuous/contiguous stacking hybridization technique; detection;
XX mutation; diagnosis; primer; ss.
XX Synthetic.
XX US5908745-A.
XX 01-JUN-1999.
XX 16-JAN-1996; 96US-0587332.
XX 16-JAN-1996; 96US-0587332.
XX (UYCH-) UNIV CHICAGO.
XX Barski VE, Kirillov EV, Lysov YP, Mirzabekov AD;
XX Parinov SV, Yerшов GM;
XX WPI; 1999-347002/29.
```

```
XX This invention describes novel methods for sequencing and analysing DNA
XX samples to detect disease-associated alleles, by continuous/contiguous
XX stacking hybridization techniques (utilizing universal bases) with
XX oligonucleotides immobilized on polyacrylamide matrices. The methods may
XX be used to detect multiple DNA base mutations which are specific for
```

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XX Detecting disease-associated alleles using continuous/contiguous
XX stacking hybridization as a diagnostic tool
XX Example 1; Column 9; 16pp; English.
```

```
XX This invention describes novel methods for sequencing and analysing DNA
XX samples to detect disease-associated alleles, by continuous/contiguous
XX stacking hybridization techniques (utilizing universal bases) with
XX oligonucleotides immobilized on polyacrylamide matrices. The methods may
XX be used to detect multiple DNA base mutations which are specific for
XX certain diseases. The methods of the invention provide accurate and
XX efficient and sensitive methods for diagnosing disease by detecting
XX multiple mutation sequences in patient DNA. The method require the
XX minimum number of oligonucleotides and few stacking hybridization steps
XX than prior art methods. The methods are also efficient enough to
XX discriminate between perfect and imperfect duplexes. The methods also
XX obviate the need for the fabrication and array placement of large numbers
XX of immobilized oligomers.
```

```
XX Sequence 5 BP; 2 A; 3 C; 0 G; 0 U; 0 other;
```

```
Query Match 100.0%; Score 1; DB 20; Length 5;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1 g 1
Db 5 G 5
```

```
RESULT 32
AAV72350/c
ID AAV72350 standard; DNA; 5 BP.
XX 28-JUL-1999 (first entry)
XX US5908745 primer #7.
XX DNA sequencing; disease-associated allele; polyacrylamide matrix;
XX continuous/contiguous stacking hybridization technique; detection;
XX mutation; diagnosis; primer; ss.
XX Synthetic.
XX US5908745-A.
XX 01-JUN-1999.
XX 16-JAN-1996; 96US-0587332.
XX 16-JAN-1996; 96US-0587332.
XX (UYCH-) UNIV CHICAGO.
XX Barski VE, Kirillov EV, Lysov YP, Mirzabekov AD;
XX Parinov SV, Yerшов GM;
XX WPI; 1999-347002/29.
XX Detecting disease-associated alleles using continuous/contiguous
XX stacking hybridization as a diagnostic tool
XX Example 1; Column 9; 16pp; English.
```

```
XX This invention describes novel methods for sequencing and analysing DNA
XX samples to detect disease-associated alleles, by continuous/contiguous
XX stacking hybridization techniques (utilizing universal bases) with
XX oligonucleotides immobilized on polyacrylamide matrices. The methods may
XX be used to detect multiple DNA base mutations which are specific for
```

CC certain diseases. The methods of the invention provide accurate and
 CC efficient and sensitive methods for diagnosing disease by detecting
 CC multiple mutation sequences in patient DNA. The method require the
 CC minimum number of oligonucleotides and few stacking hybridization steps
 CC than prior art methods. The methods are also efficient enough to
 CC discriminate between perfect and imperfect duplexes. The methods also
 CC obviate the need for the fabrication and array placement of large numbers
 CC of immobilized oligomers.

XX
 SQ Sequence 5 BP; 3 A; 2 C; 0 G; 0 U; 0 other;

Query Match 100.0%; Score 1; DB 20; Length 5;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1
 |
 Db 5 G 5

RESULT 33

AAX56964
 ID AAX56964 standard; DNA; 5 BP.

XX
 AC AAX56964;

XX
 DT 16-JUL-1999 (first entry)

XX
 DE Ras gene modulating liposomal entrapped oligonucleotide primer 8.

XX
 KW Ras gene; modulator; liposome; primer; antisense; anticancer; inhibition;
 cell growth inhibitor; treatment; cancer; ras protein; ss.

XX
 OS Synthetic.

XX
 PN WO9922772-A1.

XX
 PD 14-MAY-1999.

XX
 PF 28-OCT-1998; 98WO-US22821.

XX
 PR 31-OCT-1997; 97US-0961469.

XX
 PA (ISIS-) ISIS PHARM INC.

XX
 PI Geary RS, Hardee GE, Howard R, Levin A, Mehta RC;
 Templin MV;

XX
 PI WPI; 1999-313181/26.

XX
 PT Liposome-encapsulated oligonucleotides useful for treating or
 preventing cancers associated with ras gene activation

XX
 PS Example 1; Page 107; 120pp; English.

XX This invention describes novel compositions comprising oligonucleotides
 CC (AAX56957-X57017), entrapped within liposomes, that hybridize
 CC specifically to a target DNA or mRNA which encodes a mutant or wild-type
 CC ras protein. The products of the invention have anticancer activity and
 CC specifically bring about the antisense inhibition of ras genes or mRNA.
 CC The products of the invention are used to modulate expression of a ras
 CC gene in cells, tissue, organs or organisms, particularly to inhibit cell
 CC growth and especially to treat or prevent cancers associated with
 CC activation of a ras gene. Encapsulating the oligonucleotide reduces the
 CC rate at which it is cleared from the blood when compared with
 CC non-encapsulated material, and the oligonucleotides become distributed to
 CC practically all parts of the body.

XX
 SQ Sequence 5 BP; 1 A; 2 C; 2 G; 0 U; 0 other;

Query Match 100.0%; Score 1; DB 20; Length 5;

Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1
 |
 Db 2 g 2

RESULT 34

AAX56964/C
 ID AAX56964 standard; DNA; 5 BP.

XX
 AC AAX56964;

XX
 DT 16-JUL-1999 (first entry)

XX
 DE Ras gene modulating liposomal entrapped oligonucleotide primer 8.

XX
 KW Ras gene; modulator; liposome; primer; antisense; anticancer; inhibition;
 cell growth inhibitor; treatment; cancer; ras protein; ss.

XX
 OS Synthetic.

XX
 PN WO9922772-A1.

XX
 PD 14-MAY-1999.

XX
 PF 28-OCT-1998; 98WO-US22821.

XX
 PR 31-OCT-1997; 97US-0961469.

XX
 PA (ISIS-) ISIS PHARM INC.

XX
 PI Geary RS, Hardee GE, Howard R, Levin A, Mehta RC;
 Templin MV;

XX
 PI WPI; 1999-313181/26.

XX
 PT Liposome-encapsulated oligonucleotides useful for treating or
 preventing cancers associated with ras gene activation

XX
 PS Example 1; Page 107; 120pp; English.

XX This invention describes novel compositions comprising oligonucleotides
 CC (AAX56957-X57017), entrapped within liposomes, that hybridize
 CC specifically to a target DNA or mRNA which encodes a mutant or wild-type
 CC ras protein. The products of the invention have anticancer activity and
 CC specifically bring about the antisense inhibition of ras genes or mRNA.
 CC The products of the invention are used to modulate expression of a ras
 CC gene in cells, tissue, organs or organisms, particularly to inhibit cell
 CC growth and especially to treat or prevent cancers associated with
 CC activation of a ras gene. Encapsulating the oligonucleotide reduces the
 CC rate at which it is cleared from the blood when compared with
 CC non-encapsulated material, and the oligonucleotides become distributed to
 CC practically all parts of the body.

XX
 SQ Sequence 5 BP; 1 A; 2 C; 2 G; 0 U; 0 other;

Query Match 100.0%; Score 1; DB 20; Length 5;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 g 1
 |
 Db 4 G 4

RESULT 35

AAX21608
 ID AAX21608 standard; DNA; 5 BP.

XX
 AC AAX21608;

```

XX DT 14-MAY-1999 (first entry)
XX DE Mutant H-ras specific antisense oligo ISIS #2563.
XX KW Human; N-ras; inhibition; pharmaceutical; modulation; cancer; oncogene;
XX KW diagnostic; therapeutic; tumour; mutant; H-ras; antisense; ss.
XX OS Synthetic.
XX PN WO9902732-A1.
XX PD 21-JAN-1999.
XX PF 06-JUL-1998; 98WO-US13966.
XX PR 08-JUL-1997; 97US-0889296.
XX PA (ISIS-) ISIS PHARM INC.
XX PI Cowsert LM, Manoharan M, Monia BP;
XX DR WPI: 1999-120932/10.
XX PT New oligonucleotide targetting human N-ras nucleic acid - is
XX PT capable of inhibiting human N-ras expression, useful for preventing
XX PT or treating conditions arising from the activation of a human N-ras
XX PT oncogene
XX PS Disclosure; Page 22; 97pp; English.
XX CC The invention relates to oligonucleotides, which target a nucleic acid
XX CC encoding human N-ras, and are capable of inhibiting human N-ras
XX CC expression. The antisense oligonucleotides form a pharmaceutical
XX CC composition, which is useful for modulating the expression of human
XX CC N-ras, inhibiting the proliferation of cancer cells, and preventing or
XX CC treating conditions arising from the activation of a human N-ras
XX CC oncogene. The oligonucleotides are also useful in diagnostics,
XX CC therapeutics, and as research reagents and kits. The oligonucleotides
XX CC enable the specific modulation of activated human N-ras expression,
XX CC which is associated with tumour formation. Sequences AAX21601-619
XX CC represent antisense oligonucleotides targeted to mutant H-ras.
XX SQ Sequence 5 BP; 1 A; 2 C; 2 G; 0 U; 0 other;

Query Match 100.0%; Score 1; DB 20; Length 5;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
Db 2 g 2

RESULT 36
AAX21608/c
ID AAX21608 standard; DNA; 5 BP.
XX AC AAX21608;
XX DT 14-MAY-1999 (first entry)
XX DE Mutant H-ras specific antisense oligo ISIS #2563.
XX KW Human; N-ras; inhibition; pharmaceutical; modulation; cancer; oncogene;
XX KW diagnostic; therapeutic; tumour; mutant; H-ras; antisense; ss.
XX OS Synthetic.
XX PN WO9902732-A1.
XX PD 21-JAN-1999.

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XX PF 06-JUL-1998; 98WO-US13966.
XX PR 08-JUL-1997; 97US-0889296.
XX PA (ISIS-) ISIS PHARM INC.
XX PI Cowsert LM, Manoharan M, Monia BP;
XX DR WPI: 1999-120932/10.
XX PT New oligonucleotide targetting human N-ras nucleic acid - is
XX PT capable of inhibiting human N-ras expression, useful for preventing
XX PT or treating conditions arising from the activation of a human N-ras
XX PT oncogene
XX PS Disclosure; Page 22; 97pp; English.
XX CC The invention relates to oligonucleotides, which target a nucleic acid
XX CC encoding human N-ras, and are capable of inhibiting human N-ras
XX CC expression. The antisense oligonucleotides form a pharmaceutical
XX CC composition, which is useful for modulating the expression of human
XX CC N-ras, inhibiting the proliferation of cancer cells, and preventing or
XX CC treating conditions arising from the activation of a human N-ras
XX CC oncogene. The oligonucleotides are also useful in diagnostics,
XX CC therapeutics, and as research reagents and kits. The oligonucleotides
XX CC enable the specific modulation of activated human N-ras expression,
XX CC which is associated with tumour formation. Sequences AAX21601-619
XX CC represent antisense oligonucleotides targeted to mutant H-ras.
XX SQ Sequence 5 BP; 1 A; 2 C; 2 G; 0 U; 0 other;

Query Match 100.0%; Score 1; DB 20; Length 5;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
Db 4 G 4

RESULT 37
AAA56981
ID AAA56981 standard; cDNA; 5 BP.
XX AC AAA56981;
XX DT 14-NOV-2000 (first entry)
XX DE Human colon cancer cell cDNA sequence #109.
XX KW Human; arbitrary primer; cDNA synthesis; contig sequence construction;
XX KW open reading frame; ORF; low stringency; cDNA sequencing; ss.
XX OS Homo sapiens.
XX PN WO200031299-A2.
XX PD 02-JUN-2000.
XX PF 19-NOV-1999; 99WO-US27430.
XX PR 20-NOV-1998; 98US-0196716.
XX PA (LUDW-) LUDWIG INST CANCER RES.
XX PI Simpson AJG, Dias Neto E, Brentani RR;
XX DR WPI: 2000-400100/34.
XX PT Method for determining open reading frames of the genome of an organism
XX PT using primers at low stringency conditions, useful in the construction
XX PT

```

PT of contigs or constructs of sequenced nucleic acid molecules -
 PS Example 6; Page 47; 113pp; English.

XX The present sequence is a cDNA sequence obtained using a method for
 CC determining open reading frames (ORFs) of the genome of an
 CC organism. An aliquot of mRNA from human colon cancer cells was mixed
 CC with a single, arbitrary primer, Moloney murine leukaemia virus reverse
 CC transcriptase, reverse transcriptase buffer and dNTPs. The mixture was
 CC incubated under low stringency conditions to yield single stranded
 CC cDNA. The same primer was then used to amplify the cDNA by PCR. Rather
 CC than providing nucleotide sequence information from the non-coding
 CC termini of nucleic acid molecules, the method provides information on
 CC the more interesting and relevant internal portions, such as ORFs. The
 CC method also permits the construction of contigs of sequenced nucleic
 CC acid molecules.

XX Sequence 5 BP; 0 A; 3 C; 1 G; 1 T; 0 other;

Query Match 100.0%; Score 1; DB 21; Length 5;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
 Db 3 g 3

RESULT 38

AAA56981/c
 ID AAA56981 standard; cDNA; 5 BP.

XX
 AC AAA56981;

XX 14-NOV-2000 (first entry)

XX Human colon cancer cell cDNA sequence #109.

XX Human; arbitrary primer; cDNA synthesis; contig sequence construction;
 KW open reading frame; ORF; low stringency; cDNA sequencing; ss.

XX Homo sapiens.

XX WO200031299-A2.

XX 02-JUN-2000.

XX 19-NOV-1999; 99WO-US27430.

XX 20-NOV-1998; 98US-0196716.

XX (LUDW-) LUDWIG INST CANCER RES.

XX Simpson AJG, Dias Neto E, Brentani RR;

XX WPI; 2000-400100/34.

XX Method for determining open reading frames of the genome of an organism
 PT using primers at low stringency conditions, useful in the construction
 PT of contigs or constructs of sequenced nucleic acid molecules -

PS Example 6; Page 47; 113pp; English.

XX The present sequence is a cDNA sequence obtained using a method for
 CC determining open reading frames (ORFs) of the genome of an
 CC organism. An aliquot of mRNA from human colon cancer cells was mixed
 CC with a single, arbitrary primer, Moloney murine leukaemia virus reverse
 CC transcriptase, reverse transcriptase buffer and dNTPs. The mixture was
 CC incubated under low stringency conditions to yield single stranded
 CC cDNA. The same primer was then used to amplify the cDNA by PCR. Rather
 CC than providing nucleotide sequence information from the non-coding
 CC termini of nucleic acid molecules, the method provides information on

CC the more interesting and relevant internal portions, such as ORFs. The
 CC method also permits the construction of contigs of sequenced nucleic
 CC acid molecules.

XX Sequence 5 BP; 0 A; 3 C; 1 G; 1 T; 0 other;

Query Match 100.0%; Score 1; DB 21; Length 5;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
 Db 5 g 5

RESULT 39

AAZ93601
 ID AAZ93601 standard; DNA; 5 BP.

XX
 AC AAZ93601;

XX 24-JUL-2000 (first entry)

XX Transcription factor binding site of tobacco gene promoter sequence.

XX Regulatory sequence; meristem; genetic engineering;
 KW gene expression; crop protection; transgenic plant; resistance;
 KW tobacco; transcription factor; alcohol dehydrogenase-1; Adh1; ss.

XX Synthetic.

XX Nicotiana glauca.

XX WO200012713-A1.

XX 09-MAR-2000.

XX 26-AUG-1999; 99WO-AU000692.

XX 26-AUG-1998; 98AU-0005498.

XX (UYQU) UNIV QUEENSLAND.

XX Mudge SR, Birch RG;

XX WPI; 2000-237875/20.

XX Meristem-expressible nucleic acid sequences, useful for producing
 PT transgenic plants with improved characteristics such as resistance to
 PT pathogens

XX Example 9; Page 51; 102pp; English.

XX Isolated regulatory sequences of plants that are operable in
 CC dividing cells, in particular the meristem cells of plants are useful
 CC in the genetic engineering of plants. The regulatory sequences can
 CC be used to control the expression of foreign genes placed under their
 CC control. Such methods are useful for producing transgenic plants with
 CC altered shape and/or size. The sequences are also useful for
 CC producing transgenic plants capable of rapid regeneration following
 CC harvest or plants having improved resistance to pathogens. This
 CC sequence has been shown to bind a factor involved in the activation
 CC of the maize alcohol dehydrogenase-1 gene (adh1). It occurs three
 CC times in the meristem regulatory sequence of Tobacco described in
 CC GENESEQ record AAZ93567.

XX Sequence 5 BP; 1 A; 3 C; 1 G; 0 U; 0 other;

Query Match 100.0%; Score 1; DB 21; Length 5;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1
 |
 Db 5 g 5

RESULT 40
 AA293601/c
 ID AA293601 standard; DNA; 5 BP.
 XX
 AC AA293601;
 XX
 DT 24-JUL-2000 (first entry)
 XX
 DE Transcription factor binding site of tobacco gene promoter sequence.
 XX
 KW Regulatory sequence; meristem; genetic engineering;
 KW gene expression; crop protection; transgenic plant; resistance;
 KW tobacco; transcription factor; alcohol dehydrogenase-1; Adhl; ss.
 XX
 OS Synthetic.
 OS Nicotiana acuminata.
 XX
 PN WO200012713-A1.
 XX
 PD 09-MAR-2000.
 XX
 PF 26-AUG-1999; 99WO-AU00692.
 XX
 PR 26-AUG-1998; 98AU-0005498.
 XX
 PA (UYQU) UNIV QUEENSLAND.
 XX
 PI Mudge SR, Birch RG;
 XX
 DR WPI; 2000-237875/20.
 XX
 PT Meristem-expressible nucleic acid sequences, useful for producing
 PT transgenic plants with improved characteristics such as resistance to
 PT pathogens
 XX
 PS Example 9; Page 51; 102pp; English.
 XX
 CC Isolated regulatory sequences of plants that are operable in
 CC dividing cells, in particular the meristem cells of plants are useful
 CC in the genetic engineering of plants. The regulatory sequences can
 CC be used to control the expression of foreign genes placed under their
 CC control. Such methods are useful for producing transgenic plants with
 CC altered shape and/or size. The sequences are also useful for
 CC producing transgenic plants capable of rapid regeneration following
 CC harvest or plants having improved resistance to pathogens. This
 CC sequence has been shown to bind a factor involved in the activation
 CC of the maize alcohol dehydrogenase-1 gene (adh1). It occurs three
 CC times in the meristem regulatory sequence of tobacco described in
 CC GENESEQ record AA293567.
 XX
 SQ Sequence 5 BP; 1 A; 3 C; 1 G; 0 U; 0 other;

Query Match 100.0%; Score 1; DB 21; Length 5;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1
 |
 Db 4 G 4

RESULT 41
 AA293602/c
 ID AA293602 standard; DNA; 5 BP.
 XX
 AC AA293602;
 XX

DT 24-JUL-2000 (first entry)
 XX
 DE Transcription factor binding site of tobacco gene promoter sequence.
 XX
 KW Regulatory sequence; meristem; genetic engineering;
 KW gene expression; crop protection; transgenic plant; resistance;
 KW tobacco; transcription factor; NIT2; nitrate; ss.
 XX
 OS Synthetic.
 OS Nicotiana acuminata.
 XX
 PN WO200012713-A1.
 XX
 PD 09-MAR-2000.
 XX
 PF 26-AUG-1999; 99WO-AU00692.
 XX
 PR 26-AUG-1998; 98AU-0005498.
 XX
 PA (UYQU) UNIV QUEENSLAND.
 XX
 PI Mudge SR, Birch RG;
 XX
 DR WPI; 2000-237875/20.
 XX
 PT Meristem-expressible nucleic acid sequences, useful for producing
 PT transgenic plants with improved characteristics such as resistance to
 PT pathogens
 XX
 PS Example 9; Page 51; 102pp; English.
 XX
 CC Isolated regulatory sequences of plants that are operable in
 CC dividing cells, in particular the meristem cells of plants are useful
 CC in the genetic engineering of plants. The regulatory sequences can
 CC be used to control the expression of foreign genes placed under their
 CC control. Such methods are useful for producing transgenic plants with
 CC altered shape and/or size. The sequences are also useful for
 CC producing transgenic plants capable of rapid regeneration following
 CC harvest or plants having improved resistance to pathogens. This
 CC sequence has been shown to regulate nitrate metabolism in the
 CC fungus Neurospora crassa. It occurs multiple times in the meristem
 CC regulatory sequence of tobacco described in GENESEQ record AA293567.
 XX
 SQ Sequence 5 BP; 1 A; 1 C; 0 G; 3 T; 0 other;

Query Match 100.0%; Score 1; DB 21; Length 5;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1
 |
 Db 4 G 4

RESULT 42
 AA289330/c
 ID AA289330 standard; DNA; 5 BP.
 XX
 AC AA289330;
 XX
 DT 13-JUN-2000 (first entry)
 XX
 DE Human UCP3 promoter fragment #10.
 XX
 KW UCP3; uncoupling protein 3; human; promoter; fat cell; transcription;
 KW fat metabolism; ss.
 XX
 OS Homo sapiens.
 XX
 PN DE19838837-A1.
 XX
 PD 02-MAR-2000.

XX 27-AUG-1998; 98DE-1038837.
XX 27-AUG-1998; 98DE-1038837.
XX (BOEH) BOEHRINGER INGELHEIM INT GMBH.
PA (NOVO) NOVO-NORDISK AS.
PI Esterbauer H, Oberkofler H, Patsch W;
XX WPI; 2000-272214/24.
XX Recombinant fat and muscle tissue specific uncoupling protein 3
PT promoters useful for identifying UCP3 modulators -
XX
PS Claim 25; Page 12; 38pp; German.
XX This invention describes novel recombinant DNA molecules containing
CC an uncoupling protein 3 (UCP-3) promoter DNA sequence active in fat
CC cells but not functional in muscle cells or vice versa. The recombinant
CC DNA molecules are useful for transcription of genes and, with host cells,
CC to test for substances that can influence transcription. They can also be
CC used to identify modulators of UCP3 promoters. UCP3 plays a role in fat
CC metabolism and control of the promoter is useful in combating diseases
CC with inappropriate fat tissue metabolism. This sequence represents a
CC fragment of the human UCP-3 promoter which is used to illustrate the
CC method of the invention.
XX Sequence 5 BP; 2 A; 2 C; 0 G; 1 T; 0 other;
SQ

Query Match 100.0%; Score 1; DB 21; Length 5;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 g 1
Db 2 G 2

RESULT 43
AAZ89331
ID AAZ89331 standard; DNA; 5 BP.
XX
AC AAZ89331;
XX
DT 13-JUN-2000 (first entry)
XX
DE Human UCP3 promoter fragment #11.
XX
KW UCP3; uncoupling protein 3; human; promoter; fat cell; transcription;
KW fat metabolism; ss.
XX
OS Homo sapiens.
XX
PN DE19838837-A1.
XX
PD 02-MAR-2000.
XX
PF 27-AUG-1998; 98DE-1038837.
XX
PR 27-AUG-1998; 98DE-1038837.
XX
PA (BOEH) BOEHRINGER INGELHEIM INT GMBH.
PA (NOVO) NOVO-NORDISK AS.
XX
PI Esterbauer H, Oberkofler H, Patsch W;
XX WPI; 2000-272214/24.
XX Recombinant fat and muscle tissue specific uncoupling protein 3
PT promoters useful for identifying UCP3 modulators -
XX

PS Claim 28; Page 12; 38pp; German.
XX This invention describes novel recombinant DNA molecules containing
CC an uncoupling protein 3 (UCP-3) promoter DNA sequence active in fat
CC cells but not functional in muscle cells or vice versa. The recombinant
CC DNA molecules are useful for transcription of genes and, with host cells,
CC to test for substances that can influence transcription. They can also be
CC used to identify modulators of UCP3 promoters. UCP3 plays a role in fat
CC metabolism and control of the promoter is useful in combating diseases
CC with inappropriate fat tissue metabolism. This sequence represents a
CC fragment of the human UCP-3 promoter which is used to illustrate the
CC method of the invention.
XX Sequence 5 BP; 1 A; 0 C; 2 G; 2 T; 0 other;
SQ

Query Match 100.0%; Score 1; DB 21; Length 5;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 g 1
Db 4 g 4

RESULT 44
AAZ89332
ID AAZ89332 standard; DNA; 5 BP.
XX
AC AAZ89332;
XX
DT 13-JUN-2000 (first entry)
XX
DE Human UCP3 promoter fragment #12.
XX
KW UCP3; uncoupling protein 3; human; promoter; fat cell; transcription;
KW fat metabolism; ss.
XX
OS Homo sapiens.
XX
PN DE19838837-A1.
XX
PD 02-MAR-2000.
XX
PF 27-AUG-1998; 98DE-1038837.
XX
PR 27-AUG-1998; 98DE-1038837.
XX
PA (BOEH) BOEHRINGER INGELHEIM INT GMBH.
PA (NOVO) NOVO-NORDISK AS.
XX
PI Esterbauer H, Oberkofler H, Patsch W;
XX WPI; 2000-272214/24.
XX Recombinant fat and muscle tissue specific uncoupling protein 3
PT promoters useful for identifying UCP3 modulators -
XX
PS Claim 31; Page 12; 38pp; German.
XX This invention describes novel recombinant DNA molecules containing
CC an uncoupling protein 3 (UCP-3) promoter DNA sequence active in fat
CC cells but not functional in muscle cells or vice versa. The recombinant
CC DNA molecules are useful for transcription of genes and, with host cells,
CC to test for substances that can influence transcription. They can also be
CC used to identify modulators of UCP3 promoters. UCP3 plays a role in fat
CC metabolism and control of the promoter is useful in combating diseases
CC with inappropriate fat tissue metabolism. This sequence represents a
CC fragment of the human UCP-3 promoter which is used to illustrate the
CC method of the invention.
XX Sequence 5 BP; 1 A; 0 C; 2 G; 2 T; 0 other;
SQ

Query Match 100.0%; Score 1; DB 21; Length 5;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1
Db 4 g 4

RESULT 45
AAZ48433
ID AA248433 standard; DNA; 5 BP.
XX
AC AA248433;
XX
DT 27-MAR-2000 (first entry)
XX
DE First DNA arm segment.
XX
KW Microorganism; virus; polymerase chain reaction; food; cosmetic;
KW clinical diagnostic; molecular beacon; PCR primer; ss.
XX

OS Synthetic.

PN WO9963112-A2.

PD 09-DEC-1999.

XX

PF 18-MAY-1999; 99WO-US10940.

XX

PR 18-MAY-1998; 98US-0086025.

PR 17-MAY-1999; 99US-0086025.

XX (HUNT-) HUNT WESSON INC.

XX

PI Romick TL, Fraser MS;

DR WPI; 2000-086985/07.

XX

PT Detection of microorganisms and viruses, for use in the food and

PT cosmetic industries and for clinical diagnostics -

XX

PS Claim 51; Page 40; 63pp; English.

XX The invention provides a novel in vitro method for the detection of
CC microorganisms and viruses. The method comprises: (1) forming a
CC polymerase chain reaction (PCR) mixture by combining a predetermined
CC volume of a sample to be tested for the presence of a nucleic acid
CC sequence comprising 5'-TAGAAGC-3', known amounts of a first primer
CC comprising 5'-GCTAGGTCCCAAGT-3', and a second primer comprising
CC 5'-AGAAGCTCTCTACC-3', and PCR reagents; (2) forming a PCR product by
CC cycling the PCR mixture to amplify the nucleic acid sequence, if present,
CC to replicate and attain 0.25-10000mg nucleotide product/mul mixture; (3)
CC adding a probe containing DNA comprising 5'-GGTGGTCTTCTAAGCCACC-3' to
CC the PCR mixture or to the PCR product to cause the DNA to hybridize with
CC the nucleic acid sequence, if present, and change the conformation of the
CC probe; and (4) determining whether or not bacteria are present in the
CC sample by detecting the conformational change of the probe, a
CC conformational change indicating the presence of bacteria in the sample.
CC The methods can be used for the detection of viruses and microorganisms,
CC including bacteria, yeast, molds and protista. They can be used in the
CC food and cosmetic industry and in clinical diagnostics. Using the method
CC it is not necessary to remove non-hybridized probe from the system.

XX Sequence 5 BP; 1 A; 1 C; 2 G; 1 T; 0 other;

Query Match 100.0%; Score 1; DB 21; Length 5;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1

Db 1 g 1

Search completed: July 15, 2002, 23:10:11
Job time: 18429 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: July 15, 2002, 23:28:08 ; Search time 9532.94 Seconds
(without alignments)
2.195 Million cell updates/sec

Title: US-09-375-248-l_COPY_2588_2588

Perfect score: 1

Sequence: 1 g 1

Scoring table: OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 1797656 seqs, 10463268293 residues

Word size : 0

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

GenEmbl:*

- 1: gb_ba:*
- 2: gb_htg:*
- 3: gb_in:*
- 4: gb_om:*
- 5: gb_ov:*
- 6: gb_pat:*
- 7: gb_ph:*
- 8: gb_pl:*
- 9: gb_pr:*
- 10: gb_ro:*
- 11: gb_sts:*
- 12: gb_sy:*
- 13: gb_un:*
- 14: gb_vi:*
- 15: em_ba:*
- 16: em_fun:*
- 17: em_hum:*
- 18: em_in:*
- 19: em_mu:*
- 20: em_om:*
- 21: em_or:*
- 22: em_ov:*
- 23: em_pat:*
- 24: em_ph:*
- 25: em_pi:*
- 26: em_ro:*
- 27: em_sts:*
- 28: em_un:*
- 29: em_vi:*
- 30: em_htg_hum:*
- 31: em_htg_inv:*
- 32: em_htg_other:*
- 33: em_htgo_inv:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
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C	1	1	100.0	6	AX092441	Sequence
C	2	1	100.0	6	AX092442	Sequence
C	3	1	100.0	6	AX092443	Sequence
C	4	1	100.0	6	AX092444	Sequence
C	5	1	100.0	6	AX092445	Sequence
C	6	1	100.0	6	AX092446	Sequence
C	7	1	100.0	6	AX092447	Sequence
C	8	1	100.0	6	AX092448	Sequence
C	9	1	100.0	6	AX092449	Sequence
C	10	1	100.0	6	AX092450	Sequence
C	11	1	100.0	6	AX092451	Sequence
C	12	1	100.0	6	AX092452	Sequence
C	13	1	100.0	6	AX092453	Sequence
C	14	1	100.0	6	AX092454	Sequence
C	15	1	100.0	6	AX092455	Sequence
C	16	1	100.0	6	AX092456	Sequence
C	17	1	100.0	6	AX092457	Sequence
C	18	1	100.0	6	AX092458	Sequence
C	19	1	100.0	6	AX092459	Sequence
C	20	1	100.0	6	AX092460	Sequence
C	21	1	100.0	6	AX092461	Sequence
C	22	1	100.0	6	AX092462	Sequence
C	23	1	100.0	6	AX092463	Sequence
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C	25	1	100.0	6	AX092465	Sequence
C	26	1	100.0	6	AX092466	Sequence
C	27	1	100.0	6	AX092467	Sequence
C	28	1	100.0	6	AX092468	Sequence
C	29	1	100.0	6	AX092469	Sequence
C	30	1	100.0	6	AX092470	Sequence
C	31	1	100.0	6	AX092471	Sequence
C	32	1	100.0	6	AX092472	Sequence
C	33	1	100.0	6	AX092473	Sequence
C	34	1	100.0	6	AX092474	Sequence
C	35	1	100.0	6	AX092475	Sequence
C	36	1	100.0	6	AX092476	Sequence
C	37	1	100.0	6	AX092477	Sequence
C	38	1	100.0	6	AX092478	Sequence
C	39	1	100.0	6	AX092479	Sequence
C	40	1	100.0	6	AX092480	Sequence
C	41	1	100.0	6	AX092481	Sequence
C	42	1	100.0	6	AX092482	Sequence
C	43	1	100.0	6	AX092483	Sequence
C	44	1	100.0	6	AX092484	Sequence
C	45	1	100.0	6	AX092485	Sequence

ALIGNMENTS

RESULT 1

AX092441/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

1. 2

/organism="unidentified"

/db_xref="taxon:32644"

/note="synthetic oligonucleotide;"

1 a 1 c 0 g 0 t

BASE COUNT

AX092441

Sequence 2 from Patent WO0116366.

AX092441

AX092441.1 GI:13444536

unidentified.

unclassified.

1 (bases 1 to 2)

Kless, H.

Template-dependent nucleic acid polymerization using

oligonucleotide triphosphates building blocks

Patent: WO 0116366-A 2 08-MAR-2001;

YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar

(IL)

Location/Qualifiers

1. 2

/organism="unidentified"

/db_xref="taxon:32644"

/note="synthetic oligonucleotide;"

1 a 1 c 0 g 0 t

BASE COUNT

ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
|
Db 2 G 2

RESULT 2

AX092442
LOCUS AX092442
DEFINITION Sequence 3 from Patent WO0116366.
ACCESSION AX092442
VERSION AX092442.1 GI:13444537
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 2)
AUTHORS Kless, H.
TITLE Template-dependent nucleic acid polymerization using oligonucleotide triphosphates building blocks
JOURNAL Patent: WO 0116366-A 3 08-MAR-2001;
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar (IL)

FEATURES
source
1..2
Location/Qualifiers
/organism="unidentified"
/db_xref="taxon:32644"
/note="synthetic oligonucleotide;"
1 a 0 c 1 g 0 t

BASE COUNT
ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
|
Db 2 G 2

RESULT 3

AX092444/c
LOCUS AX092444
DEFINITION Sequence 5 from Patent WO0116366.
ACCESSION AX092444
VERSION AX092444.1 GI:13444539
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 2)
AUTHORS Kless, H.
TITLE Template-dependent nucleic acid polymerization using oligonucleotide triphosphates building blocks
JOURNAL Patent: WO 0116366-A 5 08-MAR-2001;
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar (IL)

FEATURES
source
1..2
Location/Qualifiers
/organism="unidentified"
/db_xref="taxon:32644"
/note="synthetic oligonucleotide;"
1 a 1 c 0 g 0 t

BASE COUNT
ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
|
Db 1 G 1

RESULT 4

AX092445/c
LOCUS AX092445
DEFINITION Sequence 6 from Patent WO0116366.
ACCESSION AX092445
VERSION AX092445.1 GI:13444540
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 2)
AUTHORS Kless, H.
TITLE Template-dependent nucleic acid polymerization using oligonucleotide triphosphates building blocks
JOURNAL Patent: WO 0116366-A 6 08-MAR-2001;
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar (IL)

FEATURES
source
1..2
Location/Qualifiers
/organism="unidentified"
/db_xref="taxon:32644"
/note="synthetic oligonucleotide;"
0 a 2 c 0 g 0 t

BASE COUNT
ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
|
Db 2 G 2

RESULT 5

AX092446
LOCUS AX092446
DEFINITION Sequence 7 from Patent WO0116366.
ACCESSION AX092446
VERSION AX092446.1 GI:13444541
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 2)
AUTHORS Kless, H.
TITLE Template-dependent nucleic acid polymerization using oligonucleotide triphosphates building blocks
JOURNAL Patent: WO 0116366-A 7 08-MAR-2001;
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar (IL)

FEATURES
source
1..2
Location/Qualifiers
/organism="unidentified"
/db_xref="taxon:32644"
/note="synthetic oligonucleotide;"
0 a 1 c 1 g 0 t

BASE COUNT
ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 g 1
Db      2 G 2

RESULT 6
AX092446/c
LOCUS   AX092446          2 bp      DNA      linear      PAT 21-MAR-2001
DEFINITION   Sequence 7 from Patent WO0116366.
ACCESSION   AX092446
VERSION     AX092446.1 GI:13444541
KEYWORDS    .
SOURCE      .
ORGANISM    .
REFERENCE   1 (bases 1 to 2)
AUTHORS     Kless,H.
TITLE       Template-dependent nucleic acid polymerization using
            oligonucleotide triphosphates building blocks
JOURNAL     Patent: WO 0116366-A 7 08-MAR-2001;
            YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar
            (IL)
FEATURES    Location/Qualifiers
            source          1..2
                        /organism="unidentified"
                        /db_xref="taxon:32644"
                        /note="synthetic oligonucleotide;"
BASE COUNT  0 a 1 c 1 g 0 t

Query Match      100.0%; Score 1; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 g 1
Db      1 G 1

RESULT 7
AX092447/c
LOCUS   AX092447          2 bp      DNA      linear      PAT 21-MAR-2001
DEFINITION   Sequence 8 from Patent WO0116366.
ACCESSION   AX092447
VERSION     AX092447.1 GI:13444542
KEYWORDS    .
SOURCE      .
ORGANISM    .
REFERENCE   1 (bases 1 to 2)
AUTHORS     Kless,H.
TITLE       Template-dependent nucleic acid polymerization using
            oligonucleotide triphosphates building blocks
JOURNAL     Patent: WO 0116366-A 8 08-MAR-2001;
            YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar
            (IL)
FEATURES    Location/Qualifiers
            source          1..2
                        /organism="unidentified"
                        /db_xref="taxon:32644"
                        /note="synthetic oligonucleotide;"
BASE COUNT  0 a 1 c 0 g 1 t

Query Match      100.0%; Score 1; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 g 1
Db      1 G 1

RESULT 8
AX092448
LOCUS   AX092448          2 bp      DNA      linear      PAT 21-MAR-2001
DEFINITION   Sequence 9 from Patent WO0116366.
ACCESSION   AX092448
VERSION     AX092448.1 GI:13444543
KEYWORDS    .
SOURCE      .
ORGANISM    .
REFERENCE   1 (bases 1 to 2)
AUTHORS     Kless,H.
TITLE       Template-dependent nucleic acid polymerization using
            oligonucleotide triphosphates building blocks
JOURNAL     Patent: WO 0116366-A 9 08-MAR-2001;
            YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar
            (IL)
FEATURES    Location/Qualifiers
            source          1..2
                        /organism="unidentified"
                        /db_xref="taxon:32644"
                        /note="synthetic oligonucleotide;"
BASE COUNT  1 a 0 c 1 g 0 t

Query Match      100.0%; Score 1; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 g 1
Db      1 G 1

RESULT 9
AX092449
LOCUS   AX092449          2 bp      DNA      linear      PAT 21-MAR-2001
DEFINITION   Sequence 10 from Patent WO0116366.
ACCESSION   AX092449
VERSION     AX092449.1 GI:13444544
KEYWORDS    .
SOURCE      .
ORGANISM    .
REFERENCE   1 (bases 1 to 2)
AUTHORS     Kless,H.
TITLE       Template-dependent nucleic acid polymerization using
            oligonucleotide triphosphates building blocks
JOURNAL     Patent: WO 0116366-A 10 08-MAR-2001;
            YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar
            (IL)
FEATURES    Location/Qualifiers
            source          1..2
                        /organism="unidentified"
                        /db_xref="taxon:32644"
                        /note="synthetic oligonucleotide;"
BASE COUNT  0 a 1 c 1 g 0 t

Query Match      100.0%; Score 1; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 g 1
Db      1 G 1

```

RESULT 10
AX092449/c
LOCUS AX092449 2 bp DNA linear PAT 21-MAR-2001
DEFINITION Sequence 10 from Patent WO0116366.
ACCESSION AX092449
VERSION AX092449.1 GI:13444544
KEYWORDS
SOURCE .
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 2)
AUTHORS Kless, H.
TITLE Template-dependent nucleic acid polymerization using oligonucleotide triphosphates building blocks
JOURNAL Patent: WO 0116366-A 10 08-MAR-2001;
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar (IL)
FEATURES
source Location/Qualifiers
1..2
/organism="unidentified"
/db_xref="taxon:32644"
/note="synthetic oligonucleotide;"
BASE COUNT 0 a 1 c 1 g 0 t
ORIGIN
Query Match 100.0%; Score 1; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 g 1
Db 2 G 2
RESULT 11
AX092450
LOCUS AX092450 2 bp DNA linear PAT 21-MAR-2001
DEFINITION Sequence 11 from Patent WO0116366.
ACCESSION AX092450
VERSION AX092450.1 GI:13444545
KEYWORDS
SOURCE .
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 2)
AUTHORS Kless, H.
TITLE Template-dependent nucleic acid polymerization using oligonucleotide triphosphates building blocks
JOURNAL Patent: WO 0116366-A 11 08-MAR-2001;
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar (IL)
FEATURES
source Location/Qualifiers
1..2
/organism="unidentified"
/db_xref="taxon:32644"
/note="synthetic oligonucleotide;"
BASE COUNT 0 a 0 c 2 g 0 t
ORIGIN
Query Match 100.0%; Score 1; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 g 1
Db 1 G 1
RESULT 12
AX092451
LOCUS AX092451 2 bp DNA linear PAT 21-MAR-2001

DEFINITION Sequence 12 from Patent WO0116366.
ACCESSION AX092451
VERSION AX092451.1 GI:13444546
KEYWORDS
SOURCE .
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 2)
AUTHORS Kless, H.
TITLE Template-dependent nucleic acid polymerization using oligonucleotide triphosphates building blocks
JOURNAL Patent: WO 0116366-A 12 08-MAR-2001;
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar (IL)
FEATURES
source Location/Qualifiers
1..2
/organism="unidentified"
/db_xref="taxon:32644"
/note="synthetic oligonucleotide;"
BASE COUNT 0 a 0 c 1 g 1 t
ORIGIN
Query Match 100.0%; Score 1; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 g 1
Db 1 G 1
RESULT 13
AX092453/c
LOCUS AX092453 2 bp DNA linear PAT 21-MAR-2001
DEFINITION Sequence 14 from Patent WO0116366.
ACCESSION AX092453
VERSION AX092453.1 GI:13444548
KEYWORDS
SOURCE .
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 2)
AUTHORS Kless, H.
TITLE Template-dependent nucleic acid polymerization using oligonucleotide triphosphates building blocks
JOURNAL Patent: WO 0116366-A 14 08-MAR-2001;
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar (IL)
FEATURES
source Location/Qualifiers
1..2
/organism="unidentified"
/db_xref="taxon:32644"
/note="synthetic oligonucleotide;"
BASE COUNT 0 a 1 c 0 g 1 t
ORIGIN
Query Match 100.0%; Score 1; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 g 1
Db 2 G 2
RESULT 14
AX092454
LOCUS AX092454 2 bp DNA linear PAT 21-MAR-2001
DEFINITION Sequence 15 from Patent WO0116366.
ACCESSION AX092454
VERSION AX092454.1 GI:13444549

KEYWORDS
SOURCE
ORGANISM
unidentified.
unidentified
unclassified.
REFERENCE
1 (bases 1 to 2)
AUTHORS
Kless, H.
TITLE
Template-dependent nucleic acid polymerization using oligonucleotide triphosphates building blocks
JOURNAL
Patent: WO 0116366-A 15 08-MAR-2001;
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar (IL)
FEATURES
source
Location/Qualifiers
1..2
/organism="unidentified"
/db_xref="taxon:32644"
/note="synthetic oligonucleotide;"
BASE COUNT
ORIGIN
0 a 0 c 1 g 1 t
Query Match 100.0%; Score 1; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 g 1
Db 2 G 2
RESULT 15
AX092528/c
LOCUS
AX092528
DEFINITION
Sequence 89 from Patent WO0116366.
ACCESSION
AX092528
VERSION
AX092528.1 GI:13444623
KEYWORDS
unidentified.
ORGANISM
unidentified.
REFERENCE
1 (bases 1 to 2)
AUTHORS
Kless, H.
TITLE
Template-dependent nucleic acid polymerization using oligonucleotide triphosphates building blocks
JOURNAL
Patent: WO 0116366-A 89 08-MAR-2001;
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar (IL)
FEATURES
source
Location/Qualifiers
1..2
/organism="unidentified"
/db_xref="taxon:32644"
/note="synthetic oligonucleotide;"
BASE COUNT
ORIGIN
1 a 1 c 0 g 0 t
Query Match 100.0%; Score 1; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 g 1
Db 1 G 1
RESULT 16
AX092529/c
LOCUS
AX092529
DEFINITION
Sequence 90 from Patent WO0116366.
ACCESSION
AX092529
VERSION
AX092529.1 GI:13444624
KEYWORDS
unidentified.
ORGANISM
unidentified.

KEYWORDS
SOURCE
ORGANISM
unclassified.
unclassified
unclassified.
REFERENCE
1 (bases 1 to 2)
AUTHORS
Kless, H.
TITLE
Template-dependent nucleic acid polymerization using oligonucleotide triphosphates building blocks
JOURNAL
Patent: WO 0116366-A 90 08-MAR-2001;
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar (IL)
FEATURES
source
Location/Qualifiers
1..2
/organism="unidentified"
/db_xref="taxon:32644"
/note="synthetic oligonucleotide;"
BASE COUNT
ORIGIN
0 a 2 c 0 g 0 t
Query Match 100.0%; Score 1; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 g 1
Db 2 G 2
RESULT 17
AX092530
LOCUS
AX092530
DEFINITION
Sequence 91 from Patent WO0116366.
ACCESSION
AX092530
VERSION
AX092530.1 GI:13444625
KEYWORDS
unidentified.
ORGANISM
unidentified.
REFERENCE
1 (bases 1 to 2)
AUTHORS
Kless, H.
TITLE
Template-dependent nucleic acid polymerization using oligonucleotide triphosphates building blocks
JOURNAL
Patent: WO 0116366-A 91 08-MAR-2001;
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar (IL)
FEATURES
source
Location/Qualifiers
1..2
/organism="unidentified"
/db_xref="taxon:32644"
/note="synthetic oligonucleotide;"
BASE COUNT
ORIGIN
1 a 0 c 1 g 0 t
Query Match 100.0%; Score 1; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 g 1
Db 2 G 2
RESULT 18
AX092538
LOCUS
AX092538
DEFINITION
Sequence 99 from Patent WO0116366.
ACCESSION
AX092538
VERSION
AX092538.1 GI:13444633
KEYWORDS
unidentified.
ORGANISM
unidentified.
REFERENCE
1 (bases 1 to 2)
AUTHORS
Kless, H.

TITLE Template-dependent nucleic acid polymerization using
oligonucleotide triphosphates building blocks
JOURNAL Patent: WO 0116366-A 99 08-MAR-2001;
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL); Kless, Hadar
(IL)

FEATURES
Source Location/Qualifiers
1..2
/organism="unidentified"
/db_xref="taxon:32644"
/note="synthetic oligonucleotide;"

BASE COUNT 0 a 0 c 1 g 1 t
ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1
|
Db 1 G 1

RESULT 19
AXI75286
LOCUS AXI75286 2 bp DNA linear PAT 03-JUL-2001
DEFINITION Sequence 50 from Patent WO014465.
ACCESSION AXI75286
VERSION AXI75286.1 GI:14598654

KEYWORDS synthetic construct.
SOURCE synthetic construct.
ORGANISM artificial sequence.
REFERENCE 1 (bases 1 to 2)
AUTHORS Phillips, N.C. and Fillion, M.C.

TITLE Therapeutically useful synthetic oligonucleotides
JOURNAL Patent: WO 0144465-A 50 21-JUN-2001;
Bioniche Life Sciences Inc. (CA)

FEATURES
Source Location/Qualifiers
1..2
/organism="synthetic construct"
/db_xref="taxon:32630"

BASE COUNT 0 a 0 c 1 g 1 t
ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1
|
Db 1 G 1

RESULT 20
AXI75287
LOCUS AXI75287 2 bp DNA linear PAT 03-JUL-2001
DEFINITION Sequence 51 from Patent WO014465.
ACCESSION AXI75287
VERSION AXI75287.1 GI:14598655

KEYWORDS synthetic construct.
SOURCE synthetic construct.
ORGANISM artificial sequence.
REFERENCE 1 (bases 1 to 2)
AUTHORS Phillips, N.C. and Fillion, M.C.

TITLE Therapeutically useful synthetic oligonucleotides
JOURNAL Patent: WO 0144465-A 51 21-JUN-2001;
Bioniche Life Sciences Inc. (CA)

FEATURES
Source Location/Qualifiers
1..2
/organism="synthetic construct"

BASE COUNT 0 a 0 c 1 g 1 t
ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1
|
Db 2 G 2

RESULT 21
BD009609/c
LOCUS BD009609 2 bp DNA linear PAT 31-JAN-2002
DEFINITION Probes, methods and kits for detection and typing of *Helicobacter*
pylori nucleic acids in biological samples.

ACCESSION BD009609
VERSION BD009609.1 GI:18637982
KEYWORDS JP 2001502536-A/201.
SOURCE unidentified.
ORGANISM unclassified.

REFERENCE 1 (bases 1 to 2)
AUTHORS Quint, W. and Doorn, L.J.V.
TITLE Probes, methods and kits for detection and typing of *Helicobacter*
pylori nucleic acids in biological samples
JOURNAL Patent: JP 2001502536-A 201 27-FEB-2001;
COMMENT INNOGENETICS NV, DDL BV

OS Unidentified
PN JP 2001502536-A/201
PD 27-FEB-2001
PF 10-OCT-1997 JP 1998518004
PR 16-OCT-1996 EP 96870131.8
PI WILHELMUS QUINT, LEENDERT JAN VAN DOORN
PC C1201/68, C07K14/205, C12N15/11
CC

FEATURES
Source Location/Qualifiers
1..2
/organism="unidentified"
/db_xref="taxon:32644"

BASE COUNT 0 a 1 c 0 g 0 t 1 others
ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 g 1
|
Db 2 G 2

RESULT 22
CNS01C99

LOCUS CNS01C99 2 bp mRNA linear PLN 02-SEP-1999
DEFINITION Botrytis cinerea strain T4 cDNA library under conditions of
nitrogen deprivation.

ACCESSION AL115237
VERSION AL115237.1 GI:5829856
KEYWORDS cDNA library; nitrogen deprivation.
SOURCE Botryotinia fuckeliana.

ORGANISM Botryotinia fuckeliana
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Leotiomycetes;
Helotiales; Sclerotiniaceae; Botryotinia.
REFERENCE 1 (bases 1 to 2)
AUTHORS Bitton, F., Levis, C., Fortini, D., Pradier, J.M. and Brygoo, Y.

TITLE Direct Submission
JOURNAL Submitted (01-SEP-1999) Phytopathologie, INRA, route de St Cyr, 78026 Versailles, France
REFERENCE 2 (bases 1 to 2)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (01-SEP-1999) Genoscope - Centre National de Sequencage : CP 5706 91057 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - web : www.genoscope.cns.fr)

COMMENT The cDNA library to be analyzed within the framework of this project was created using a Botrytis cinerea strain which was grown under conditions of nitrogen deprivation, which is the normal situation for B. cinerea during its development on its host plant. The library was produced in an oriented direction, in the pBSII vector.

FEATURES

source 1. .2
 /organism="Botryotinia fuckelliana"
 /strain="T4"
 /db_xref="taxon:40559"
 /note="Genoscope sequence ID : W04F091"
BASE COUNT 0 a 0 c 1 g 1 t
ORIGIN

Query Match 100.0%; Score 1; DB 8; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1

I |

Db 1 G 1

RESULT 23

AC079635 AC079635 3 bp DNA linear HTG 14-AUG-2001
LOCUS Mus musculus clone RP23-152L20, LOW-PASS SEQUENCE SAMPLING.
DEFINITION AC079635
ACCESSION AC079635.3 GI:14647267
VERSION HTG: HTGS_PHASE0.
KEYWORDS house mouse.
SOURCE Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 3)
AUTHORS McCombie, W.R., Baker, J.P., Bahret, A., Yang, C., Ballia, V., Dedhia, N.N., de la Bastide, M., Kuit, K., King, L., Kirchoff, K.A., Miller, B., Nascimento, L.U., O'Shaughnessy, A.L., Preston, R.R., Rodriguez, S., Santos, L., Shah, R.S., Spiegel, L.A., Palmer, L., Vil, M.D. and Zutavern, T.
TITLE Mouse Genomic Sequence
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 3)
AUTHORS McCombie, W.R.

TITLE Direct Submission
JOURNAL Submitted (06-SEP-2000) Lita Annenberg Hazen Genome Sequencing Center, Cold Spring Harbor Laboratory, 1 Bungtown Road, Cold Spring Harbor, NY 11724, USA
AUTHORS On Jul 10, 2001 this sequence version replaced gi:14595773.

COMMENT

* NOTE: This record contains 1 individual
 * sequencing reads that have not been assembled into
 * contigs. Runs of N are used to separate the reads
 * and the order in which they appear is completely
 * arbitrary. Low-pass sequence sampling is useful for
 * identifying clones that may be gene-rich and allows
 * overlap relationships among clones to be deduced.
 * However, it should not be assumed that this clone
 * will be sequenced to completion. In the event that
 * the record is updated, the accession number will
 * be preserved.

* 1 3: contig of 3 bp in length.
 * This entry has been temporarily removed. An update for RP23-152L20

will be submitted as soon as it becomes available.

FEATURES
source 1. .3
 /organism="Mus musculus"
 /db_xref="taxon:10090"
 /clone="RP23-152L20"
BASE COUNT 1 a 0 c 1 g 1 t
ORIGIN

Query Match 100.0%; Score 1; DB 2; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1

I |

Db 1 G 1

RESULT 24

CHKNCAMC5 CHKNCAMC5 3 bp DNA linear VRT 17-JUL-2000
LOCUS Chicken cardiac neural cell adhesion (NCAM) gene, exon 12D.
DEFINITION M23994 J04140
ACCESSION M23994.1 GI:212442
VERSION M23994.1
KEYWORDS chicken.
SEGMENT 5 of 6
SOURCE Gallus gallus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
AUTHORS Prediger, E.A., Hoffman, S., Edelman, G.M. and Cunningham, B.A.
TITLE Four exons encode a 93-base-pair insert in three neural cell adhesion molecule mRNAs specific for chicken heart and skeletal muscle

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 85 (24), 9616-9620 (1988)
MEDLINE 89071747
PUBMED 3200847
COMMENT Exon 12D represents a very small exon.
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 /organism="Gallus gallus"
 /db_xref="taxon:9031"
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BASE COUNT 2 a 0 c 1 g 0 t
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Qy 1 g 1

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Db 3 G 3

RESULT 25

A97991 A97991 3 bp DNA linear PAT 26-JAN-2000
LOCUS Sequence 21 from Patent WO9914366.
DEFINITION A97991
ACCESSION A97991
VERSION A97991.1 GI:6781229
KEYWORDS .
SOURCE unidentified.
ORGANISM unidentified

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REFERENCE 1 (bases 1 to 3)
AUTHORS Pongers-Willemsse,M.J. and Van,D.J.
TITLE DETECTION OF MINIMAL RESIDUAL DISEASE IN LYMPHOID MALIGNANCIES
JOURNAL Patent: WO 9914366-A 21 25-MAR-1999;
DONGEN JACOBUS JOHANNES MARIA (NL); UNIV ERASMUS (NL)
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Qy 1 g 1
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RESULT 26
LOCUS A97991/c A97991 3 bp DNA linear PAT 26-JAN-2000
DEFINITION Sequence 21 from Patent WO9914366.
ACCESSION A97991
VERSION A97991.1 GI:6781229
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 3)
AUTHORS Pongers-Willemsse,M.J. and Van,D.J.
TITLE DETECTION OF MINIMAL RESIDUAL DISEASE IN LYMPHOID MALIGNANCIES
JOURNAL Patent: WO 9914366-A 21 25-MAR-1999;
DONGEN JACOBUS JOHANNES MARIA (NL); UNIV ERASMUS (NL)
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Best Local Similarity 100.0%; Pred. No. 0;
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Qy 1 g 1
Db 1 G 1

RESULT 27
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DEFINITION Sequence 18 from Patent WO0116366.
ACCESSION AX092457
VERSION AX092457.1 GI:13444552
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 3)
AUTHORS Kless,H.
TITLE Template-dependent nucleic acid polymerization using oligonucleotide triphosphates building blocks
JOURNAL Patent: WO 0116366-A 18 08-MAR-2001;
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar (IL)
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Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
Db 3 G 3

RESULT 28
LOCUS AX092458 AX092458 3 bp DNA linear PAT 21-MAR-2001
DEFINITION Sequence 19 from Patent WO0116366.
ACCESSION AX092458
VERSION AX092458.1 GI:13444553
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 3)
AUTHORS Kless,H.
TITLE Template-dependent nucleic acid polymerization using oligonucleotide triphosphates building blocks
JOURNAL Patent: WO 0116366-A 19 08-MAR-2001;
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar (IL)
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Qy 1 g 1
Db 3 G 3

RESULT 29
LOCUS AX092460/c AX092460 3 bp DNA linear PAT 21-MAR-2001
DEFINITION Sequence 21 from Patent WO0116366.
ACCESSION AX092460
VERSION AX092460.1 GI:13444555
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 3)
AUTHORS Kless,H.
TITLE Template-dependent nucleic acid polymerization using oligonucleotide triphosphates building blocks
JOURNAL Patent: WO 0116366-A 21 08-MAR-2001;
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar (IL)
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BASE COUNT 2 a 1 c 0 g 0 t
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Qy 1 g 1
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 Db 2 G 2

RESULT 30
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 LOCUS AX092461 3 bp DNA linear PAT 21-MAR-2001
 DEFINITION Sequence 22 from Patent WO0116366.
 ACCESSION AX092461
 VERSION AX092461.1 GI:13444556
 KEYWORDS
 SOURCE
 ORGANISM
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 unclassified.
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 1 (bases 1 to 3)
 Kless,H.
 Template-dependent nucleic acid polymerization using
 oligonucleotide triphosphates building blocks
 Patent: WO 0116366-A 22 08-MAR-2001;
 JOURNAL YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar
 (IL)

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Qy 1 g 1
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 Db 3 G 3

RESULT 31
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 LOCUS AX092462 3 bp DNA linear PAT 21-MAR-2001
 DEFINITION Sequence 23 from Patent WO0116366.
 ACCESSION AX092462
 VERSION AX092462.1 GI:13444557
 KEYWORDS
 SOURCE
 ORGANISM
 unclassified.
 unclassified.
 unclassified.
 1 (bases 1 to 3)
 Kless,H.
 Template-dependent nucleic acid polymerization using
 oligonucleotide triphosphates building blocks
 Patent: WO 0116366-A 23 08-MAR-2001;
 JOURNAL YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar
 (IL)

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 Location/Qualifiers
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Qy 1 g 1
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 Db 3 G 3

RESULT 32
 AX092462/c
 LOCUS AX092462 3 bp DNA linear PAT 21-MAR-2001
 DEFINITION Sequence 23 from Patent WO0116366.
 ACCESSION AX092462
 VERSION AX092462.1 GI:13444557
 KEYWORDS
 SOURCE
 ORGANISM
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 unclassified.
 1 (bases 1 to 3)
 Kless,H.
 Template-dependent nucleic acid polymerization using
 oligonucleotide triphosphates building blocks
 Patent: WO 0116366-A 23 08-MAR-2001;
 JOURNAL YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar
 (IL)

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 Location/Qualifiers
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 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
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 Db 2 G 2

RESULT 33
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 LOCUS AX092463 3 bp DNA linear PAT 21-MAR-2001
 DEFINITION Sequence 24 from Patent WO0116366.
 ACCESSION AX092463
 VERSION AX092463.1 GI:13444558
 KEYWORDS
 SOURCE
 ORGANISM
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 1 (bases 1 to 3)
 Kless,H.
 Template-dependent nucleic acid polymerization using
 oligonucleotide triphosphates building blocks
 Patent: WO 0116366-A 24 08-MAR-2001;
 JOURNAL YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar
 (IL)

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Best Local Similarity 100.0%; Pred. No. 0;
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Qy 1 g 1
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Db 2 G 2

RESULT 34
AX092464 LOCUS AX092464 3 bp DNA linear PAT 21-MAR-2001
DEFINITION Sequence 25 from Patent WO0116366.
ACCESSION AX092464
VERSION AX092464.1 GI:13444559
KEYWORDS
SOURCE .
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 3)
AUTHORS Kless, H.
TITLE Template-dependent nucleic acid polymerization using
JOURNAL oligonucleotide triphosphates building blocks
PATENT: WO 0116366-A 25 08-MAR-2001;
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar
(IL)
FEATURES
Source Location/Qualifiers
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/note="synthetic oligonucleotide;"
BASE COUNT 2 a 0 c 1 g 0 t
ORIGIN

Query Match 100.0%; Score 1; DB 6; Length 3;
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Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
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Db 2 G 2

RESULT 35
AX092465 LOCUS AX092465 3 bp DNA linear PAT 21-MAR-2001
DEFINITION Sequence 26 from Patent WO0116366.
ACCESSION AX092465
VERSION AX092465.1 GI:13444560
KEYWORDS
SOURCE .
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 3)
AUTHORS Kless, H.
TITLE Template-dependent nucleic acid polymerization using
JOURNAL oligonucleotide triphosphates building blocks
PATENT: WO 0116366-A 26 08-MAR-2001;
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar
(IL)
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/note="synthetic oligonucleotide;"
BASE COUNT 1 a 1 c 1 g 0 t
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Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
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Db 2 G 2

RESULT 36
AX092465/c LOCUS AX092465 3 bp DNA linear PAT 21-MAR-2001
DEFINITION Sequence 26 from Patent WO0116366.
ACCESSION AX092465
VERSION AX092465.1 GI:13444560
KEYWORDS
SOURCE .
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 3)
AUTHORS Kless, H.
TITLE Template-dependent nucleic acid polymerization using
JOURNAL oligonucleotide triphosphates building blocks
PATENT: WO 0116366-A 26 08-MAR-2001;
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar
(IL)
FEATURES
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/note="synthetic oligonucleotide;"
BASE COUNT 1 a 1 c 1 g 0 t
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Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
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Db 3 G 3

RESULT 37
AX092466 LOCUS AX092466 3 bp DNA linear PAT 21-MAR-2001
DEFINITION Sequence 27 from Patent WO0116366.
ACCESSION AX092466
VERSION AX092466.1 GI:13444561
KEYWORDS
SOURCE .
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 3)
AUTHORS Kless, H.
TITLE Template-dependent nucleic acid polymerization using
JOURNAL oligonucleotide triphosphates building blocks
PATENT: WO 0116366-A 27 08-MAR-2001;
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar
(IL)
FEATURES
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Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
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Db 2 G 2

RESULT 38
AX092466 LOCUS AX092466 3 bp DNA linear PAT 21-MAR-2001
DEFINITION Sequence 27 from Patent WO0116366.
ACCESSION AX092466
VERSION AX092466.1 GI:13444561
KEYWORDS
SOURCE .
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 3)
AUTHORS Kless, H.
TITLE Template-dependent nucleic acid polymerization using
JOURNAL oligonucleotide triphosphates building blocks
PATENT: WO 0116366-A 27 08-MAR-2001;
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar
(IL)
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Db 2 G 2

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RESULT 38
AX092467
LOCUS AX092467 3 bp DNA linear PAT 21-MAR-2001
DEFINITION Sequence 28 from Patent WO0116366.
ACCESSION AX092467
VERSION AX092467.1 GI:13444562
KEYWORDS
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REFERENCE
AUTHORS
TITLE
JOURNAL
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Location/Qualifiers
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/note="synthetic oligonucleotide;"
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
Db 2 G 2

RESULT 39
AX092469/c
LOCUS AX092469 3 bp DNA linear PAT 21-MAR-2001
DEFINITION Sequence 30 from Patent WO0116366.
ACCESSION AX092469
VERSION AX092469.1 GI:13444564
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
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Location/Qualifiers
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Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
Db 3 G 3

RESULT 40
AX092473/c
LOCUS AX092473 3 bp DNA linear PAT 21-MAR-2001
DEFINITION Sequence 34 from Patent WO0116366.

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AX092470
LOCUS AX092470 3 bp DNA linear PAT 21-MAR-2001
DEFINITION Sequence 31 from Patent WO0116366.
ACCESSION AX092470
VERSION AX092470.1 GI:13444565
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
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Db 3 G 3

RESULT 41
AX092472/c
LOCUS AX092472 3 bp DNA linear PAT 21-MAR-2001
DEFINITION Sequence 33 from Patent WO0116366.
ACCESSION AX092472
VERSION AX092472.1 GI:13444567
KEYWORDS
SOURCE
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REFERENCE
AUTHORS
TITLE
JOURNAL
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/note="synthetic oligonucleotide;"
BASE COUNT 2 a 1 c 0 g 0 t
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 g 1
Db 1 G 1

RESULT 42
AX092473/c
LOCUS AX092473 3 bp DNA linear PAT 21-MAR-2001
DEFINITION Sequence 34 from Patent WO0116366.

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VERSION        AX092473.1  GI:13444568
KEYWORDS
SOURCE         unidentified.
ORGANISM       unclassified.
REFERENCE      1 (bases 1 to 3)
AUTHORS       Kless,H.
TITLE         Template-dependent nucleic acid polymerization using
              oligonucleotide triphosphates building blocks
JOURNAL        Patent: WO 0116366-A 34 08-MAR-2001;
              YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar
              (IL)
FEATURES       source
              Location/Qualifiers
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                /note="synthetic oligonucleotide;"
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Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 g 1
Db 3 g 3
RESULT 43
AX092474
LOCUS          AX092474          3 bp      DNA      linear      PAT 21-MAR-2001
DEFINITION     Sequence 35 from Patent WO0116366.
ACCESSION      AX092474
VERSION        AX092474.1  GI:13444569
KEYWORDS
SOURCE         unidentified.
ORGANISM       unclassified.
REFERENCE      1 (bases 1 to 3)
AUTHORS       Kless,H.
TITLE         Template-dependent nucleic acid polymerization using
              oligonucleotide triphosphates building blocks
JOURNAL        Patent: WO 0116366-A 35 08-MAR-2001;
              YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar
              (IL)
FEATURES       source
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Qy 1 g 1
Db 3 g 3
RESULT 44
AX092474/c
LOCUS          AX092474/c      3 bp      DNA      linear      PAT 21-MAR-2001
DEFINITION     Sequence 35 from Patent WO0116366.
ACCESSION      AX092474
VERSION        AX092474.1  GI:13444569
KEYWORDS
SOURCE         unidentified.
ORGANISM       unclassified.
REFERENCE      1 (bases 1 to 3)
AUTHORS       Kless,H.
TITLE         Template-dependent nucleic acid polymerization using
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JOURNAL        Patent: WO 0116366-A 35 08-MAR-2001;
              YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar
              (IL)
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Qy 1 g 1
Db 3 g 3
RESULT 45
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LOCUS          AX092475          3 bp      DNA      linear      PAT 21-MAR-2001
DEFINITION     Sequence 36 from Patent WO0116366.
ACCESSION      AX092475
VERSION        AX092475.1  GI:13444570
KEYWORDS
SOURCE         unidentified.
ORGANISM       unclassified.
REFERENCE      1 (bases 1 to 3)
AUTHORS       Kless,H.
TITLE         Template-dependent nucleic acid polymerization using
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JOURNAL        Patent: WO 0116366-A 36 08-MAR-2001;
              YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL) ; Kless, Hadar
              (IL)
FEATURES       source
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Job time: 24541 sec
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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 15, 2002, 20:07:24 ; Search time 7067.1 seconds
(without alignments)
578.678 Million cell updates/sec

Title: US-09-375-248-1_COPY_2546_2848
Perfect score: 303
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Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 13736207 seqs, 6748477542 residues

Word size : 0

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0
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Post-processing: Listing first 45 summaries

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- 3: em_estin:*
- 4: em_estnu:*
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- 15: em_gss_pln:*
- 16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	24	7.9	270	10	R86469
5	24	7.9	309	10	R86465
6	24	7.9	314	10	R86522
7	24	7.9	1036	10	B1100914
8	23	7.6	441	10	RG384720
9	23	7.6	512	10	RG384715
10	21	6.9	488	10	BF652351
11	21	6.9	498	10	BF652352
12	21	6.9	531	10	BM482403
13	21	6.9	538	9	AV601195
14	21	6.9	544	9	AV601196
15	20	6.6	293	10	W57847
16	20	6.6	434	10	B1182263
17	20	6.6	558	10	BM261245

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20	20	6.6	856	10	BG746729
21	20	6.6	862	10	BG615859
22	20	6.6	864	10	B1763816
23	20	6.6	885	10	BM048480
24	19	6.3	201	10	BF927018
25	19	6.3	208	10	BF925651
26	19	6.3	1257	10	B1524514
27	18	5.9	244	9	AV321924
28	18	5.9	261	10	BM241884
29	18	5.9	271	10	BM409650
30	18	5.9	319	9	AW009058
31	18	5.9	360	12	AQ216651
32	18	5.9	369	9	AI744037
33	18	5.9	470	10	BE460395
34	18	5.9	478	12	BH392477
35	18	5.9	480	10	B1405811
36	18	5.9	498	10	BG767090
37	18	5.9	498	10	BM417681
38	18	5.9	505	10	BM089435
39	18	5.9	509	12	AQ154758
40	18	5.9	512	10	BE435943
41	18	5.9	517	10	BG280611
42	18	5.9	521	10	BF265245
43	18	5.9	524	10	BM410739
44	18	5.9	525	10	BF513456
45	18	5.9	528	10	BH187298

ALIGNMENTS

RESULT 1	AA367842	284 bp	mRNA	linear	EST 21-APR-1997
LOCUS	EST79262	Placenta I Homo sapiens	cDNA similar to tyrosine kinase,		
DEFINITION	receptor FLT4, class III, mRNA sequence.				
ACCESSION	AA367842				
VERSION	AA367842.1	GI:2020386			
KEYWORDS	EST.				
SOURCE	human.				
ORGANISM	Homo sapiens				

REFERENCE	1 (bases 1 to 284)
AUTHORS	Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A., Bult

ADDITIONAL	Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A., Bult
ADDITIONAL	,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D., White
ADDITIONAL	,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C., Clayton,R.A.,
ADDITIONAL	Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D., Fitzgerald
ADDITIONAL	,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S., Glodak,A.,
ADDITIONAL	Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S., Jr., Kelley,J.M.,
ADDITIONAL	Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M.,
ADDITIONAL	Moreno-Palauques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M.,
ADDITIONAL	Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R.,
ADDITIONAL	Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y.,
ADDITIONAL	Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,
ADDITIONAL	Dimke,D., Feng,D.-F., Ferrile,A., Fischer,C., Hastings,G.A., He,W.W.
ADDITIONAL	,Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K., Kozak,D.L.,
ADDITIONAL	Kunsch,C., Hungjun,J., Li,H., Weissner,P.S., Olsen,H., Raymond,L.,
ADDITIONAL	Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M., Dillon,P.J., Fannon
ADDITIONAL	,M.R., Rosen,C.A., Haseltine,W.A., Fields,C., Fraser,C.M. and
ADDITIONAL	Venter,J.C.

TITLE	Initial assessment of human gene diversity and expression patterns
JOURNAL	based upon 83 million nucleotides of cDNA sequence
MEDLINE	Nature 377 (6547 Suppl), 3-174 (1995)
COMMENT	Other ESTs: 96026280
COMMENT	Contact: Kerlavage, AR
COMMENT	Bioinformatics
COMMENT	The Institute for Genomic Research
COMMENT	9712 Medical Center Drive, Rockville, MD 20850 USA
COMMENT	Tel: 3018699056

Fax: 3018699423

Email: arkerlav@tigr.org

For clone availability, additional sequence and expression

information related to this EST, please check the TIGR Human Gene

Index (<http://www.tigr.org/tdb/hgi/hgi.html>)

Seq primer: M13-21.

FEATURES

Location/Qualifiers

1..284
/organism="Homo sapiens"
/db_xref="ATCC (inhost):172752"
/db_xref="taxon:9606"
/clone_lib="Placenta 1"
/tissue_type="placenta"
/dev_stage="fetus"
/note="Organ: placenta; Vector: pBluescript SK-; Site:1:
EcoRI; Site_2: EcoRI"

BASE COUNT 56 a 91 c 91 g 46 t
ORIGIN

Query Match 60.7%; Score 184; DB 9; Length 284;
Best Local Similarity 99.6%; Pred. No. 1.3e-81;
Matches 234; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 gagcgctgcacctgggagagtgctcgctacgcgccttcggaaagtgtggaagcc 60

|||||
Db 6 GAGCGCTGCGACCTGGGAGAGTGTCTCGCTACGGCGCTTCGGGAAGGTGGTGAAGCC 65

Qy 61 Lccgcttcgcgcacccacaaagggcagcagctgtgacacgltggcgtgaaatgctgaaa 120

|||||
Db 66 TCCCGTTTCGGCATCCACGAGGCGGACAGCTGTGACACCGTGGCGTGCAAAATGCTGAAA 125

Qy 121 gagggcgccagggcagcagcagccgcgcgtgtgtcggagctcgaagatcctcattcac 180

|||||
Db 126 GAGGGCGCCAGCGGCGAGCCAGCACCGCGCGCTGTGTCTGGAGCTCAAGATCCTCATTTCC 185

Qy 181 atcggcaaccactcaacgtgtgtaacctctcggcggtgcacacgaagccagcag 235

|||||
Db 186 ATCGGCACACCACTCAACGTGTCNAACCTCTCGGGGCGTGCACCAAGCCGCGAG 240

RESULT 2

LOCUS BM285802 448 bp mRNA linear EST 28-DEC-2001
DEFINITION 524533 MARC 3BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION BM285802
VERSION BM285802.1 GI:17994828
KEYWORDS EST.
SOURCE cow.

ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.
1 (bases 1 to 448)
Smith, T.P.L., Grosse, M., Freking, B.A., Roberts, A.J., Stone, R.T.,
Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett,
G.L., Heaton, M.P., Laegreid, W., Rohrer, G.A., Chitko-McKown, C.G.,
Perte, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and
Keene, J.W.

TITLE Sequence evaluation of four pooled-tissue normalized bovine cDNA
libraries and construction of a gene index for cattle
JOURNAL Genome Res. 11 (4), 626-630 (2001)
MEDLINE 21180013

COMMENT Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390

Email: smith@email.marc.usda.gov

Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
PCR Primers

FORWARD: AGGAACAGCCTATGACCAT

BACKWARD: GTTTCCTCCAGTCAGCAGC

Plate: 130 row: 0 column: 20

Seq primer: ATTTAGGTGACACTATAG.

Location/Qualifiers

1..448

/organism="Bos taurus"

/db_xref="taxon:9913"

/clone_lib="MARC 3BOV"

/tissue_type="pooled"

/lab_host="DH10B"

/note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI;

Library made from pooled tissue from marrow, alveolar,

macrophage, ovary, fetal semitendinosus muscle, and fetal

longissimus muscle."

BASE COUNT 104 a 134 c 131 g 78 t 1 others
ORIGIN

Query Match 10.6%; Score 32; DB 10; Length 448;
Best Local Similarity 100.0%; Pred. No. 2e-05;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 100 gtggccgtgaaatgctgaaagagggcgccac 131

|||||
Db 42 GTGCCGTGAAATGCTGAAAGAGGGCGCCAC 73

RESULT 3

LOCUS R86582

DEFINITION R86582 233 bp mRNA linear EST 17-AUG-1995

cdna clone pRABOC157 5' similar to c-fms, mRNA sequence.

ACCESSION R86582

VERSION R86582.1 GI:947236

KEYWORDS EST.

SOURCE rabbit.

ORGANISM Oryctolagus cuniculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.

REFERENCE 1 (bases 1 to 233)

AUTHORS Sakai, D., Tong, H.-S. and Minkin, C.

TITLE Osteoclast Molecular Phenotyping by Random cDNA Sequencing

JOURNAL Bone 17 (2), 111-119 (1995)

MEDLINE 96021365

COMMENT Other_ESTS: RABEST035T, RABEST040T, RABEST075T

Contact: Sakai D

Basic Sciences

University of Southern California

USC School of Dentistry, 925 West 34th Street, DEN-4220, Los

Angeles, CA 90089-0641

Tel: 2137405563

Fax: 2137407560

Email: sakai@molbio.usc.edu

Seq primer: T7 promoter.

Location/Qualifiers

1..233

/organism="Oryctolagus cuniculus"

/strain="New Zealand White"

/db_xref="taxon:9986"

/clone="pRABOC157"

/clone_lib="Rabbit Osteoclast, Dennis Sakai"

/lab_host="E. coli DH12S"

/note="Vector: pSPORT1; Site_1: SalI; Site_2: NotI; Poly(A

) + RNA was purified from a 97% pure population of

osteoclasts prepared from the long bones of 10 day old

rabbits. First strand cDNA was synthesized by priming

with an oligo(dT)-NotI anchor-primer and second strand

cDNA was synthesized by replacement synthesis as described

by Gubler and Hoffman (Gene 25:283, 1983). Following the

addition of SalI adapters and NotI digestion, the cDNA was

cloned between the SalI (50) and NotI (30) sites of the

pSPORT1 (BRL) plasmid vector."

BASE COUNT 53 a 61 c 79 g 40 t

Query Match 7.9%; Score 24; DB 10; Length 233;
Best Local Similarity 100.0%; Pred. No. 0.18; Mismatches 0; Indels 0; Gaps 0;
Matches 24; Conservative 0

Qy 33 cggcgcccttcgggaagtggtgga 56
|||||
Db 75 CGGCGCCTTCGGGAAGTGCTGGA 98

RESULT 4

R86469 270 bp mRNA linear EST 17-AUG-1995
LOCUS RABEST040T Rabbit Osteoclast, Dennis Sakai Oryctolagus cuniculus
DEFINITION cDNA clone PRABOC040 5' similar to c-fms, mRNA sequence.

ACCESSION R86469
VERSION R86469.1 GI:947151
KEYWORDS EST.
SOURCE rabbit.
ORGANISM Oryctolagus cuniculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.

REFERENCE 1 (bases 1 to 270)
AUTHORS Sakai,D., Tong,H.-S. and Minkin,C.
TITLE Osteoclast Molecular Phenotyping by Random cDNA Sequencing
JOURNAL Bone 17 (2), 111-119 (1995)
MEDLINE 96021365

COMMENT Other_ESTs: RABEST035T, RABEST075T, RABEST157T
Contact: Sakai D
Basic Sciences
University of Southern California
USC School of Dentistry, 925 West 34th Street, DEN-4220, Los Angeles, CA 90089-0641
Tel: 2137407560
Fax: 2137407560
Email: sakai@molbio.usc.edu
Seq primer: T7 promoter.
Location/Qualifiers
1. .270
/organism="Oryctolagus cuniculus"
/strain="New Zealand White"
/db_xref="taxon:9986"
/clone_lib="Rabbit Osteoclast, Dennis Sakai"
/lab_host="E. coli DH12S"
/note="vector: pSPORT1; Site_1: Sali; Site_2: NotI; Poly(A)+ RNA was purified from a 97% pure population of osteoclasts prepared from the long bones of 10 day old rabbits. First strand cDNA was synthesized by priming with an oligo(dT)-NotI anchor-primer and second strand cDNA was synthesized by replacement synthesis as described by Gubler and Hoffman (Gene 25:283, 1983). Following the addition of Sali adapters and NotI digestion, the cDNA was cloned between the Sali (50) and NotI (30) sites of the pSPORT1 (BRL) plasmid vector."

BASE COUNT 62 a 73 c 89 g 46 t

Query Match 7.9%; Score 24; DB 10; Length 270;
Best Local Similarity 100.0%; Pred. No. 0.18; Mismatches 0; Indels 0; Gaps 0;
Matches 24; Conservative 0

Qy 33 cggcgcccttcgggaagtggtgga 56
|||||
Db 74 CGGCGCCTTCGGGAAGTGCTGGA 97

RESULT 5

R86465 314 bp mRNA linear EST 17-AUG-1995
LOCUS RABEST075T Rabbit Osteoclast, Dennis Sakai Oryctolagus cuniculus
DEFINITION cDNA clone PRABOC075 5' similar to c-fms, mRNA sequence.

ACCESSION R86522
VERSION R86522.1 GI:947328
KEYWORDS EST.
SOURCE rabbit.
ORGANISM Oryctolagus cuniculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.

REFERENCE 1 (bases 1 to 314)
AUTHORS Sakai,D., Tong,H.-S. and Minkin,C.
TITLE Osteoclast Molecular Phenotyping by Random cDNA Sequencing
JOURNAL Bone 17 (2), 111-119 (1995)
MEDLINE 96021365

R86465 309 bp mRNA linear EST 17-AUG-1995
LOCUS RABEST035T Rabbit Osteoclast, Dennis Sakai Oryctolagus cuniculus
DEFINITION cDNA clone PRABOC035 5' similar to c-fms, mRNA sequence.

ACCESSION R86465
VERSION R86465.1 GI:947147
KEYWORDS EST.
SOURCE rabbit.
ORGANISM Oryctolagus cuniculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.

REFERENCE 1 (bases 1 to 309)
AUTHORS Sakai,D., Tong,H.-S. and Minkin,C.
TITLE Osteoclast Molecular Phenotyping by Random cDNA Sequencing
JOURNAL Bone 17 (2), 111-119 (1995)
MEDLINE 96021365

COMMENT Other_ESTs: RABEST040T, RABEST075T, RABEST157T
Contact: Sakai D
Basic Sciences
University of Southern California
USC School of Dentistry, 925 West 34th Street, DEN-4220, Los Angeles, CA 90089-0641
Tel: 2137405563
Fax: 2137407560
Email: sakai@molbio.usc.edu
Seq primer: T7 promoter.
Location/Qualifiers
1. .309
/organism="Oryctolagus cuniculus"
/strain="New Zealand White"
/db_xref="taxon:9986"
/clone_lib="Rabbit Osteoclast, Dennis Sakai"
/lab_host="E. coli DH12S"
/note="vector: pSPORT1; Site_1: Sali; Site_2: NotI; Poly(A)+ RNA was purified from a 97% pure population of osteoclasts prepared from the long bones of 10 day old rabbits. First strand cDNA was synthesized by priming with an oligo(dT)-NotI anchor-primer and second strand cDNA was synthesized by replacement synthesis as described by Gubler and Hoffman (Gene 25:283, 1983). Following the addition of Sali adapters and NotI digestion, the cDNA was cloned between the Sali (50) and NotI (30) sites of the pSPORT1 (BRL) plasmid vector."

BASE COUNT 68 a 81 c 102 g 58 t

Query Match 7.9%; Score 24; DB 10; Length 309;
Best Local Similarity 100.0%; Pred. No. 0.19; Mismatches 0; Indels 0; Gaps 0;
Matches 24; Conservative 0

Qy 33 cggcgcccttcgggaagtggtgga 56
|||||
Db 74 CGGCGCCTTCGGGAAGTGCTGGA 97

RESULT 6

R86522 314 bp mRNA linear EST 17-AUG-1995
LOCUS RABEST075T Rabbit Osteoclast, Dennis Sakai Oryctolagus cuniculus
DEFINITION cDNA clone PRABOC075 5' similar to c-fms, mRNA sequence.

ACCESSION R86522
VERSION R86522.1 GI:947328
KEYWORDS EST.
SOURCE rabbit.
ORGANISM Oryctolagus cuniculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.

REFERENCE 1 (bases 1 to 314)
AUTHORS Sakai,D., Tong,H.-S. and Minkin,C.
TITLE Osteoclast Molecular Phenotyping by Random cDNA Sequencing
JOURNAL Bone 17 (2), 111-119 (1995)
MEDLINE 96021365

COMMENT Other_ESTs: RABEST035T, RABEST040T, RABEST157T

Contact: Sakai D
Basic Sciences
University of Southern California
USC School of Dentistry, 925 West 34th Street, DEN-4220, Los
Angeles, CA 90089-0641
Tel: 2137405563
Fax: 2137407560
Email: sakai@molbio.usc.edu
Seq primer: T7 promoter.

FEATURES Location/Qualifiers

source 1..314

/organism="Oryctolagus cuniculus"
/strain="New Zealand White"
/db_xref="taxon:9986"
/clone="pRABOC075"
/lab_host="E. coli DH12S"
/note="Vector: pSPORT1; site_1: SalI; site_2: NotI; Poly(A)
) + RNA was purified from a 97% pure population of
osteoclasts prepared from the long bones of 10 day old
rabbits. First strand cDNA was synthesized by priming
with an oligo(dT)-NotI anchor-primer and second strand
cDNA was synthesized by replacement synthesis as described
by Gubler and Hoffman (Gene 25:283, 1983). Following the
addition of SalI adapters and NotI digestion, the cDNA was
cloned between the SalI (50) and NotI (30) sites of the
pSPORT1 (BRL) plasmid vector."

BASE COUNT 71 a 79 c 103 g 60 t 1 others

ORIGIN

Query Match

Best Local Similarity 7.9%; Score 24; DB 10; Length 314;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 33 cggcgccctcgggaagggtggga 56

|||||

Db 59 CGCGCCCTTCGGGAAGGTGGTGA 82

RESULT 7

B1100914

LOCUS B1100914 1036 bp mRNA linear EST 26-JUN-2001

DEFINITION 60286236P1 NCI_CGAP_Kid14 Mus musculus cDNA clone IMAGE:5041569

5', mRNA sequence.

ACCESSION B1100914

VERSION B1100914.1 GI:14551807

KEYWORDS EST.

SOURCE house mouse.

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 1036)

TITLE NIH-MGC http://mgc.nci.nih.gov/.

JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)

COMMENT Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Jeffrey E. Green, M.D.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAM1114 row: g column: 10

High quality sequence stop: 308.

Location/Qualifiers

source 1..1036

/organism="Mus musculus"

/strain="FVB/N"

/db_xref="taxon:10090"

/clone="IMAGE:5041569"

/lab_host="NCI_CGAP_Kid14"

/note="DH10B (T1 phage-resistant)"

/note="Organ: kidney; Vector: pCMV-SPORT6; Site_1: NotI;

Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.

Average insert size 1.75 kb. Constructed by Life

Technologies. Note: this is a NCI_CGAP Library. |"

BASE COUNT 322 a 247 c 298 g 169 t

ORIGIN

Query Match

Best Local Similarity 7.9%; Score 24; DB 10; Length 1036;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 42 cgggaaggtggtggaagcctccgc 65

|||||

Db 397 CGGGAAGGTGTTGGAAGCCTCCGC 420

RESULT 8

BG384720

LOCUS BG384720 441 bp mRNA linear EST 12-MAR-2001

DEFINITION 303961 MARC lPTG Sus scrofa cDNA 5', mRNA sequence.

ACCESSION BG384720

VERSION BG384720.1 GI:13309192

KEYWORDS EST.

SOURCE pig.

ORGANISM Sus scrofa

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

REFERENCE 1 (bases 1 to 441)

AUTHORS Fahrenkrug,S.C., Freking,B.A., Rohrer,G.A., Smith,T.P.L., Casas,E.,

Stone,R.T., Heaton,M.P., Grosse,W.M., Bennett,G.A., Laegreid,W.W.

and Keele,J.W.

Design and use of two pooled tissue normalized cDNA libraries for

EST discovery in swine

Unpublished (2000)

Contact: Smith TPL

PO Box 166, Clay Center, NE 68933-0166, USA

Tel: 402 762 4366

Fax: 402 762 4390

Email: smith@email.marc.usda.gov

Single pass sequencing. Bases called and alt-trimmed with phred

v0.980904.e. Vector identified by cross_match with the -minscore 18

and -minmatch 12 options.

PCR primers

FORWARD: AGGAACAGCTATGACCAT

BACKWARD: GTTTCCTCAGTCACGCG

Plate: 92 row: C column: 14

Seq primer: ATTAGGTGACACTATAG.

Location/Qualifiers

source 1..441

/organism="Sus scrofa"

/db_xref="taxon:9823"

/clone_lib="MARC lPTG"

/tissue_type="pooled"

/lab_host="DH10B"

/note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI;

Library made from pooled tissue from day 11, 13, 15, 20,

and 30 embryos."

BASE COUNT 122 a 110 c 120 g 89 t

ORIGIN

Query Match

Best Local Similarity 7.6%; Score 23; DB 10; Length 441;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 109 aaatgctgaaagagggcgccac 131

|||||

Db 218 AAAATGCTGAAGAGGCGCCAC 240

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RESULT 9
BG384715          512 bp  mRNA  linear  EST 12-MAR-2001
LOCUS
DEFINITION       303951 MARC 1PIG Sus scrofa cDNA 5', mRNA sequence.
ACCESSION        BG384715
VERSION          BG384715.1 GI:13309187
KEYWORDS         EST.
SOURCE           pig.
ORGANISM         Sus scrofa
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE
AUTHORS          Fahrenkrug, S.C., Freking, B.A., Rohrer, G.A., Smith, T.P.L., Casas, E.,
Stone, K.T., Heaton, M.P., Grosse, W.M., Bennett, G.A., Laegreid, W.W.,
and Keele, J.W.
TITLE            Design and use of two pooled tissue normalized cDNA libraries for
EST discovery in swine
JOURNAL
COMMENT          Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@mail.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
PCR Primers
FORWARD: AGGAACAGCTATGACCAT
BACKWARD: GTTTTCCCAGTCACGACG
Plate: 92 row: A column: 16
Seq primer: ATTTAGTGACACTATAG.
FEATURES
source
1..512
/organism="Sus scrofa"
/db_xref="taxon:9823"
/clone_lib="MARC 1PIG"
/tissue_type="pooled"
/lab_host="DH10B"
/notice="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI;
Library made from pooled tissue from day 11, 13, 15, 20,
and 30 embryos."
BASE COUNT      146 a 128 c 144 g 94 t
ORIGIN
1..512
/organism="Sus scrofa"
/db_xref="taxon:9823"
/clone_lib="MARC 1PIG"
/tissue_type="pooled"
/lab_host="DH10B"
/notice="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI;
Library made from pooled tissue from day 11, 13, 15, 20,
and 30 embryos."
Query Match      7.6%; Score 23; DB 10; Length 512;
Best Local Similarity 100.0%; Pred. No. 0.68;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 109 aaatgctgaaagaggcgccac 131
|||||
Db 188 AAAATGCTGAAAGAGGCGCCAC 210

RESULT 10
BF652351          498 bp  mRNA  linear  EST 25-APR-2001
LOCUS
DEFINITION       273882 MARC 3BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION        BF652351
VERSION          BF652351.1 GI:11917481
KEYWORDS         EST.
SOURCE           cow.
ORGANISM         Bos taurus
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.
REFERENCE
AUTHORS          Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T.,
Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett
, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-Mckown, C.G.,
and Keele, J.W.
TITLE            Sequence evaluation of four pooled-tissue normalized bovine cDNA
libraries and construction of a gene index for cattle
JOURNAL
COMMENT          Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@mail.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred

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Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J., and
Keele, J.W.
Sequence evaluation of four pooled-tissue normalized bovine cDNA
libraries and construction of a gene index for cattle
Genome Res. 11 (4), 626-630 (2001)
21180013
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@mail.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
PCR Primers
FORWARD: AGGAACAGCTATGACCAT
BACKWARD: GTTTTCCCAGTCACGACG
Plate: 65 row: N column: 7
Seq primer: ATTTAGTGACACTATAG.
FEATURES
source
1..498
/organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="MARC 3BOV"
/tissue_type="pooled"
/lab_host="DH10B"
/notice="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI;
Library made from pooled tissue from marrow, alveolar
macrophage, ovary, fetal semitendinosus muscle, and fetal
longissimus muscle."
BASE COUNT      108 a 149 c 149 g 92 t
ORIGIN
1..498
/organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="MARC 3BOV"
/tissue_type="pooled"
/lab_host="DH10B"
/notice="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI;
Library made from pooled tissue from marrow, alveolar
macrophage, ovary, fetal semitendinosus muscle, and fetal
longissimus muscle."
Query Match      6.9%; Score 21; DB 10; Length 498;
Best Local Similarity 100.0%; Pred. No. 6.8;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 cgcgccttcgggaagtgtgt 53
|||||
Db 394 CGCGCCTTCGGGAAGGTGTGT 414

RESULT 11
BF652352          498 bp  mRNA  linear  EST 25-APR-2001
LOCUS
DEFINITION       275883 MARC 3BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION        BF652352
VERSION          BF652352.1 GI:11917482
KEYWORDS         EST.
SOURCE           cow.
ORGANISM         Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.
REFERENCE
AUTHORS          Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T.,
Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett
, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-Mckown, C.G.,
Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J., and
Keele, J.W.
TITLE            Sequence evaluation of four pooled-tissue normalized bovine cDNA
libraries and construction of a gene index for cattle
JOURNAL
COMMENT          Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@mail.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred

```

v0.980904.e. Vector identified by cross_match with the -minscore 18 and -minmatch 12 options.

PCR Primers

FORWARD: AGGAACACGCTATGACCAT

BACKWARD: GTTTTCCAGTCAGCAGC

Plate: 65 row: N column: 8

Seq primer: ATTTAGTGACACTATAG.

Location/Qualifiers

FEATURES

source

1..498

/organism="Bos taurus"

/db_xref="taxon:9913"

/clone_lib="MARC 3BOV"

/tissue_type="pooled"

/lab_host="DH10B"

/note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI;

Library made from pooled tissue from marrow, alveolar

macrophage, ovary, fetal semitendinosus muscle, and fetal

longissimus muscle."

108 a 149 c 149 g 92 t

BASE COUNT

ORIGIN

Query Match 6.9%; Score 21; DB 10; Length 498;

Best Local Similarity 100.0%; Pred. No. 6.8;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 33 cggcgccctcgggaagtggt 53

|||||

Db 394 CGCGCCCTTCGGGAAGTGGT 414

RESULT 12

BM482403

LOCUS

DEFINITION 531 bp mRNA linear EST 05-FEB-2002

ACCESSION 535280 MARC 3BOV Bos taurus cDNA 5', mRNA sequence.

VERSION BM482403.1 GI:18532731

KEYWORDS

SOURCE

ORGANISM

Bos taurus

Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

Bovidae; Bovinae; Bos.

1 (bases 1 to 531)

Smith, T. P. L., Grosse, W. M., Freking, B. A., Roberts, A. J., Stone, R. T.,

Casas, E., Wray, J. E., White, J., Cho, J., Fahrnenkrug, S. C., Bennett

, G. L., Heaton, M. P., Laegreid, W. W., Rohrer, G. A., Chitko-McKown, C. G.,

Perle, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J., and

Keele, J. W.

Sequence evaluation of four pooled-tissue normalized bovine cDNA

libraries and construction of a gene index for cattle

Genome Res. 11 (4), 626-630 (2001)

21180013

Contact: Smith TPL

USDA, ARS, US Meat Animal Research Center

PO Box 166, Clay Center, NE 68933-0166, USA

Tel: 402 762 4366

Fax: 402 762 4390

Email: smith@mail.marc.usda.gov

Single pass sequencing. Bases called and alt_trimmed with phred

v0.980904.e. Vector identified by cross_match with the -minscore 18

and -minmatch 12 options.

PCR Primers

FORWARD: AGGAACACGCTATGACCAT

BACKWARD: GTTTTCCAGTCAGCAGC

Plate: 3 row: I column: 5

Seq primer: ATTTAGTGACACTATAG.

Location/Qualifiers

1..531

/organism="Bos taurus"

/db_xref="taxon:9913"

/clone_lib="MARC 3BOV"

/tissue_type="pooled"

FEATURES

source

Query Match 6.9%; Score 21; DB 9; Length 538;

Best Local Similarity 100.0%; Pred. No. 6.9;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 33 cggcgccctcgggaagtggt 53

|||||

Db 344 CGCGCCCTTCGGGAAGTGGT 324

RESULT 14

/lab_host="DH10B"

/note="vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI;

Library made from pooled tissue from marrow, alveolar

macrophage, ovary, fetal semitendinosus muscle, and fetal

longissimus muscle."

BASE COUNT 91 a 145 c 169 g 125 t 1 others

ORIGIN

Query Match 6.9%; Score 21; DB 10; Length 531;

Best Local Similarity 100.0%; Pred. No. 6.9;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 33 cggcgccctcgggaagtggt 53

|||||

Db 82 CGCGCCCTTCGGGAAGTGGT 102

RESULT 13

AV601195/c

LOCUS

DEFINITION 538 bp mRNA linear EST 27-NOV-2001

3', mRNA sequence.

ACCESSION AV601195

VERSION AV601195.1 GI:9723513

KEYWORDS

SOURCE

ORGANISM

Bos taurus

Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

Bovidae; Bovinae; Bos.

1 (bases 1 to 538)

Takasuga, A., Hirotsune, S., Itoh, R., Jitohzono, A., Suzuki, H., Aso, H.

and Sugimoto, Y.

Establishment of a high throughput EST sequencing system using

poly(A) tail-removed cDNA libraries and determination of 36,000

bovine ESTs

Nucleic Acids Res. 29 (22), E108 (2001)

21570554

Contact: Yoshikazu Sugimoto

Animal Genetics Division

Shirakawa Institute of Animal Genetics

Odakura, Nishigo, Nishi-shirakawa, Fukushima 961-8061, Japan

Tel: 81-248-25-5641

Fax: 81-248-25-5725

Email: kazusugie@ocn.ne.jp

Single pass sequencing.

This clone was obtained from a polyA-deleted cDNA library.

Location/Qualifiers

1..538

/organism="Bos taurus"

/db_xref="taxon:9913"

/clone="EIKI002H06"

/clone_lib="Bos taurus kidney fetus"

/tissue_type="kidney"

/dev_stage="fetus"

/lab_host="DH10B"

/note="Vector: pZL1; Site_1: SalI; Site_2: NotI; Poly A

was deleted from a NotI site"

100 a 158 c 150 g 126 t 4 others

BASE COUNT

ORIGIN

AV601196
LOCUS
DEFINITION AV601196 Bos taurus kidney fetus Bos taurus cDNA clone EIK1002H06
5', mRNA sequence.
ACCESSION AV601196
VERSION AV601196.1 GI:9723514
KEYWORDS EST.
SOURCE cow.
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.
1 (bases 1 to 544)
Takasuga,A., Hirotsune,S., Itoh,R., Jitohzono,A., Suzuki,H., Aso,H.
and Sugimoto,Y.
Establishment of a high throughput EST sequencing system using
poly(A) tail-removed cDNA libraries and determination of 36,000
bovine ESTs
Nucleic Acids Res. 29 (22), E108 (2001)
21570554
Contact: Yoshikazu Sugimoto
Animal Genetics Division
Shirakawa Institute of Animal Genetics
Odakura, Nishi-shirakawa, Fukushima 961-8061, Japan
Tel: 81-248-25-5641
Fax: 81-248-25-5725
Email: kazusugi@ocn.ne.jp
Single pass sequencing.
This clone was obtained from a polyA-deleted cDNA library.
Location/Qualifiers
1..544
/organism="Bos taurus"
/db_xref="taxon:9913"
/clone="EIK1002H06"
/clone_lib="Bos taurus kidney fetus"
/tissue_type="kidney"
/dev_stage="fetus"
/lab_host="DH10B"
/note="vector: pZL1; Site.1: SalI; Site.2: NotI; Poly A
was deleted from a NotI site"

BASE COUNT 126 a 152 c 160 g 105 t 1.others
ORIGIN

Query Match 6.9%; Score 21; DB 9; Length 544;
Best Local Similarity 100.0%; Pred. No. 6.9;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 33 cggcgccctcggaagtggtggt 53
|||||
Db 195 CGGCGCCCTCGGAAGGTGGT 215

RESULT 15
W57847
LOCUS
DEFINITION W57847 293 bp mRNA linear EST 15-OCT-1996
IMAGE:340953 5', mRNA sequence.
ACCESSION W57847
VERSION W57847.1 GI:1364581
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 293)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman
W., Hultman,M., Kucaba,T., Le.M., Lennon,G., Marra,M., Parsons,J.,
Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston
R., Williamson,A., Wohlmann,P. and Wilson,R.
The WashU-Merck EST Project
Unpublished (1995)
Contact: Wilson RK

Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LNL : contact the
IMAGE Consortium (info@image.lnl.gov) for further information..
Insert length: 788 Std Error: 0.00
Seq primer: mob.REGA+ET
High quality sequence stop: 278.
Location/Qualifiers
1..293
/organism="Homo sapiens"
/db_xref="GDB:1266328"
/db_xref="taxon:9606"
/clone="IMAGE:340953"
/clone_lib="Soares_fetal_heart_NBHH19W"
/sex="unknown"
/dev_stage="19 weeks"
/lab_host="DH10B (ampicillin resistant)"
/note="Organ: heart; Vector: pT7T3D (Pharmacia) with a
modified polylinker; Site.1: Not I; Site.2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTTACCAATCTGAAGTGGAGCGCGCATCTTTTCTTTTCTTTT 3'],
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT7T3 vector
(Pharmacia). Library went through one round of
normalization to a Cot = 5. Library constructed by
M.Patima Bonaldo. This library was constructed from the
same fetus as the fetal lung library, Soares fetal lung
NBHH19W."

FEATURES
source

BASE COUNT 71 a 78 c 52 g 89 t 3 others
ORIGIN

Query Match 6.6%; Score 20; DB 10; Length 293;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 101 tggccgtgaaaatgctgaaa 120
|||||
Db 231 TGGCCGTGAAAATGCTGAAA 250

RESULT 16
B1182263
LOCUS
DEFINITION B1182263 434 bp mRNA linear EST 10-JUL-2001
UNL-P-FN-bf-e-12-0-UNL.s1 UNL-P-FN Sus scrofa cDNA clone
UNL-P-FN-bf-e-12-0-UNL 3', mRNA sequence.
ACCESSION B1182263
VERSION B1182263.1 GI:14656672
KEYWORDS EST.
SOURCE pig.
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Sulina; Suidae; Sus.
1 (bases 1 to 434)
Cartano,A.R., Johnson,R.K. and Pomp,D.
Generation and sequence characterization of a normalized cDNA
library from swine ovarian follicles
Unpublished (2001)
Contact: Pomp, D
Department of Animal Science
University of Nebraska, Lincoln
Lincoln, NE 68583-0908, USA
Tel: 402 472 6416
Fax: 402 472 6362
Email: dpomp@unl.edu
Oligo-dT track not found, Not I site shown in beginning of sequence
is likely internal to the message.
Seq primer: M13 -29
POLYA=No.

```

FEATURES
Source
1. .434
/organism="Sus scrofa"
/strain="University of Nebraska, Lincoln Swine Selection
Lines"
/db_xref="taxon:9823"
/clone="UNL-P-FN-bf-e-12-0-UNL"
/clone_lib="UNL-P-FN"
/dev_stage="ADULT"
/lab_host="DH10B (Life Technologies)"
/notes="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; The UNL-P-FN
library is a normalized library representing porcine
ovarian follicles, ranging between 2.0 to 10.0 mm in
diameter, collected during 7 days of the follicular phase
of the pig estrous cycle. This library was derived from
the library UNL-P-F2. The tag is a string of 5-6
nucleotides present between the Not I site and the
oligo-dT track. The library was constructed as described
by Bonaldo, Lennon and Soares, Genome Research 6: 791-806
, 1996.
TAG_SEQ=None found"
BASE COUNT      103 a 114 c 120 g      97 t
ORIGIN

Query Match      6.6%; Score 20; DB 10; Length 434;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 163 ctcaagalcctcattcacat 182
DB 343 CTCAAGATCCTCATTCACAT 362

RESULT 17
BM261245
LOCUS      BM261245      558 bp      mRNA      linear      EST 18-DEC-2001
DEFINITION da145402.y1 NICHHD XGC Sp1 xenopus laevis cdna clone IMAGE:4964906
5' similar to TR:P79701 P79701 VASCULAR ENDOTHELIAL GROWTH FACTOR
RECEPTOR. ;, mRNA sequence.
ACCESSION   BM261245
VERSION     BM261245.1 GI:17924285
KEYWORDS    EST.
SOURCE      African clawed frog.
ORGANISM    Xenopus laevis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
Xenopodinae; Xenopus.
1 (bases 1 to 558)
NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
JOURNAL
COMMENT     Contact: Robert Strausberg, Ph.D.
Tissue Procurement: Martha Rebert, Steven L. Klein, Ph.D.
cdna Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA sequencing by: Washington University Genome Sequencing Center
Clone distribution: Xenopus clones from this library are available
through the I.M.A.G.E. Consortium/LLNL at: info@image.llnl.gov
Seq primer: -40RP from Gibco
High quality sequence stop: 442.
Location/Qualifiers
1. .558
/organism="Xenopus laevis"
/db_xref="taxon:8355"
/clone="IMAGE:4964906"
/clone_lib="NICHHD XGC Sp1"
/dev_stage="adult"
/lab_host="DH10B (phage-resistant)"
/notes="Organ: spleen; Vector: pCMV-SPORT6; Site_1: NotI;

Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2.4 kb. Constructed by Life
Technologies."
BASE COUNT      162 a 119 c 149 g      128 t
ORIGIN

Query Match      6.6%; Score 20; DB 10; Length 558;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 106 gtgaaatgctgaaagagg 125
DB 130 GTGAAATGCTGAAAGAGGG 149

RESULT 18
BH142039
LOCUS      BH142039      619 bp      DNA      linear      GSS 16-AUG-2001
DEFINITION TDGDK45TH cTOG Lycopersicon esculentum genomic clone cTOG23G17, DNA
sequence.
ACCESSION   BH142039
VERSION     BH142039.1 GI:15194268
KEYWORDS    GSS.
SOURCE      tomato.
ORGANISM    Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
Lycopersicon.
1 (bases 1 to 619)
van der Hoeven,R., Sun,H., Cho,J., Utterback,T., Ronning,C. and
Tanksley,S.
Tomato Demethylated Genomic DNA Sequences
Unpublished (2001)
JOURNAL
COMMENT     Contact: CUGI
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
tomato demethylated genomic DNA
Insert Length: 1270 Std Error: 0.00
Seq primer: M13F-R
Class: shotgun.
Location/Qualifiers
1. .619
/organism="Lycopersicon esculentum"
/cultivar="E6203"
/db_xref="taxon:4081"
/clone="cTOG23G17"
/clone_lib="cTOG"
/tissue_type="young leaves"
/dev_stage="12-14 weeks post harvest"
/lab_host="E.coli JM109"
/notes="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
XhoI; This library was made from short EcoRI digested
fragments of the genome of Lycopersicon esculentum ligated
into pBS (SK-). The fragments were cloned into the
methylation restrictive E.coli strain JM109 with the
purpose of enriching the library for non-methylated DNA
fragments. This procedure may enrich the pool of cloned
fragments in JM109 cells for sequences representing
expressed genes. Average insert size 1.27 kb."
BASE COUNT      233 a 102 c 121 g      163 t
ORIGIN

Query Match      6.6%; Score 20; DB 12; Length 619;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 106 gtgaaatgctgaaagagg 125
|||||

```



```

Db 392 GTGAAATGCTGAAAGAGG 411

RESULT 19
BG709462
LOCUS 810 bp mRNA linear EST 07-MAY-2001
DEFINITION 602674728F1 NIH_MGC_96 Homo sapiens cDNA clone IMAGE:4797343 5',
mRNA sequence.
A''''SSION
VLSKSION BG709462
KEYWORDS BG709462.1 GI:13987822
SOURCE EST.
ORGANISM human.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 810)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: NIH Intramural Sequencing Center
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LUCM10683 row: g column: 08
High quality sequence stop: 743.
Location/Qualifiers
FEATURES
source
1..810
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4797343"
/tissue_type="hypothalamus"
/lab_host="DH10B"
/note="Organ: brain; Vector: pBluescriptR (modified
pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI (gtcgag
); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTVN-3',
size-selected for average insert size 2.3 kb and
normalized to ROT 5. This is a primary library enriched
for full-length clones and constructed using the
Cap-trapper method (Carninci, in preparation). Library
constructed by M. Brownstein (NIH/NHGRI, National
Institutes of Health). Note: this is a NIH_MGC Library."
BASE COUNT 177 a 184 c 203 g 246 t
ORIGIN

Query Match 6.6%; Score 20; DB 10; Length 810;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 101 tggccgtgaaaatgctgaaa 120
|||||
Db 784 TGGCCGTGAAATGCTGAAA 803
|||||

RESULT 20
BG746729
LOCUS 856 bp mRNA linear EST 15-MAY-2001
DEFINITION 602704056F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:4857469 5',
mRNA sequence.
ACCESSION BG746729
VERSION BG746729.1 GI:14057382
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 856)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: CLONETECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LUCM1647 row: a column: 17
High quality sequence stop: 711.
Location/Qualifiers
FEATURES
source
1..862
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4857469"
/tissue_type="adenocarcinoma cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: colon; Vector: pOT87; Site_1: XhoI; Site_2:
EcoRI; CDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-CDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)"
BASE COUNT 192 a 198 c 199 g 267 t
ORIGIN

Query Match 6.6%; Score 20; DB 10; Length 856;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 101 tggccgtgaaaatgctgaaa 120
|||||
Db 772 TGGCCGTGAAATGCTGAAA 791
|||||

RESULT 21
BG615859
LOCUS 862 bp mRNA linear EST 18-APR-2001
DEFINITION 602643265F1 NIH_MGC_61 Homo sapiens cDNA clone IMAGE:4774168 5',
mRNA sequence.
ACCESSION BG615859
VERSION BG615859.1 GI:13667230
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 862)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: CLONETECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LUCM1647 row: a column: 17
High quality sequence stop: 711.
Location/Qualifiers
FEATURES
source
1..862

```

```
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4774168"
/clone_lib="NIH_MGC_61"
/tissue_type="embryonal carcinoma"
/lab_host="DH10B (T1 phage-resistant)"
/notes="Organ: testis; Vector: pDNR-LIB (Clontech); Site_1:
sfll (ggccgcctgcgc); Site_2: sfll (ggccattatggcc);
Double-stranded cDNA was prepared from cell line RNA. 5'
and 3' adaptors were used in cloning as follows: 5'
adaptor sequence: 5'-CAGGCCATTATGGCC-3' and 3' adaptor
sequence: 5'-ATTCTAGAGCCGAGCGGCGGCACATG-dT(30)BN-3'
(where B = A, C, or G and N = A, C, G, or T). Average
insert size 1.75 kb (range 0.9-4.0 kb). 15/15 colonies
contained inserts by PCR. This library was enriched for
full-length clones and was constructed by Clontech
Laboratories (Palo Alto, CA). Note: this is a NIH_MGC
Library."
BASE COUNT      198 a 185 c 201 g 278 t
ORIGIN

Query Match      6.6%; Score 20; DB 10; Length 862;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 101 tggccgtgaaaaatgctgaaa 120
Db 726 TGGCCGTGAAAAATGCTGAAA 745

RESULT 22
LOCUS      B1763816      864 bp      mRNA      linear      EST 25-SEP-2001
DEFINITION 603049766F1 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5189729 5',
mRNA sequence.
ACCESSION  B1763816
VERSION    B1763816.1 GI:15755394
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11474 row: d column: 18
High quality sequence stop: 862.
Location/Qualifiers
1. .864
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5189729"
/clone_lib="NIH_MGC_116"
/lab_host="DH10B"
/notes="Organ: pooled colon, kidney, stomach; Vector:
pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
source anonymous pool of 3 colons, age 26 yo male, 49 yo
female, 71 yo male colon; 46 yo male kidney, and pool of 2
stomachs, 62 yo male and 70 yo female. Library is
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.4 kb,
insert size range 1-3 kb. Library is normalized and
```

```
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
023. Note: this is a NIH_MGC Library."
BASE COUNT      195 a 198 c 210 g 260 t
ORIGIN

Query Match      6.6%; Score 20; DB 10; Length 864;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 101 tggccgtgaaaaatgctgaaa 120
Db 791 TGGCCGTGAAAAATGCTGAAA 810

RESULT 23
LOCUS      BM048480      885 bp      mRNA      linear      EST 07-NOV-2001
DEFINITION 603628170F1 NIH_MGC_40 Homo sapiens cDNA clone IMAGE:5456776 5',
mRNA sequence.
ACCESSION  BM048480
VERSION    BM048480.1 GI:16777747
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTF
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LUCM1955 row: k column: 17
High quality sequence stop: 807.
Location/Qualifiers
1. .885
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5456776"
/clone_lib="NIH_MGC_40"
/tissue_type="carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/notes="Organ: prostate; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
BASE COUNT      195 a 209 c 208 g 273 t
ORIGIN

Query Match      6.6%; Score 20; DB 10; Length 885;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 101 tggccgtgaaaaatgctgaaa 120
Db 770 TGGCCGTGAAAAATGCTGAAA 789

RESULT 24
```

BF927018
LOCUS CM2-NT0192-051200-577-f09 NT0192 Homo sapiens cDNA, mRNA sequence. EST 19-JAN-2001
ACCESSION BF927018
VERSION BF927018.1 GI:12324874
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 201)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldmann, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
Shotgun sequencing of the human transcriptome with ORF expressed

sequence tags

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

MEDLINE 20202663

COMMENT Contact: Simpson A.J.G.

Laboratory of Cancer Genetics

Ludwig Institute for Cancer Research

Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL

(<http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CM2&t2=CM2-NT0192-051200-577-f09&t3=2000-12-05&t4=1>)

Seq primer: puc 18 forward

High quality sequence start: 126

High quality sequence stop: 201.

Location/Qualifiers

1..201

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone_lib="NT0192"

/dev_stage="Adult"

/note="Organ: nervous_tumor; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application

No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of

tissue mRNA and cDNA amplification were performed under low stringency conditions."

58 a 43 c 62 g 38 t

BASE COUNT

ORIGIN

Query Match 6.3%; Score 19; DB 10; Length 201;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 74 tccacaagggcagcagctg 92

|||||

Db 171 TCCACAGGGCAGCAGCTG 189

RESULT 25

BF925651

LOCUS CM2-NT0192-291100-578-e05 NT0192 Homo sapiens cDNA, mRNA sequence. EST 19-JAN-2001

ACCESSION BF925651

VERSION BF925651.1 GI:12322186

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS

1 (bases 1 to 208)

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldmann, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
Shotgun sequencing of the human transcriptome with ORF expressed

sequence tags

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

MEDLINE 20202663

COMMENT

Contact: Simpson A.J.G.

Laboratory of Cancer Genetics

Ludwig Institute for Cancer Research

Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL

(<http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CM2&t2=CM2-NT0192-291100-578-e05&t3=2000-11-29&t4=1>)

Seq primer: puc 18 forward

High quality sequence start: 12

High quality sequence stop: 208.

Location/Qualifiers

1..208

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone_lib="NT0192"

/dev_stage="Adult"

/note="Organ: nervous_tumor; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application

No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of

tissue mRNA and cDNA amplification were performed under low stringency conditions."

57 a 44 c 62 g 45 t

BASE COUNT

ORIGIN

Query Match 6.3%; Score 19; DB 10; Length 208;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 74 tccacaagggcagcagctg 92

|||||

Db 178 TCCACAGGGCAGCAGCTG 196

RESULT 26

BF524514/c

LOCUS CM2-NT0192-1257 bp mRNA linear EST 29-AUG-2001

DEFINITION 603051580r1 NIH_MGC_122 Homo sapiens cDNA clone IMAGE:5201514 3',

mRNA sequence.

ACCESSION BF524514

VERSION BF524514.1 GI:15349306

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1257)

NIH-MGC <http://mgc.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

JOURNAL

COMMENT

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Life Technologies, Inc.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Plate: L1AM1504 row: 0 column: 19
High quality sequence stop: 38.
Location/Qualifiers
1. .1257
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5201514"
/clone_lib="NIH_MGC_122"
/lab_host="DH10B"
/note="Organ: pooled lung and spleen; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of 24 week female lung, 16 week female spleen, and 20-22 week male spleens. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 026. Note: this is a NIH_MGC Library."
367 a 466 c 235 g 189 t
BASE COUNT
ORIGIN

Query Match 6.3%; Score 19; DB 10; Length 1257;
Best Local Similarity 100.0%; Pred. No. 87;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 139 gaqccaccgcgcgtgatgt 157
|||||
DB 306 GAGCACC GCCGCTCATGT 288

RESULT 27
AV321924/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

AV321924 244 bp mRNA linear EST 09-NOV-1999
AV321924 RIKEN full-length enriched, 13 days embryo male testis Mus musculus CDNA clone 6030438L02 3' similar to X99644 M.musculus mRNA for TfPI beta protein, mRNA sequence.
AV321924
AV321924.1 GI:6291770
EST.
house mouse.
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 244)
Konno, H., Alzawa, K., Akahira, S., Akiyama, S., Akiyama, J., Carninci, P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N., Hirozane, T., Hori, F., Ishii, Y., Ishikawa, T., Itoh, M., Izawa, M., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N., Kojima, Y., Koya, S., Kusakabe, M., Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y., Owa, C., Ozawa, Y., Saito, H., Sano, M., Sato, K., Shibata, K., Shibata, Y., Shigenoto, Y., Shiraki, T., Sogabe, Y., Sugahara, Y., Suzuki, H., Suzuki, H., Takahashi, F., Tateo, M., Tomimaga, N., Tsunoda, Y., Watahiki, A., Watanabe, S., Yamamura, T., Yasunishi, A., Yokota, T., Yoshiki, A., Yoshino, M., Muramatsu, M. and Hayashizaki, Y.
RIKEN Mouse ESTs (Konno, H., et al. 1999)
Unpublished (1999)
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsr.riken.go.jp,
URL: <http://genome.gsc.riken.go.jp/>
Sasaki, N., Izawa, M., Watahiki, M., Ozawa, K., Tanaka, T., Yoneda, Y., Matsuura, S., Carninci, P., Muramatsu, M., Okazaki, Y. and Hayashizaki

Y.
Transcriptional sequencing: A method for DNA sequencing using RNA polymerase. Proc. Natl. Acad. Sci. U.S.A. 95 (7), 3455-3460 (1998)
Itoh, M., Kitsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J., Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki, Y. and Hayashizaki, Y.
Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)
Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)
Please visit our web site (<http://genome.rtc.riken.go.jp>) for further details.
Location/Qualifiers
1. .244
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="6030438L02"
/clone_lib="RIKEN full-length enriched, 13 days embryo male testis"
/sex="male"
/tissue_type="testis"
/dev_stage="13 days embryo"
/lab_host="DH10B"
/note="Site_1: SalI; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAGAGATCCAGAGCTCTTTTTTTTTTTTTTNN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 5.0 and subtraction to Rot = 100.0. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGATTCGAGTTAATTAATTAATCCCTCCCTCCCTCC 3']. cDNA was cloned into the XhoI and BamHI sites. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I. Cloning sites, 5' end: SalI; 3' end: BamHI."
41 a 75 c 50 g 78 t
BASE COUNT
ORIGIN

Query Match 5.9%; Score 18; DB 9; Length 244;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 ccttcgggaagtggtgg 55
|||||
DB 25 CCTTCGGGAAGGTGGTGG 8

RESULT 28
BM241884
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE

BM241884 261 bp mRNA linear EST 01-FEB-2002
BM241884 NTA Mouse Hematopoietic Stem Cell (Lin-/c-Kit-/Sca-1+) cDNA Library (Long) Mus musculus cDNA clone K0624A01 3', mRNA sequence.
BM241884
BM241884.1 GI:17877154
EST.
house mouse.
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 261)
Piao, Y., Kargul, G.J., Dudekula, D.B., Qian, Y., Luo, A., Carter, M.G., Taub, D., Longo, D.L., Keller, J. and Ko, M.S.H.
Systematic Analyses of NIA Mouse Hematopoietic Stem Cell (Lin-/c-Kit-/Sca-1+) cDNA Library (Long)

JOURNAL COMMENT Unpublished (2001)
Contact: Dawood B. Dudekula
Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdna@igsun.grc.nia.nih.gov
Plate: K0624 row: A column: 01
Seq primer: -21M13 Forward
High quality sequence stop: 261
POLYA-Yes.

FEATURES source Location/Qualifiers
1. .261
/organism="Mus musculus"
/strain="C57BL/6Ncr"
/db_xref="niaEST:K0624A01-3"
/db_xref="taxon:10090"
/clone="K0624A01"
/clone_lib="NIA Mouse Hematopoietic Stem Cell
(Lin-/C-Kit-/Sca-1+) cDNA Library (long)"
/tissue_type="Hematopoietic Stem Cell (Lin-/C-Kit-/Sca-1+)"
/dev_stage="Age approx.10 weeks old"
/lab_host="DH10B"
/note="Vector: pSPORT1 (Invitrogen); Site_1: SalI; Site_2: NotI; Mouse cDNA project by the Laboratory of Genetics, National Institute on Aging (NIA), Intramural Research Program, NIH (http://igsun.grc.nia.nih.gov/cDNA). This is a long-transcript enriched cDNA library (Ref. Genome Res. 11: 1553-1558 (2001). [PMID: 11544199]). Total RNAs were obtained from Drs. Dennis Taub, Dan Longo (National Institute on Aging, USA), Jonathan Keller (National Cancer Institute, USA). Double-stranded cDNAs were synthesized with an oligo(dT) primer [Invitrogen]:
5'-pGACTAGTCTGATCGGAGCGCGCCCTTTT-TTTT-3' from 1.1 ug of total RNA, treated with T4 DNA polymerase, and purified by ethanol-precipitation. The cDNAs were ligated to lone-linker Lb-Sal4, purified by phenol/chloroform, and separated from free linkers by Centricon 100. Then, the cDNAs were amplified by long-range high fidelity PCR using Ex Taq polymerase (Takara) with a primer Sal4-S. The products were purified by phenol/chloroform and Centricon 100. The cDNAs were digested with SalI and NotI enzymes and cloned into SalI/NotI site of pSPORT1 plasmid vector. The DH10B E. coli host was transformed with the ligation mixture by the standard chemical method. The average insert size is about 2.2 kb. The library was constructed by Yulan Piao (NIA)."

BASE COUNT 58 a 63 c 57 g 83 t
ORIGIN

Query Match 5.9%; Score 18; DB 10; Length 261;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 82 ggcagcagctgtgacacc 99
|||||
Db 225 GCCAGCAGCTGTGACACC 242

RESULT 29
BM409650/c
LOCUS 271 bp mRNA linear EST 22-JAN-2002
DEFINITION tomato breaker fruit Lycopersicon esculentum cDNA clone
cLEG49022 5' end, mRNA sequence.

ACCESSION BM409650.1 GI:18261280
VERSION
KEYWORDS EST.
SOURCE tomato.
ORGANISM Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;

REFERENCE AUTHORS
TITLE
JOURNAL
COMMENT

Lycopersicon.
1 (bases 1 to 271)
Alcala,J., Vrebalov,J., White,R., Vision,T., Karamycheva,S.A., Tsai
,J., Bougri,O., Kirkness,E., Utterback,T., Van Aken,S., Ronning
,C.M., Fraser,C.M., Martin,G.B., Tanksley,S.D. and Giovannoni,J.
Generation of ESTs from tomato fruit tissue, breaker stage (2002)
Unpublished (2002)
Contact: CUCI
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
This clone is available through the Clemson University Genomics
Institute
Seq primer: T3.

FEATURES source Location/Qualifiers
1. .271

/organism="Lycopersicon esculentum"
/cultivar="TA496"
/db_xref="taxon:4081"
/clone="cLEG49022"
/clone_lib="tomato breaker fruit"
/tissue_type="Pericarp"
/dev_stage="breaker"
/lab_host="SOLR"
/note="Vector: pBluescriptSKmCudapt; Site_1: EcoRI;
Site_2: XhoI; supplier: Boyce Thompson Institute;
sequencing: The Institute for Genomic Research. Fruit
were harvested at the breaker stage (first sign of
lycopene accumulation on the blossom end of fruit). Fruit
were cut in half and the seeds and locules were discarded
prior to freezing the pericarp."

BASE COUNT 73 a 56 c 60 g 82 t
ORIGIN

Query Match 5.9%; Score 18; DB 10; Length 271;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 71 gcatccacagggcgacga 88
|||||
Db 57 GCATCCACAAGGGCAGCA 40

RESULT 30
AW009058/c
LOCUS ws75g02.x1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:2503826 3',
DEFINITION mRNA sequence.

ACCESSION AW009058
VERSION AW009058.1 GI:5857836
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 319)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
JOURNAL
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbsr@mail.nih.gov
Tissue Procurement: Elias Campo, M.D., Michael R. Emmert-Buck, M.D.,
, Ph.D.

cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arraying: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution Information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 968 Std Error: 0.00

Seq primer: -40UP from Gibco
High quality sequence stop: 318.

FEATURES

Location/Qualifiers
1. .319
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="IMAGE:2503826"
/clone_lib="NCI_CGAP_Co3"
/sex="pooled"
/tissue_type="colon"
/lab_host="DH10B"

/note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was prepared from 12 pooled bulk tumor samples and primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization."
65 a 116 c 117 g 21 t

BASE COUNT

ORIGIN

Query Match 5.9%; Score 18; DB 9; Length 319;

Best Local Similarity 100.0%; Pred. No. 1.9e+02;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 32 acggcgcttcgggaagg 49

|||||

Db 55 ACGGCGCCTTCGGGAAGG 38

RESULT 31

AQ216651/c

LOCUS

DEFINITION HS_2139_A2_C03_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2139 Col=6 Row=E, DNA sequence.

ACCESSION AQ216651

VERSION AQ216651.1

KEYWORDS GSS.

SOURCE human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 360)

Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,

Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and

Hood,L.

Sequence-tagged connectors: A sequence approach to mapping and

scanning the human genome

Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)

99380589

Contact: Mahairas GG, Wallace JC, Hood L

High Throughput Sequencing Center

University of Washington

401 Queen Anne Avenue North, Seattle, WA 98109, USA

Tel: (206) 616-3618

Fax: (206) 616-3887

Email: jwallace@u.washington.edu

Sequence Tagged Connector

Plate: 2139 row: E column: 6

Class: BAC ends

High quality sequence stop: 360.

Location/Qualifiers

1. .360

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="Plate=2139 Col=6 Row=E"

/clone_lib="CIT Approved Human Genomic Sperm Library D"

/sex="male"

/note="Organ: sperm; Vector: pBelBAC11; BAC Clones in

E-Coli DH10B"

104 a 63 c 76 g 105 t 12 others

BASE COUNT

ORIGIN

Query Match 5.9%; Score 18; DB 12; Length 360;

Best Local Similarity 100.0%; Pred. No. 2e+02;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 108 gaaaatgctgaagagg 125

|||||

Db 95 GAAATGCTGAAGAGGG 78

RESULT 32

A1744037/c

LOCUS

DEFINITION wc32h11.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2316933 3',

mRNA sequence.

369 bp mRNA linear EST 17-DEC-1999

ACCESSION A1744037

VERSION A1744037.1

KEYWORDS EST.

SOURCE human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 369)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgaps@email.nih.gov

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.

cDNA Library Preparation: M. Bento Soares, Ph.D.

DNA Sequencing by: Greg Lennon, Ph.D.

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

www.bio.llnl.gov/bbrp/image/image.html

Insert Length: 1520 Std Error: 0.00

Seq primer: -40UP from Gibco

High quality sequence stop: 329.

Location/Qualifiers

1. .369

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:2316933"

/clone_lib="NCI_CGAP_Kid11"

/lab_host="DH10B"

/note="Organ: kidney; Vector: pT7T3D-Pac (Pharmacia) with

a modified polylinker; Site_1: Not I; Site_2: Eco RI;

Plasmid DNA from the normalized library NCI_CGAP_Kid3 was

prepared, and ss circles were made in vitro. Following RAP

purification, this DNA was used as tracer in a subtractive

hybridization reaction. The driver was PCR-amplified cDNAs

from a pool of 5,000 clones made from the same library

(cloneIDs 1322376-1323911, 1456007-1456775, and

1500552-1502855). Subtraction by Bento Soares and M.

Fatima Bonaldo."

77 a 131 c 131 g 30 t

BASE COUNT

ORIGIN

Query Match 5.9%; Score 18; DB 9; Length 369;

Best Local Similarity 100.0%; Pred. No. 2e+02;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 32 acggcgcttcgggaagg 49

|||||

Db 55 ACGGCGCCTTCGGGAAGG 38

RESULT 33

```

BE460395/c
LOCUS      BE460395               470 bp      mRNA      linear      EST 18-MAY-2001
DEFINITION clone CLEG29A14, tomato breaker fruit, TIGR Lycopersicon esculentum cDNA
ACCESSION BE460395
VERSION    BE460395.1  GI:9504697
KEYWORDS   EST,
SOURCE     tomato.
ORGANISM   Lycopersicon esculentum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
            Lycopersicon.
REFERENCE  1 (bases 1 to 470)
AUTHORS    Alcalá,J., Vrebalov,J., White,R., van der Hoeven,K.S., Holt,I.E.,
            Liang,F., Hansen,T.S., Craven,M.B., Bowman,C.L., Konning,C.M.,
            Nierman,W., Fraser,C.M., Martin,G.B., Giovannoni,J.J. and Tanksley
            ,S.D.
            Generation of ESTs from tomato fruit tissue, breaker stage
            Unpublished (2000)
TITLE      Contact: CUGI
JOURNAL    Clemson University Genomics Institute
COMMENT    Clemson University
            100 Jordan Hall, Clemson, SC 29634, USA
            Email: http://www.genome.clemson.edu/orders/index.html
            5 prime sequence.
FEATURES   source
            Location/Qualifiers
            1..470
            /organism="Lycopersicon esculentum"
            /cultivar="TA496"
            /db_xref="taxon:4081"
            /clone="CLEG29A14"
            /clone_lib="tomato breaker fruit, TIGR"
            /tissue_type="pericarp"
            /dev_stage="breaker"
            /lab_host="SOLR"
            /note="Vector: pBluescriptSKmCUadap; Site_1: EcoRI;
            Site_2: XhoI; Fruit were harvested at the breaker stage
            (first sign of lycopene accumulation on the blossom end of
            the fruit). Fruit were cut in half and the seeds and
            locules were discarded prior to freezing the pericarp."
BASE COUNT 134 a 81 c 118 g 137 t
ORIGIN

Query Match      5.9%; Score 18; DB 10; Length 470;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 71 gcatccacaagggcagca 88
      |||||||
Db 422 GCATCCACAGGCACGA 405

RESULT 34
BH392477
LOCUS      BH392477               478 bp      DNA      linear      GSS 11-DEC-2001
DEFINITION AG-ND-142N21.TF ND-TAM Anopheles gambiae genomic clone AG-ND-142N21
            , DNA sequence.
ACCESSION  BH392477
VERSION     BH392477.1  GI:17338618
KEYWORDS    GSS.
SOURCE      African malaria mosquito.
ORGANISM    Anopheles gambiae
            Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
            Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea
            ; Anopheles.
REFERENCE  1 (bases 1 to 478)
AUTHORS    Shetty,J., Malek,J., Koo,H., Collins,F., Gardner,M. and Loftus,B.J.
TITLE      Direct Submission of BAC-end sequences from Anopheles gambiae
JOURNAL    Unpublished (2001)
COMMENT    Contact: Brendan J Loftus
            Department of Eukaryotic Genomics

```

```

The Institute for Genomic Research
712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Fax: 301 838 3543
Email: bjoftus@tigr.org
This clone is from an A. gambiae BAC library (ND-TAM) provided by
F.H. Collins and sequenced by The Institute for Genomic Research
(TIGR). The BAC library was generated from A. gambiae PEST strain
DNA. All DNA was extracted from newly hatched first instar larvae
to minimize the inclusion of DNA from microorganisms that inhabit
the gut. The DNA is derived from mixed sexes of larvae. The BAC
library was constructed at Texas A&M University BAC Center
University, College Station, Texas 77843-2123, USA using a HindIII
partial digest.
Seq primer: M13 For
Class: BAC ends.
FEATURES   source
            Location/Qualifiers
            1..478
            /organism="Anopheles gambiae"
            /strain="PEST"
            /db_xref="taxon:7165"
            /clone="AG-ND-142N21"
            /clone_lib="ND-TAM"
            /note="vector: pECBAC1; Site_1: HindIII"
BASE COUNT 121 a 121 c 131 g 105 t
ORIGIN

Query Match      5.9%; Score 18; DB 12; Length 478;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 139 gagcacgcgcgcgatg 156
      |||||||
Db 106 GAGCACCGCGCGCTGATG 123

RESULT 35
BH405811/c
LOCUS      BH405811               480 bp      mRNA      linear      EST 14-AUG-2001
DEFINITION 146C09 Mature tuber lambda ZAP Solanum tuberosum cDNA, mRNA
            sequence.
ACCESSION  BH405811
VERSION     BH405811.1  GI:15185225
KEYWORDS    EST.
SOURCE      potato.
ORGANISM    Solanum tuberosum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
REFERENCE  1 (bases 1 to 480)
AUTHORS    Nielsen,K.L., Crookshanks,M., Emmersen,J. and Wellinder,K.G.
TITLE      EST-sequencing of mature potato tuber (Var. Kuras)
JOURNAL    Unpublished (2000)
COMMENT    Contact: Karen G. Wellinder
            Institut for bioteknologi
            Aalborg Universitet
            Sohngaardsholmsvej 49, 9000 Aalborg, Denmark
            Tel: +45 96358467
            Fax: +45 96141808
            Email: kgw@bio.auc.dk
            Sequenced from the 5' end.
            High quality sequence stop: 480
POLYA=No.
FEATURES   source
            Location/Qualifiers
            1..480
            /organism="Solanum tuberosum"
            /cultivar="Field grown Kuras"
            /db_xref="taxon:4113"
            /clone_lib="Mature tuber lambda ZAP"
            /tissue_type="Tuber"
            /note="vector: Lambda ZAP"
BASE COUNT 141 a 86 c 114 g 139 t

```

ORIGIN

Query Match 5.9%; Score 18; DB 10; Length 480;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 71 gcatccacaagggcagca 88
 |||||
 Db 430 GCATCCACAGGCGACGA 413

RESULT 36

BG767090
 LOCUS 602740451F1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4870260 5',
 DEFINITION mRNA sequence.

ACCESSION BG767090
 VERSION BG767090.1 GI:14077743
 KEYWORDS EST.
 SOURCE human.

ORGANISM

Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Euthera; Primates; Catarrhini; Hominoidea; Homo.

REFERENCE 1 (bases 1 to 498)
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: c9apbs@remail.nih.gov

Tissue Procurement: ATCC/DCTD/DTF
 cDNA Library Preparation: Ling Hong/Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov

Plate: LLCMI743 row: e column: 13
 High quality sequence stop: 484.
 Location/Qualifiers

FEATURES

source

1..498
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:4870260"
 /clone_lib="NIH_MGC_49"
 /tissue_type="melanotic melanoma, high MDR (cell line)"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: skin; Vector: pORF7; Site_1: XhoI; Site_2:
 EcoRI; cDNA made by oligo-dT priming. Directionally cloned
 into EcoRI/XhoI sites using the following 5' adaptor:
 GGCACGAG(G). Size-selected >500bp for average insert size
 1.8kb. Library constructed by Ling Hong in the laboratory
 of Gerald M. Rubin (University of California, Berkeley)
 using ZAP-cDNA synthesis kit (Stratagene) and Superscript
 II RT (Life Technologies). Note: this is a NIH_MGC
 Library. |"

BASE COUNT 50 a 161 c 218 g 69 t

ORIGIN

Query Match 5.9%; Score 18; DB 10; Length 498;
 Best Local Similarity 100.0%; Pred. No. 2.2e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 32 acggcgcccttcgggaagg 49
 |||||
 Db 202 ACCGGCCCTTCGGGAAGG 219

RESULT 37

BG767090
 LOCUS 602740451F1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4870260 5',
 DEFINITION mRNA sequence.

ACCESSION BG767090
 VERSION BG767090.1 GI:14077743
 KEYWORDS EST.
 SOURCE human.

ORGANISM

Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Euthera; Primates; Catarrhini; Hominoidea; Homo.

REFERENCE 1 (bases 1 to 498)
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: c9apbs@remail.nih.gov

Tissue Procurement: ATCC/DCTD/DTF
 cDNA Library Preparation: Ling Hong/Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov

Plate: LLCMI743 row: e column: 13
 High quality sequence stop: 484.
 Location/Qualifiers

FEATURES

source

1..498
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:4870260"
 /clone_lib="NIH_MGC_49"
 /tissue_type="melanotic melanoma, high MDR (cell line)"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: skin; Vector: pORF7; Site_1: XhoI; Site_2:
 EcoRI; cDNA made by oligo-dT priming. Directionally cloned
 into EcoRI/XhoI sites using the following 5' adaptor:
 GGCACGAG(G). Size-selected >500bp for average insert size
 1.8kb. Library constructed by Ling Hong in the laboratory
 of Gerald M. Rubin (University of California, Berkeley)
 using ZAP-cDNA synthesis kit (Stratagene) and Superscript
 II RT (Life Technologies). Note: this is a NIH_MGC
 Library. |"

mays cDNA, mRNA sequence.

ACCESSION BM417681
 VERSION BM417681.1 GI:18384482
 KEYWORDS EST.
 SOURCE Zea mays.
 ORGANISM Zea mays.

REFERENCE 1 (bases 1 to 498)
 AUTHORS Walbot,V.
 TITLE Maize ESTs from various cDNA libraries sequenced at Stanford University
 JOURNAL Unpublished (1999)
 COMMENT Contact: Walbot V
 Department of Biological Sciences
 Stanford University
 855 California Ave, Palo Alto, CA 94304, USA
 Tel: 650 723 2227
 Fax: 650 725 8221
 Email: walbot@stanford.edu

Plate: 952005 row: A column: 05.

Location/Qualifiers

1..498
 /organism="Zea mays"
 /cultivar="BMS (Black Mexican Sweet)"
 /db_xref="taxon:4577"
 /clone_lib="952 - BMS tissue from Walbot Lab (reduced rRNA)"
 /tissue_type="suspension culture"
 /dev_stage="mixed logarithmic and stationary growth phases"
 /lab_host="DH10B"
 /note="Vector: pUC19; Site_1: EcoRI; Site_2: EcoRI; The library was prepared by George Rudenko using poly (A) selected RNA and Universal Riboclone cDNA Synthesis System (Promega). cDNA was synthesized using both random and oligo(dT) primers in separate reactions and equipped with EcoRI adaptors. Library was size-fractionated on agarose gels (for insert size >400bp) and non-directionally cloned into EcoRI-digested pUC19 vector. Blue/white selection on carbenicillin-containing plates was used to recover positive clones."

BASE COUNT 87 a 171 c 87 g 152 t

ORIGIN

Query Match 5.9%; Score 18; DB 10; Length 498;
 Best Local Similarity 100.0%; Pred. No. 2.2e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 72 catccacaagggcagcag 89
 |||||
 Db 115 CATCCACAAGGCGACGAG 132

BASE COUNT 87 a 171 c 87 g 152 t

ORIGIN

Query Match 5.9%; Score 18; DB 10; Length 498;
 Best Local Similarity 100.0%; Pred. No. 2.2e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 72 catccacaagggcagcag 89
 |||||
 Db 115 CATCCACAAGGCGACGAG 132

RESULT 38

LOCUS

BM089435
 DEFINITION 503183 MARC 280V Bos taurus cDNA 5', mRNA sequence.
 ACCESSION BM089435
 VERSION BM089435.1 GI:17000063
 KEYWORDS EST.
 SOURCE cow.

ORGANISM

Bos taurus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Euthera; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 Bovidae; Bovinae; Bos.
 1 (bases 1 to 505)
 Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T.,
 Casas,J.E., White,J., Cho,J., Fahrenkrug,S.C., Bennett,
 G.L., Heaton,M.P., Laegreid,W.W., Rohrer,G.A., Chitko-McKown,C.G.,
 Perle,G., Holt,I., Karamycheva,S., Liang,F., Quackenbush,J. and

REFERENCE

AUTHORS

Keele,J.W.
Sequence evaluation of four pooled-tissue normalized bovine cDNA
libraries and construction of a gene index for cattle
Genome Res. 11 (4), 626-630 (2001)
21180013
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt.trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
PCR Primers
FORWARD: AGGAACAGCTATGACCAT
BACKWARD: GTTTCCAGTCACGACG
Plate: 4 row: G column: 10
Seq primer: ATTTAGCTGACACTATAG.
Location/Qualifiers
1..505
/organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="MARC 2BOV"
/tissue_type="pooled"
/lab_host="DH10B"
/note="Vector: PCMV SPORT6; Site_1: XbaI; Site_2: XhoI;
Library made from pooled tissue from testis, thymus,
semitendonsus muscle, longissimus muscle, pancreas,
adrenal, and endometrium."
BASE COUNT 76 a 135 c 194 g 100 t
ORIGIN

Query Match 5.9%; Score 18; DB 10; Length 505;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 tgggaagagtgcgcgtc 31
|||||
Db 1 TCGGGAGAGTGTGGCT 18

RESULT 39
A0154758/c
LOCUS
DEFINITION
HS_3027_A2_D08_MF CIT Approved Human Genomic Sperm Library D Homo
sapiens genomic clone Plate-3027 Col-16 Row-G, DNA sequence.
ACCESSION
A0154758
VERSION
A0154758.1 GI:3547428
KEYWORDS
GSS.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 509)
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
Hood,L.
Sequence-tagged connectors: A sequence approach to mapping and
scanning the human genome
Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
99380599
Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Sequence Tagged Connector
Plate: 3027 row: G column: 16
Class: BAC ends

FEATURES
source
High quality sequence stop: 509.
Location/Qualifiers
1..509
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_plate="3027 Col-16 Row-G"
/clone_lib="CIT Approved Human Genomic Sperm Library D"
/sex="male"
/note="Organ: sperm; Vector: pBelOBAC11; BAC Clones in
E-Coli DH10B"
BASE COUNT 111 a 129 c 126 g 139 t 4 others
ORIGIN

Query Match 5.9%; Score 18; DB 12; Length 509;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 cacctggggagagtgcctc 27
|||||
Db 199 CACCTGGGGAGAGTGTCTC 182

RESULT 40
BE435943/c
LOCUS
DEFINITION
EST406937 tomato breaker fruit, TIGR Lycopersicon esculentum cDNA
clone cLEG29H11, mRNA sequence.
ACCESSION
BE435943
VERSION
BE435943.1 GI:9433702
KEYWORDS
EST.
SOURCE
tomato.
ORGANISM
Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
Lycopersicon.
1 (bases 1 to 512)
Alcala,J., Vrebalov,J., White,R., van der Hoeven,R.S., Holt,I.E.,
Liang,F., Hansen,T.S., Craven,M.B., Bowman,C.L., Ronning,C.M.,
Nierman,W., Fraser,C.M., Martin,G.B., Giovannoni,J.J. and Tanksley
,S.D.
Generation of ESTs from tomato fruit tissue, breaker stage
Unpublished (2000)
Contact: CUGI
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
5 prime sequence.
Location/Qualifiers
1..512
/organism="Lycopersicon esculentum"
/cultivar="TA496"
/db_xref="taxon:4081"
/clone="cLEG29H11"
/clone_lib="tomato breaker fruit, TIGR"
/tissue_type="pericarp"
/dev_stage="breaker"
/lab_host="SOLR"
/note="Vector: pBluescriptSKmCuadapt; Site_1: EcoRI;
Site_2: XhoI; Fruit were harvested at the breaker stage
(first sign of lycopene accumulation on the blossom end of
the fruit). Fruit were cut in half and the seeds and
locules were discarded prior to freezing the pericarp."
BASE COUNT 150 a 94 c 126 g 142 t
ORIGIN

Query Match 5.9%; Score 18; DB 10; Length 512;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Oy 71 gcatccacaaggcgagca 88
    |||||||
Db 372 GCATCCACAAGGGCAGCA 355

RESULT 41
BG280611
LOCUS
DEFINITION
  BG280611 517 bp mRNA linear EST 21-FEB-2001
  system Neurospora crassa sexual cDNA library, Uni-zap vector
ACCESSION
  BG280611
VERSION
  BG280611.1 GI:13079190
KEYWORDS
  EST.
SOURCE
  Neurospora crassa
  Neurospora crassa
  Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
  Sordariales; Sordariaceae; Neurospora.
  1 (bases 1 to 517)
REFERENCE
  Kupfer,D., Lai,H., Nelson,M. and Roe,B.
  ESTs from a Neurospora crassa Sexual cDNA Library
  Unpublished (2001)
JOURNAL
  Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu
  Department of Chemistry and Biochemistry
  Advanced Center for Genome Technology, University of Oklahoma
  620 Parrington Oval, Norman, OK 73019, USA
  Tel: 405 325 4912
  Fax: 405 325 7762
  Email: broe@ou.edu
  Contact Dr. Mary Anne Nelson, Department of Biology, University of
  New Mexico, Albuquerque, NM 87131 (e-mail address manelson@unm.edu)
  regarding clone availability
  Seq primer: M13 Universal Reverse Primer
  High quality sequence stop: 426.
  Location/Qualifiers
    1..517
    /organism="Neurospora crassa"
    /strain="wild type"
    /db_xref="taxon:5141"
    /clone_lib="c5006np"
    /clone_lib="Neurospora crassa sexual cDNA library, Uni-zap
    vector system"
    /tissue_type="perithecia (fruiting bodies)"
    /dev_stage="sexual"
    /lab_host="E. coli strain SOLR"
    /note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
    XhoI; 5' end of cDNA cloned into EcoRI site of pBluescript
    ; 3' end of cDNA cloned into XhoI site of pBluescript"
BASE COUNT      84 a 177 c 129 g 127 t
ORIGIN
    5.9%; Score 18; DB 10; Length 517;
    Query Match
    Best Local Similarity 100.0%; Pred. No. 2.2e+02;
    Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 270 cggcaacctctccaactt 287
Db 158 CGGCAACCTCTCCAACTT 175

RESULT 42
BF265245/c
LOCUS
DEFINITION
  BF265245 521 bp mRNA linear EST 23-OCT-2001
  HV_CEA0011P07f Hordeum vulgare seedling green leaf EST library
  HVCDA0004 (Blumeria challenged) Hordeum vulgare cDNA clone
ACCESSION
  BF265245
VERSION
  BF265245.2 GI:13262032
KEYWORDS
  EST.
SOURCE
  barley.
  Hordeum vulgare
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae

```

```

: Triticeae; Hordeum.
1 (bases 1 to 521)
Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Wei,F., Begum,D., Choi
Frisch,D., Yu,Y., Henry,D., Palmer,M., Rambo,T., Simmons,J., Choi
,D.W., Fenton,R.D., Oates,R. and Main,D.
Development of a genetically and physically anchored EST resource
for barley genomics: Blumeria infected incompatible (Mia13)
seedling leaf cDNA library
Unpublished (2001)
On Nov 17, 2000 this sequence version replaced gi:11196335.
Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Total hg bases = 287
Seq primer: AATTAAACCTCACTAAAGG
High quality sequence stop: 486.
  Location/Qualifiers
    1..521
    /organism="Hordeum vulgare"
    /cultivar="C116155 (Mia13)"
    /db_xref="taxon:4513"
    /clone_lib="HV_CEA0011P07f"
    /clone_lib="Hordeum vulgare seedling green leaf EST
    library HVCDA0004 (Blumeria challenged)"
    /tissue_type="seedling green leaf"
    /lab_host="TJC121"
    /note="Vector: lambdaZAP; Site_1: EcoRI; Site_2: XhoI;
    C.I. 16155 (Mia13) plants were greenhouse grown in the R
    Wise lab at Iowa State University, Ames, IA; 7 day old
    green seedlings were challenged with isolate A27 (AvrMla13
    ) of Blumeria graminis f. sp. hordei, and leaves were
    harvested 20 and 24 hr post-inoculation and snap frozen;
    uninoculated leaves were harvested 20 hr post-inoculation
    (Wei, Wise). In the TJ Close lab at the University of
    California, Riverside, total RNA was prepared from each
    sample pool, equal quantities of all three RNA pools were
    combined, poly(A) RNA was purified from the mixture, one
    cDNA library was made, and 1 million pfu were in vivo
    excised to give pBluescript SK(-) cDNA phagemids (Choi,
    Close). Phagemids were plated and picked at the Clemson
    University Genomics Institute (CUGI) (Begum, Palmer,
    Frisch, Atkins and Wing). Plasmid DNA preparations, DNA
    sequencing and sequence analysis were performed at CUGI
    (Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main).
    The sequence has been trimmed to remove vector sequence
    and contains a minimum of 100 bases of phred value 20 or
    above. For more details on library preparation and
    sequence analysis see
    http://www.genome.clemson.edu/projects/barley. To order
    this clone see http://www.genome.clemson.edu/orders Also
    see Close TJ, Wing R, Kleinhofs A, Wise R (2001)
    Genetically and physically anchored EST resources for
    barley genomics. Barley Genetics Newsletter 31:29-30.
    (http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)*
BASE COUNT      97 a 198 c 143 g 83 t
ORIGIN
    5.9%; Score 18; DB 10; Length 521;
    Query Match
    Best Local Similarity 100.0%; Pred. No. 2.2e+02;
    Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 41 tcgggaagtggtggaag 58
Db 388 TCGGGAAGTGGTGGAAG 371

RESULT 43
BM410739/c

```

LOCUS BM410739 524 bp mRNA linear EST 22-JAN-2002
 DEFINITION EST585066 tomato breaker fruit Lycopersicon esculentum cDNA clone
 CLEGS4K24 5' end, mRNA sequence.
 ACCESSION BM410739
 VERSION BM410739.1 GI:18262369
 KEYWORDS EST.
 SOURCE tomato.
 ORGANISM Lycopersicon esculentum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
 Lycopersicon.
 1 (bases 1 to 524)
 REFERENCE Alcalá, J., Vrebalov, J., White, R., Vision, T., Karamycheva, S.A., Tsai
 J., Bougri, O., Kirkness, E., Utterback, T., Van Aken, S., Renning
 , C.M., Fraser, C.M., Martin, G.B., Tanksley, S.D. and Giovannoni, J.
 Generation of ESTs from tomato fruit tissue, breaker stage (2002)
 Unpublished (2002)
 JOURNAL Contact: CUGI
 COMMENT Clemson University Genomics Institute
 Clemson University
 100 Jordan Hall, Clemson, SC 29634, USA
 Email: <http://www.genome.clemson.edu/orders/index.html>
 This clone is available through the Clemson University Genomics
 Institute
 Seq primer: T3.
 FEATURES Location/Qualifiers
 1..524
 /organism="Lycopersicon esculentum"
 /cultivar="TA496"
 /db_xref="taxon:4081"
 /clone="CLEGS4K24"
 /clone_lib="tomato breaker fruit"
 /tissue_type="Pericarp"
 /dev_stage="breaker"
 /lab_host="SOUR"
 /note="Vector: pBluescriptSKmCudapt; Site_1: EcoRI;
 Site_2: XhoI; supplier: Boyce Thompson Institute;
 sequencing: The Institute for Genomic Research. Fruit
 were harvested at the breaker stage (first sign of
 lycopene accumulation on the blossom end of fruit). Fruit
 were cut in half and the seeds and locules were discarded
 prior to freezing the pericarp."
 BASE COUNT 153 a 98 c 125 g 148 t
 ORIGIN
 Query Match 5.9%; Score 18; DB 10; Length 524;
 Best Local Similarity 100.0%; Pred. No. 2.2e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 71 qcaccacaaagggcagca 88
 |||||||||
 Db 372 GCATCCACAAGGGCAGCA 355
 RESULT 44
 BF513456/c
 LOCUS BF513456 525 bp mRNA linear EST 07-DEC-2000
 DEFINITION UI-H-BW1-ams-e-03-0-UI-s1 NCI_CGAP_Sub7 Homo sapiens cDNA clone
 IMAGE:3070948 3', mRNA sequence.
 ACCESSION BF513456
 VERSION BF513456.1 GI:11598635
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 525)
 REFERENCE NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 TITLE Unpublished (1997)
 JOURNAL

COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapsb@mai.nih.gov
 Oligo-dT track not found, Not 1 site shown in beginning of sequence
 is likely internal to the message. cDNA Library Preparation: M.B.
 Soares Lab Clone distribution: NCI-CGAP clone distribution
 Information can be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
 Seq primer: M13 Forward
 POLYA-No. Location/Qualifiers
 1..525
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:3070948"
 /clone_lib="NCI_CGAP_Sub7"
 /lab_host="DH10B (Life Technologies)"
 /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
 polylinker; Site_1: Not I; Site_2: Eco RI; NCI_CGAP_Sub7
 is a subtracted library derived from NCI_CGAP_Sub6. The
 NCI_CGAP_Sub7 library had 12 million recombinants. A
 single-stranded DNA preparation of NCI_CGAP_Sub6 was used
 as a tracer in a subtractive hybridization with a driver
 comprising: the IMAGE pool (NCI_CGAP_Kid3 pool 1 LLAM
 3334-3337, 3682-3683, 3798-3803 (IMAGE Clones)
 1322376-1323911, 1456008-1456775, 1500552-1502855);
 NCI_CGAP_Kid3 pool 1 LLAM 3338-3342, 3722-3725, 3776-3778
 (IMAGE Clones) 1323912-1325831, 1471368-1472803,
 1492104-1493255); NCI_CGAP_Lus pool 1 LLAM 3575-3582,
 3851-3854 (IMAGE Clones) 1414920-1417991, 1520904-1522439
); NCI_CGAP_GC4 pool 1 LLAM 3164-3167, 3716-3720,
 3733-3735 (IMAGE Clones) 1257096-1258631, 1469064-1470983
 , 1475592-1476743); NCI_CGAP_Pr22 pool 1 LLAM 2457-2459,
 2758-2759, 3062-3068 (IMAGE Clones) 985608-986759,
 1101152-1101959, 1217928-1220615); NCI_CGAP_Colo pool 1
 LLAM 2644-2653, 2871-2872 (IMAGE Clones) 1037416-1061255
 , 1144584-1145351). (6% of the driver population), plus a
 pool of 3,840 arrayed clones from NCI_CGAP_Sub1 (IMAGE
 Clones) 2708616-2710535) and NCI_CGAP_Sub2 (IMAGE
 Clones) 2710536-2712455) (4% of the driver population
), plus a pool of 11,136 clones from NCI_CGAP_Sub3 (IMAGE
 Clones) 2712456-2723591) (10% of the driver population),
 plus a pool of 5,472 clones from NCI_CGAP_Sub4 (IMAGE
 Clones) 2723592-2729326) (40% of the driver population),
 plus a pool of 4032 clones from NCI_CGAP_Sub6 (IMAGE
 Clones) 2728969-2733190) (40% of the driver population).
 Subtraction was performed as previously described [Bonaldi
 , Lennon & Soares (1996)]: Normalization and Subtraction:
 Two Approaches To Facilitate Gene Discovery. Genome
 Research 6, 791-806.
 TAG_SEQ=None found".
 BASE COUNT 94 a 195 c 179 g 57 t
 ORIGIN
 Query Match 5.9%; Score 18; DB 10; Length 525;
 Best Local Similarity 100.0%; Pred. No. 2.2e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 32 acggcgcttcgggaagg 49
 |||||||||
 Db 97 ACGGCGCTTCGGGAAGG 80
 RESULT 45
 BJ187298/c
 LOCUS BJ187298 528 bp mRNA linear EST 24-JAN-2002
 DEFINITION BJ187298 normalized full length cDNA library, chloronemata,
 caulonemata and malformed buds Physcomitrella patens subsp. patens
 cDNA clone phb40108 5', mRNA sequence.
 ACCESSION BJ187298
 VERSION BJ187298.1 GI:18355239
 KEYWORDS EST.
 SOURCE Physcomitrella patens subsp. patens.

ORGANISM Physcomitrella patens subsp. patens
 Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
 Bryopsida: Funariidae; Funariales; Funariaceae; Physcomitrella.
 REFERENCE 1 (bases 1 to 528)
 AUTHORS Fujita,T., Shin-i,T., Seki,M., Kamiya,A., Uchiyama,I., Nishiyama,T.,
 Carninci,P., Hayashizaki,Y., Shinozaki,K., Kohara,Y. and Hasebe,
 M.
 TITLE Comparison of the moss Physcomitrella patens genome with flowering
 plants genome
 JOURNAL Unpublished (2002)
 COMMENT Contact: Tadasu Shin-i
 Center For Genetic Resource Information
 National Institute of Genetics
 1111 Yata, Mishima, Shizuoka 411-8540, Japan
 Tel: 81-559-81-6856
 Fax: 81-559-81-6855
 Email: tshini@genes.nig.ac.jp
 A backbone of the vector is pBluescript II, that was in vivo
 excised from a modified lps phage vector (Mo bi Tec, Germany). XhoI
 digested-5' end of cDNA is ligated to SalI site of the vector, and
 the BamHI digested-3' end including poly-A tail is ligated to BamHI
 site of the vector. cDNA insert could be amplified with
 conventional T7 and T3 primers. This normalized full-length cDNA
 library was generated basically according to the method described
 in Genome Research 10, 1617-1630 (2000). Carninci, P. et al.
 Protonemata were blended by the POLYTRON, and then cultivated on
 the BCD medium containing 0.5uM BA (benzylaminopurine) for 8 to 13
 days under the continuous light.
 FEATURES
 source Location/Qualifiers
 1..528
 /organism="Physcomitrella patens subsp. patens"
 /db_xref="taxon:145481"
 /clone="ppb40108"
 /clone_lib="normalized full length cDNA library,
 chloronemata, caulonemata and malformed buds"
 /tissue_type="mixture of chloronemata, caulonemata and
 malformed buds"
 BASE COUNT 124 a 114 c 166 g 124 t
 ORIGIN

Query Match 5.9%; Score 18; DB 10; Length 528;
 Best Local Similarity 100.0%; Pred. No. 2.2e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 71 gcatccacaaggccagca 88
 |||||
 Db 92 GCATCCACAAGGCAGCA 75

Search completed: July 15, 2002, 20:07:28
 Job time: 14486 sec

Db 2726 atcggaacacacctcaacgtggtcaacctctctcggtggtgacccaagccgcagggcccc 2785
Qy 241 ctcattggtatcgtggagttctcaagtacgcgaacctctcacaacttctctgcgcgccaag 300
Db 2786 ctcattggtatcgtggagttctcaagtacgcgaacctctcacaacttctctgcgcgccaag 2845
Qy 301 cgg 303
Db 2846 cgg 2848
RESULT 2
US-09-442-384B-447
; Sequence 447, Application US/09442384B
; GENERAL INFORMATION:
; APPLICANT: Chenchik, Alex
; APPLICANT: Lukashov, Matvey
; TITLE OF INVENTION: Hematology/Immunology Array
; FILE REFERENCE: CLON-006CIP15
; CURRENT APPLICATION NUMBER: US/09/442,384B
; CURRENT FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: 09/053,375
; PRIOR FILING DATE: 1998-03-31
; NUMBER OF SEQ ID NOS: 830
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 447
; LENGTH: 4416
; TYPE: DNA
; ORGANISM: homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 4243
; OTHER INFORMATION: n = A,T,C or G
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 4243
; OTHER INFORMATION: n = A,T,C or G
US-09-442-384B-447

Query Match 100.0%; Score 303; DB 5; Length 4416;
Best Local Similarity 100.0%; Pred. No. 4.6e-152; Mismatches 0; Indels 0; Gaps 0;
Matches 303; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 gacggctcacctggggagagtgctcggtacgcgcgcttcgggaagtggtggaagcc 60
Db 2546 gacggctcacctggggagagtgctcggtacgcgcgcttcgggaagtggtggaagcc 2605
Qy 61 tccgctttcggcatccacaaaggcagcagctgtgacacgtggtggaatgctgaaa 120
Db 2606 tccgctttcggcatccacaaaggcagcagctgtgacacgtggtggaatgctgaaa 2665
Qy 121 gggggccacggccagcgagcaccgcgcgtgatgtcgagctcaagatcctcattcac 180
Db 2666 gggggccacggccagcgagcaccgcgcgtgatgtcgagctcaagatcctcattcac 2725
Qy 181 atcggaacacacctaactggttcaacctctctcggtggtgacccaagccgcagggcccc 240
Db 2726 atcggaacacacctaactggttcaacctctctcggtggtgacccaagccgcagggcccc 2785
Qy 241 ctcattggtatcgtggagttctcaagtacgcgaacctctcacaacttctctgcgcgccaag 300
Db 2786 ctcattggtatcgtggagttctcaagtacgcgaacctctcacaacttctctgcgcgccaag 2845
Qy 301 cgg 303
Db 2846 cgg 2848
RESULT 3
US-09-704-167A-7
; Sequence 7, Application US/09704167A
; GENERAL INFORMATION:

; APPLICANT: Havemann, Klaus
; TITLE OF INVENTION: Production and Use of Endothelial-like Cells
; FILE REFERENCE: BPD-100
; CURRENT APPLICATION NUMBER: US/09/704,167A
; CURRENT FILING DATE: 2000-11-01
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: VEGFR-3 5'-primer for RT-PCR, VEGFR-3 GenBank accession no. U009704.1
; OTHER INFORMATION: 020
US-09-704-167A-7

Query Match 7.6%; Score 23; DB 5; Length 23;
Best Local Similarity 100.0%; Pred. No. 0.028; Mismatches 0; Indels 0; Gaps 0;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 249 gatcgtggagttctgcaagtacg 271
Db 1 gatcgtggagttctgcaagtacg 23

RESULT 4
US-10-172-118-711
; Sequence 711, Application US/10172118
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yudong
; APPLICANT: Linsley, Peter
; APPLICANT: Mao, Mao
; APPLICANT: Roberts, Chris
; APPLICANT: Van 't Veer, Laura
; APPLICANT: Van de Vijver, Marc
; APPLICANT: Bernards, Rene
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 9301-175-999
; CURRENT APPLICATION NUMBER: US/10/172,118
; CURRENT FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: 60/380,770
; PRIOR FILING DATE: 2002-05-14
; NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 711
; LENGTH: 7680
; TYPE: DNA
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: NM_002019
; DATABASE ENTRY DATE: 2001-06-18
US-10-172-118-711

Query Match 6.6%; Score 20; DB 6; Length 7680;
Best Local Similarity 100.0%; Pred. No. 0.9; Mismatches 0; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 106 gtgaaaatgctgaagaggg 125
Db 2827 gtgaaaatgctgaagaggg 2846

RESULT 5
US-10-027-632-10882
; Sequence 10882, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129

; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10882
; LENGTH: 992
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-10882

Query Match 5.9%; Score 18; DB 6; Length 992;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 cacctggggagagtgctc 27
|||||

Db 928 cacctggggagagtgctc 945

RESULT 6
US-10-027-632-10883
; Sequence 10883, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10883
; LENGTH: 992
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-10883

Query Match 5.9%; Score 18; DB 6; Length 992;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 cacctggggagagtgctc 27
|||||

Db 928 cacctggggagagtgctc 945

RESULT 7
US-10-172-118-116
; Sequence 116, Application US/10172118
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yudong
; APPLICANT: Linsley, Peter
; APPLICANT: Mao, Mao
; APPLICANT: Roberts, Chris
; APPLICANT: Van 't Veer, Laura
; APPLICANT: Van de Vijver, Marc
; APPLICANT: Bernards, Rene
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 9301-175-999
; CURRENT APPLICATION NUMBER: US/10/172,118
; CURRENT FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: 60/380,770
; PRIOR FILING DATE: 2002-05-14
; NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 116
; LENGTH: 2329
; TYPE: DNA
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: AF049460
; DATABASE ENTRY DATE: 2001-06-18
US-10-172-118-116

Query Match 5.9%; Score 18; DB 6; Length 2329;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 32 acggcgcttcgggaagg 49
|||||

Db 324 acggcgcttcgggaagg 341

RESULT 8
US-10-138-674-1913
; Sequence 1913, Application US/10138674
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1913
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-138-674-1913

Query Match 5.6%; Score 17; DB 6; Length 17;
Best Local Similarity 70.6%; Pred. No. 46;
Matches 12; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 163 ctcaagatctcatcca 179
|:|:|:|:|:|:|:|:|:|

Db 1 cucaagaucuccauuca 17

```
RESULT 9
US-10-138-674-4731
; Sequence 4731, Application US/10138674
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE REFERENCE: MBH00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4731
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-138-674-4731

Query Match      5.6%; Score 17; DB 6; Length 17;
Best Local Similarity 88.2%; Pred. No. 46;
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 108 gaaaatgctgaaagagg 124
      |||||:||||:|||||
Db 1 gaaaaugcugaaagagg 17

RESULT 10
US-10-138-674-7615
; Sequence 7615, Application US/10138674
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE REFERENCE: MBH00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7615
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-138-674-7615

Query Match      5.6%; Score 17; DB 6; Length 17;
Best Local Similarity 82.4%; Pred. No. 46;
Matches 14; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 106 gtgaaaaatgctgaaaga 122
      |||||:||||:|||||
Db 1 gugaaaaaugcugaaaga 17

RESULT 11
US-09-721-544-11540/c
; Sequence 11540, Application US/09721544
; GENERAL INFORMATION:
; APPLICANT: Arterburn, Matthew
; APPLICANT: Asghari, Vida
; APPLICANT: Damavandi, Simin
; APPLICANT: Dickson, Mark
; APPLICANT: Drake, Jim
```

```
; APPLICANT: Drmanac, Radoje
; APPLICANT: Engleman, Carrie
; APPLICANT: Faulkner, Brandy
; APPLICANT: Garcia, Veronica
; APPLICANT: Giedt, Gretchen
; APPLICANT: Hunter, Kelly
; APPLICANT: Jessen, Aaron
; APPLICANT: Jones, Lee
; APPLICANT: Kita, David
; APPLICANT: Labat, Ivan
; APPLICANT: Laroya, Mimi
; APPLICANT: Lomelli, Michelle
; APPLICANT: Nguyen, Phuong
; APPLICANT: Nogra, Margie
; APPLICANT: Palencia, Servando
; APPLICANT: Raisi, Fariba
; APPLICANT: Smith, Benjamin
; APPLICANT: Tkach, Joe
; APPLICANT: Tran, Lien
; APPLICANT: Verna, Ron
; APPLICANT: Yang, Fel
; APPLICANT: Yim, Kenneth
; TITLE OF INVENTION: Novel Nucleic Acid Sequences Obtained
; FILE REFERENCE: 728CIP
; CURRENT APPLICATION NUMBER: US/09/721,544
; CURRENT FILING DATE: 2000-11-21
; PRIOR APPLICATION NUMBER: 09/515,128
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: 09/034,341
; PRIOR FILING DATE: 1998-02-13
; NUMBER OF SEQ ID NOS: 24489
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 11540
; LENGTH: 345
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-721-544-11540

Query Match      5.6%; Score 17; DB 5; Length 345;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 95 acaccgtgcccgtgaaa 111
      |||||:||||:|||||
Db 139 ACACCGTGGCGGTGAAA 123

RESULT 12
US-09-918-995-28414
; Sequence 28414, Application US/09918995
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 28414
; LENGTH: 439
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)-(439)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-28414
```



```
Query Match          5.6%:  Score 17;  DB 5;  Length 439;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 197 acgtggtcaacctctc 213
    |||
Db 117 acgtggtcaacctctc 133

RESULT 13
US-10-027-632-125688
; Sequence 125688, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: Polymorphisms in the Human Genome
; CURRENT APPLICATION NUMBER: 108827.129
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 125688
; LENGTH: 583
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-125688

Query Match          5.6%:  Score 17;  DB 6;  Length 583;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 93 tgacaccgtgcccgtga 109
    |||
Db 495 tgacaccgtgcccgtga 511

RESULT 14
US-60-360-039-40648
; Sequence 40648, Application US/60360039
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Chen, Xianfeng
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: PLANTS WITH IMPROVED PROPERTIES
; CURRENT APPLICATION NUMBER: US/60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 40648
; LENGTH: 1080
; TYPE: DNA
; ORGANISM: Caulobacter crescentus
US-60-360-039-40648
```

```
Query Match          5.6%:  Score 17;  DB 7;  Length 1080;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 281 ccaacttctctgcgcgc 297
    |||
Db 179 ccaacttctctgcgcgc 195

RESULT 15
US-09-663-870A-5
; Sequence 5, Application US/09663870A
; GENERAL INFORMATION:
; APPLICANT: Tang, Y Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Zhou, Ping
; APPLICANT: Asundi, Vinod
; APPLICANT: Zhang, Jie
; APPLICANT: Wehrman, Tom
; APPLICANT: Drmanac, Radolje T
; TITLE OF INVENTION: Novel Nucleic Acids and Peptides
; FILE REFERENCE: 21272-017 CIP2C
; CURRENT APPLICATION NUMBER: US/09/663.870A
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: 09/491,404
; PRIOR FILING DATE: 2000-01-25
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 1101
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1098)
US-09-663-870A-5

Query Match          5.6%:  Score 17;  DB 5;  Length 1101;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 197 acgtggtcaacctctc 213
    |||
Db 311 acgtggtcaacctctc 327

RESULT 16
US-10-155-881-36848
; Sequence 36848, Application US/10155881
; GENERAL INFORMATION:
; APPLICANT: Dotson, Stanton B.
; APPLICANT: Kovalic, David K.
; APPLICANT: Liu, Jingdong
; APPLICANT: Lutfiyya, Linda L.
; APPLICANT: McIninch, James
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
; FILE REFERENCE: TRANSCRIPTION IN PLANTS
; CURRENT APPLICATION NUMBER: US/10/155,881
; PRIOR FILING DATE: 2002-05-22
; NUMBER OF SEQ ID NOS: 37595
; SEQ ID NO 36848
; LENGTH: 1269
; TYPE: DNA
; ORGANISM: Glycine max
US-10-155-881-36848

Query Match          5.6%:  Score 17;  DB 6;  Length 1269;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

Tue Jul 16 09:39:23 2002

QY 54 ggaagcctccgcttctg 70
|||||
Db 671 ggaagcctccgcttctg 687

RESULT 17
US-09-980-285A-19
; Sequence 19, Application US/09980285A
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: HODGSON, David M.
; APPLICANT: LINCOLN, Stephen E.
; APPLICANT: RUSSO, Frank D.
; APPLICANT: SPIRO, Peter A.
; APPLICANT: BANVILLE, Steve C.
; APPLICANT: BRATCHER, Shawn R.
; APPLICANT: DUFOR, Gerard E.
; APPLICANT: COHEN, Howard J.
; APPLICANT: ROSEN, Bruce
; APPLICANT: CHALUP, Michael S.
; APPLICANT: HILLMAN, Jennifer L.
; APPLICANT: JONES, Annisa L.
; APPLICANT: YU, Jimmy Y.
; APPLICANT: GREENAWALT, Lila B.
; APPLICANT: PANZER, Scott R.
; APPLICANT: ROSEBERRY, Ann M.
; APPLICANT: WRIGHT, Rachel J.
; APPLICANT: DANIELS, Susan E.
; TITLE OF INVENTION: MOLECULES FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: PT-1022 PCT
; CURRENT FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: 60/137,109; 60/137,337; 60/137,258; 60/137,250; 60/137,113;
; 60/137,417; 60/137,259; 60/137,396; 60/137,114; 60/137,173; 60/137,411;
; 60/147,436; 60/147,549; 60/147,377; 60/147,527; 60/147,520; 60/147,536;
; 60/147,530; 60/147,547; 60/147,824; 60/147,541; 60/147,542; 60/147,500
; PRIOR FILING DATE: 1999-06-02; 1999-06-03; 1999-06-02; 1999-06-02; 1999-06-03;
; 1999-06-03; 1999-06-02; 1999-06-03; 1999-06-02; 1999-06-02; 1999-06-03;
; 1999-08-04; 1999-08-05; 1999-08-04; 1999-08-05; 1999-08-05; 1999-08-05;
; 1999-08-05; 1999-08-05; 1999-08-05; 1999-08-05; 1999-08-05;
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PERL Program
; SEQ ID NO 19
; LENGTH: 1406
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: 366739.2
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 311
; OTHER INFORMATION: a, t, c, g, or other
US-09-980-285A-19

Query Match 5.6%; Score 17; DB 5; Length 1406;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 276 ccttccaaactctctgc 292
|||||
Db 227 ccttccaaactctctgc 243

RESULT 18
US-10-155-881-17149
; Sequence 17149, Application US/10155881
; GENERAL INFORMATION:
; APPLICANT: Dotson, Stanton B.
; APPLICANT: Kovalic, David K.
; APPLICANT: Liu, Jingdong

; APPLICANT: Lutfiyya, Linda L.
; APPLICANT: McIninch, James
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
; TRANSCRIPTION IN PLANTS
; FILE REFERENCE: 38-21(15300)J
; CURRENT APPLICATION NUMBER: US/10/155,881
; CURRENT FILING DATE: 2002-05-22
; NUMBER OF SEQ ID NOS: 37595
; SEQ ID NO 17149
; LENGTH: 1557
; TYPE: DNA
; ORGANISM: Glycine max
US-10-155-881-17149

Query Match 5.6%; Score 17; DB 6; Length 1557;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 54 ggaagcctccgcttctg 70
|||||
Db 705 ggaagcctccgcttctg 721

RESULT 19
US-10-155-881-17151
; Sequence 17151, Application US/10155881
; GENERAL INFORMATION:
; APPLICANT: Dotson, Stanton B.
; APPLICANT: Kovalic, David K.
; APPLICANT: Liu, Jingdong
; APPLICANT: Lutfiyya, Linda L.
; APPLICANT: McIninch, James
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
; TRANSCRIPTION IN PLANTS
; FILE REFERENCE: 38-21(15300)J
; CURRENT APPLICATION NUMBER: US/10/155,881
; CURRENT FILING DATE: 2002-05-22
; NUMBER OF SEQ ID NOS: 37595
; SEQ ID NO 17151
; LENGTH: 1683
; TYPE: DNA
; ORGANISM: Glycine max
US-10-155-881-17151

Query Match 5.6%; Score 17; DB 6; Length 1683;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 54 ggaagcctccgcttctg 70
|||||
Db 895 ggaagcctccgcttctg 911

RESULT 20
US-10-105-299-8613
; Sequence 8613, Application US/10105299
; GENERAL INFORMATION:
; APPLICANT: Rosen, et. al
; TITLE OF INVENTION: Human Secreted Proteins
; FILE REFERENCE: PS950
; CURRENT APPLICATION NUMBER: US/10/105,299
; CURRENT FILING DATE: 2002-03-26
; NUMBER OF SEQ ID NOS: 15197
; Prior Application removed - See File Wrapper or Palm
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8613
; LENGTH: 1901
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-105-299-8613

Query Match 5.6%; Score 17; DB 6; Length 1901;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 276 cctctccaactctctgc 292
|||||

Db 620 cctctccaactctctgc 636

RESULT 21

US-10-105-299-8616
; Sequence 8616, Application US/10105299

; GENERAL INFORMATION:

; APPLICANT: Rosen, et. al

; TITLE OF INVENTION: Human Secreted Proteins

; FILE REFERENCE: PS950

; CURRENT APPLICATION NUMBER: US/10/105,299

; CURRENT FILING DATE: 2002-03-26

; NUMBER OF SEQ ID NOS: 15197

; Prior Application removed - See File Wrapper or Palm

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 8616

; LENGTH: 1901

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-105-299-8616

Query Match 5.6%; Score 17; DB 6; Length 1901;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 276 cctctccaactctctgc 292
|||||

Db 620 cctctccaactctctgc 636

RESULT 22

US-10-105-299-9023/c
; Sequence 9023, Application US/10105299

; GENERAL INFORMATION:

; APPLICANT: Rosen, et. al

; TITLE OF INVENTION: Human Secreted Proteins

; FILE REFERENCE: PS950

; CURRENT APPLICATION NUMBER: US/10/105,299

; CURRENT FILING DATE: 2002-03-26

; NUMBER OF SEQ ID NOS: 15197

; Prior Application removed - See File Wrapper or Palm

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 9023

; LENGTH: 1901

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-105-299-9023

Query Match 5.6%; Score 17; DB 6; Length 1901;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 276 cctctccaactctctgc 292
|||||

Db 1282 CCTCTCCAACCTCTCTGC 1266

RESULT 23

US-10-022-939-1

; Sequence 1, Application US/10022939

; GENERAL INFORMATION:

; APPLICANT: Kendall, Richard L.

; APPLICANT: Thomas, Kenneth A.

; APPLICANT: Mao, Xianzhi

; APPLICANT: Tebben, Andrew
; TITLE OF INVENTION: HUMAN RECEPTOR TYROSINE KINASE, KDR
; FILE REFERENCE: 19963YDB
; CURRENT APPLICATION NUMBER: US/10/022,939
; CURRENT FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: 09/483,539
; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: 09/098,707
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/050,962
; PRIOR FILING DATE: 1997-06-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 4071
; TYPE: DNA
; ORGANISM: Human
US-10-022-939-1

Query Match 5.6%; Score 17; DB 6; Length 4071;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 163 ctcaagatctctcatcca 179
|||||

Db 2656 ctcaagatctctcatcca 2672

RESULT 24

US-09-053-375B-136

; Sequence 136, Application US/09053375B

; GENERAL INFORMATION:

; APPLICANT: Chenchik, Alex

; APPLICANT: Bibilashvili, Robert

; TITLE OF INVENTION: Nucleic Acid Arrays

; FILE REFERENCE: CLON-006

; CURRENT APPLICATION NUMBER: US/09/053,375B

; CURRENT FILING DATE: 1998-08-31

; NUMBER OF SEQ ID NOS: 1543

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 136

; LENGTH: 4230

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-053-375B-136

Query Match 5.6%; Score 17; DB 5; Length 4230;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 163 ctcaagatctctcatcca 179
|||||

Db 2650 ctcaagatctctcatcca 2666

RESULT 25

US-10-141-260-7

; Sequence 7, Application US/10141260

; GENERAL INFORMATION:

; APPLICANT: Yu, Xuanchuan

; APPLICANT: Wilganowski, Nathaniel L.

; TITLE OF INVENTION: Novel Human Semaphorin Receptors and Polynucleotides Encoding

; FILE REFERENCE: LEX-0341-USA

; CURRENT APPLICATION NUMBER: US/10/141,260

; CURRENT FILING DATE: 2002-05-07

; PRIOR APPLICATION NUMBER: US 60/289,424

; PRIOR FILING DATE: 2001-05-08

; NUMBER OF SEQ ID NOS: 12

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 7
; LENGTH: 5685
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-141-260-7

Query Match 5.6%; Score 17; DB 6; Length 5685;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 72 catccacaaggcgagca 88
|||||
DB 5280 catccacaaggcgagca 5296

RESULT 26
US-10-141-260-11
; Sequence 11, Application US/10141260
; GENERAL INFORMATION:
; APPLICANT: Yu, Xuanchuan
; APPLICANT: Miranda, Maricar
; APPLICANT: Wilganowski, Nathaniel L.
; TITLE OF INVENTION: Novel Human Semaphorin Receptors and Polynucleotides Encoding the
; FILE REFERENCE: LEX-0341-USA
; CURRENT APPLICATION NUMBER: US/10/141,260
; CURRENT FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: US 60/289,424
; PRIOR FILING DATE: 2001-05-08
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 5730
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-141-260-11

Query Match 5.6%; Score 17; DB 6; Length 5730;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 72 catccacaaggcgagca 88
|||||
DB 5325 catccacaaggcgagca 5341

RESULT 27
US-10-116-802-18
; Sequence 18, Application US/10116802
; GENERAL INFORMATION:
; APPLICANT: Amy Lasek
; TITLE OF INVENTION: GENES EXPRESSED IN LUNG CANCER
; FILE REFERENCE: PA-0045 US
; CURRENT APPLICATION NUMBER: US/10/116,802
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: 60/281,593
; PRIOR FILING DATE: 2001-04-04
; NUMBER OF SEQ ID NOS: 519
; SOFTWARE: PERL Program
; SEQ ID NO 18
; LENGTH: 5832
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: 247817.4
US-10-116-802-18

Query Match 5.6%; Score 17; DB 6; Length 5832;
Best Local Similarity 100.0%; Pred. No. 37;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 163 ctcaagatctctattca 179
|||||
DB 2959 ctcaagatctctattca 2975

RESULT 28
US-10-133-013-269
; Sequence 269, Application US/10133013
; GENERAL INFORMATION:
; APPLICANT: Astromoff, Anna
; APPLICANT: Bandman, Olga
; APPLICANT: Cocks, Benjamin G.
; TITLE OF INVENTION: GENES ASSOCIATED WITH VASCULAR DISEASE
; FILE REFERENCE: PA-0049 US
; CURRENT APPLICATION NUMBER: US/10/133,013
; CURRENT FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: 60/287,067
; PRIOR FILING DATE: 2001-04-27
; NUMBER OF SEQ ID NOS: 271
; SOFTWARE: PERL Program
; SEQ ID NO 269
; LENGTH: 5841
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: 247817.4
US-10-133-013-269

Query Match 5.6%; Score 17; DB 6; Length 5841;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 163 ctcaagatctctattca 179
|||||
DB 2959 ctcaagatctctattca 2975

RESULT 29
US-10-141-260-3
; Sequence 3, Application US/10141260
; GENERAL INFORMATION:
; APPLICANT: Yu, Xuanchuan
; APPLICANT: Miranda, Maricar
; APPLICANT: Wilganowski, Nathaniel L.
; TITLE OF INVENTION: Novel Human Semaphorin Receptors and Polynucleotides Encoding
; FILE REFERENCE: LEX-0341-USA
; CURRENT APPLICATION NUMBER: US/10/141,260
; CURRENT FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: US 60/289,424
; PRIOR FILING DATE: 2001-05-08
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 5847
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-141-260-3

Query Match 5.6%; Score 17; DB 6; Length 5847;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 72 catccacaaggcgagca 88
|||||
DB 5442 catccacaaggcgagca 5458

```
RESULT 30
US-10-141-260-5
; Sequence 5, Application US/10141260
; GENERAL INFORMATION:
; APPLICANT: Yu, Xuanchuan
; APPLICANT: Miranda, Maricar
; APPLICANT: Wilganowski, Nathaniel L.
; TITLE OF INVENTION: Novel Human Semaphorin Receptors and Polynucleotides Encoding the
; FILE OF INVENTION: Same
; FILE REFERENCE: LEX-0341-USA
; CURRENT APPLICATION NUMBER: US/10/141,260
; CURRENT FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: US 60/289,424
; PRIOR FILING DATE: 2001-05-08
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 5880
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-141-260-5
```

```
Query Match 5.6%; Score 17; DB 6; Length 5880;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 72 catccacaaggcgagca 88
Db 5475 catccacaaggcgagca 5491
|||||

RESULT 31
US-10-141-260-9
; Sequence 9, Application US/10141260
; GENERAL INFORMATION:
; APPLICANT: Yu, Xuanchuan
; APPLICANT: Miranda, Maricar
; APPLICANT: Wilganowski, Nathaniel L.
; TITLE OF INVENTION: Novel Human Semaphorin Receptors and Polynucleotides Encoding the
; FILE OF INVENTION: Same
; FILE REFERENCE: LEX-0341-USA
; CURRENT APPLICATION NUMBER: US/10/141,260
; CURRENT FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: US 60/289,424
; PRIOR FILING DATE: 2001-05-08
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 5925
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-141-260-9
```

```
Query Match 5.6%; Score 17; DB 6; Length 5925;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 72 catccacaaggcgagca 88
Db 5520 catccacaaggcgagca 5536
|||||

RESULT 32
US-10-141-260-1
; Sequence 1, Application US/10141260
; GENERAL INFORMATION:
; APPLICANT: Yu, Xuanchuan
; APPLICANT: Miranda, Maricar
; APPLICANT: Wilganowski, Nathaniel L.
; TITLE OF INVENTION: Novel Human Semaphorin Receptors and Polynucleotides Encoding the
; FILE OF INVENTION: Same
```

```
; FILE REFERENCE: LEX-0341-USA
; CURRENT APPLICATION NUMBER: US/10/141,260
; CURRENT FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: US 60/289,424
; PRIOR FILING DATE: 2001-05-08
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 6042
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-141-260-1
```

```
Query Match 5.6%; Score 17; DB 6; Length 6042;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 72 catccacaaggcgagca 88
Db 5637 catccacaaggcgagca 5653
|||||
```

```
RESULT 33
PCT-US02-09944-259
; Sequence 259, Application PC/TUS0209944
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: DAFEO, Abel
; APPLICANT: JONES, Anissa L.
; APPLICANT: TRAN, Alanna-Phung B.
; APPLICANT: DAHL, Christopher R.
; APPLICANT: GIETZEN, Barryl
; APPLICANT: CHINN, Joyce
; APPLICANT: DUFOUR, Gerard E.
; APPLICANT: HILLMAN, Jennifer L.
; APPLICANT: YU, Jimmy Y.
; APPLICANT: TUASON, Olivia
; APPLICANT: YAP, Pierre E.
; APPLICANT: AMSHEY, Stefan R.
; APPLICANT: DAUGHERTY, Sean C.
; APPLICANT: LIU, Tommy F.
; APPLICANT: NGUYEN, Duy-Viet An
; APPLICANT: KLEEFELD, Yael
; APPLICANT: GERSTIN, JR., Edward H.
; APPLICANT: PERALTA, Careyana H.
; APPLICANT: DAVID, Marie H.
; APPLICANT: LEWIS, Samantha A.
; APPLICANT: CHEN, Alice J.
; APPLICANT: PANZER, Scott R.
; APPLICANT: HARRIS, Bernard
; APPLICANT: FLORES, Vincent
; APPLICANT: MARWAHA, Rakesh
; APPLICANT: LO, Audrey
; APPLICANT: LAN, Ruth Y.
; APPLICANT: URASHKA, Michael E.
; TITLE OF INVENTION: MOLECULES FOR DISEASE DETECTION AND TREATMENT
; FILE REFERENCE: PT-1231 PCT
; CURRENT APPLICATION NUMBER: PCT/US02/09944
; CURRENT FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: 60/280,067; 60/279,619; 60/280,068; 60/291,280; 60/291,8
; 60/291,829; 60/299,428; 60/300,001; 60/299,776
; PRIOR FILING DATE: 2001-03-29; 2001-03-28; 2001-03-29; 2001-05-16; 2001-05-17;
; 2001-05-17; 2001-06-19; 2001-06-20; 2001-06-20
; NUMBER OF SEQ ID NOS: 792
; SOFTWARE: PERL Program
; SEQ ID NO 259
; LENGTH: 7136
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
```

; OTHER INFORMATION: Incyte ID NO: LI:355693.18:2001MAY17
PCT-US02-09944-259

Query Match 5.6%; Score 17; DB 1; Length 7136;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 72 catccacaaggcgagca 88
|||||
Db 5985 catccacaaggcgagca 6001

RESULT 34

US-10-172-118-988/c
; Sequence 988, Application US/10172118
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yudong
; APPLICANT: Linsley, Peter
; APPLICANT: Mao, Mao
; APPLICANT: Roberts, Chris
; APPLICANT: Van 't Veer, Laura
; APPLICANT: Van de Vijver, Marc
; APPLICANT: Bernards, Rene
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 9301-175-999
; CURRENT APPLICATION NUMBER: US/10/172,118
; CURRENT FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: 60/380,770
; PRIOR FILING DATE: 2002-05-14
; NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 988
; LENGTH: 7515
; TYPE: DNA
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: NM_004104
; DATABASE ENTRY DATE: 2001-06-18
US-10-172-118-988

Query Match 5.6%; Score 17; DB 6; Length 7515;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 83 gcagcagctgtgacacc 99
|||||
Db 1612 GCAGCAGCTGTGACACC 1596

RESULT 35

US-10-138-674-5819
; Sequence 5819, Application US/10138674
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE REFERENCE: MBH800-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5819
; LENGTH: 16
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-138-674-5819

Query Match 5.3%; Score 16; DB 6; Length 16;
Best Local Similarity 81.2%; Pred. No. 1.6e+02;
Matches 13; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 107 tgaataatgctgaaaga 122
:||||:|:|||||
Db 1 ugaaaaugcugaaaga 16

RESULT 36

US-10-138-674-6641
; Sequence 6641, Application US/10138674
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Condition
; FILE REFERENCE: MBH800-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6641
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-138-674-6641

Query Match 5.3%; Score 16; DB 6; Length 17;
Best Local Similarity 68.8%; Pred. No. 1.6e+02;
Matches 11; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 164 tcaagatctctcatcca 179
:||||:|:|||||
Db 1 ucaagaucuccauca 16

RESULT 37

US-09-539-800C-4548/c
; Sequence 4548, Application US/09539800C
; GENERAL INFORMATION:
; APPLICANT: Seilhamer, Jeffrey J.
; APPLICANT: Delegeane, Angelo M.
; APPLICANT: Stuart, Susan G.
; APPLICANT: Stuve, Laura L.
; APPLICANT: Mullahy, Sara J.
; APPLICANT: Naughton, Rebecca E.
; TITLE OF INVENTION: POLYNUCLEOTIDES OF CONNECTIVE TISSUE
; FILE REFERENCE: PD-1023 CIP
; CURRENT APPLICATION NUMBER: US/09/539,800C
; CURRENT FILING DATE: 2000-03-30
; PRIOR APPLICATION NUMBER: 08/521,383
; PRIOR FILING DATE: August 16, 1995
; PRIOR APPLICATION NUMBER: 08/271,217
; PRIOR FILING DATE: June 27, 1994
; PRIOR APPLICATION NUMBER: 08/334,881
; PRIOR FILING DATE: November 4, 1994
; PRIOR APPLICATION NUMBER: 08/943,978
; PRIOR FILING DATE: October 3, 1997
; PRIOR APPLICATION NUMBER: 60/028,732
; PRIOR FILING DATE: October 4, 1996
; PRIOR APPLICATION NUMBER: 08/943,979
; PRIOR FILING DATE: October 4, 1997
; PRIOR APPLICATION NUMBER: 60/027,782
; PRIOR FILING DATE: October 4, 1996
; PRIOR APPLICATION NUMBER: 08/993,774
; PRIOR FILING DATE: December 18, 1997
; PRIOR APPLICATION NUMBER: 60/034,975

; PRIOR FILING DATE: December 20, 1996
; PRIOR APPLICATION NUMBER: 09/250,003
; PRIOR FILING DATE: February 10, 1999
; PRIOR APPLICATION NUMBER: 60/074,364
; PRIOR FILING DATE: February 12, 1998
; PRIOR APPLICATION NUMBER: 09/452,747
; PRIOR FILING DATE: December 1, 1999
; PRIOR APPLICATION NUMBER: 60/111,910
; PRIOR FILING DATE: December 10, 1998
; NUMBER OF SEQ ID NOS: 19698
; SOFTWARE: PERL Program
; SEQ ID NO 4548
; LENGTH: 198
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; OTHER INFORMATION: Incyte ID No: hu00608208
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 54, 66-67, 85
; OTHER INFORMATION: a, t, c, g, or other
US-09-539-800C-4548

Query Match 5.3%; Score 16; DB 5; Length 198;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 81 gggcagcagctgtgac 96
|||||
DB 163 GGCACGACGCTGTGAC 148

RESULT 38

US-09-540-210B-7506/c
; Sequence 7506, Application US/09540210B
; GENERAL INFORMATION:
; APPLICANT: Selihamer, Jeffrey J.
; APPLICANT: Delegeane, Angelo M.
; APPLICANT: Stuart, Susan G.
; APPLICANT: Stuve, Laura L.
; APPLICANT: Mullahy, Sara J.
; APPLICANT: Naughton, Rebecca E.
; TITLE OF INVENTION: POLYNUCLEOTIDES OF URINARY TRACT TISSUE
; FILE REFERENCE: PD-1037 CIP
; CURRENT APPLICATION NUMBER: US/09/540,210B
; CURRENT FILING DATE: 2002-04-03
; PRIOR APPLICATION NUMBER: 08/972,899
; PRIOR FILING DATE: November 18, 1997
; PRIOR APPLICATION NUMBER: 08/395,244
; PRIOR FILING DATE: February 27, 1995
; PRIOR APPLICATION NUMBER: 08/722,922
; PRIOR FILING DATE: September 27, 1996
; PRIOR APPLICATION NUMBER: 60/005,526
; PRIOR FILING DATE: September 29, 1995
; PRIOR APPLICATION NUMBER: 08/824,029
; PRIOR FILING DATE: March 25, 1997
; PRIOR APPLICATION NUMBER: 60/014,010
; PRIOR FILING DATE: March 25, 1996
; PRIOR APPLICATION NUMBER: 08/826,847
; PRIOR FILING DATE: April 10, 1997
; PRIOR APPLICATION NUMBER: 60/015,533
; PRIOR FILING DATE: April 10, 1996
; PRIOR APPLICATION NUMBER: 08/903,555
; PRIOR FILING DATE: July 31, 1997
; PRIOR APPLICATION NUMBER: 60/023,308
; PRIOR FILING DATE: July 31, 1996
; PRIOR APPLICATION NUMBER: 08/862,178
; PRIOR FILING DATE: May 22, 1997
; PRIOR APPLICATION NUMBER: 60/018,217
; PRIOR FILING DATE: May 23, 1996
; PRIOR APPLICATION NUMBER: 08/881,589

; PRIOR FILING DATE: June 24, 1997
; PRIOR APPLICATION NUMBER: 60/021,275
; PRIOR FILING DATE: June 25, 1996
; PRIOR APPLICATION NUMBER: 08/903,802
; PRIOR FILING DATE: July 31, 1997
; PRIOR APPLICATION NUMBER: 60/023,308
; PRIOR FILING DATE: July 31, 1996
; PRIOR APPLICATION NUMBER: 08/905,881
; PRIOR FILING DATE: August 1, 1997
; PRIOR APPLICATION NUMBER: 60/025,204
; PRIOR FILING DATE: August 1, 1996
; PRIOR APPLICATION NUMBER: 08/903,471
; PRIOR FILING DATE: July 30, 1997
; PRIOR APPLICATION NUMBER: 60/025,478
; PRIOR FILING DATE: July 31, 1996
; PRIOR APPLICATION NUMBER: 08/903,556
; PRIOR FILING DATE: July 31, 1997
; PRIOR APPLICATION NUMBER: 60/025,217
; PRIOR FILING DATE: August 22, 1996
; PRIOR APPLICATION NUMBER: 08/937,142
; PRIOR FILING DATE: September 23, 1997
; PRIOR APPLICATION NUMBER: 60/026,598
; PRIOR FILING DATE: September 24, 1996
; PRIOR APPLICATION NUMBER: 08/960,746
; PRIOR FILING DATE: October 29, 1997
; PRIOR APPLICATION NUMBER: 60/030,144
; PRIOR FILING DATE: October 30, 1996
; PRIOR APPLICATION NUMBER: 08/826,847
; PRIOR FILING DATE: April 10, 1997
; PRIOR APPLICATION NUMBER: 60/015,533
; PRIOR FILING DATE: April 10, 1996
; PRIOR APPLICATION NUMBER: 08/755,524
; PRIOR FILING DATE: November 22, 1996
; PRIOR APPLICATION NUMBER: 60/007,495
; PRIOR FILING DATE: November 22, 1995
; PRIOR APPLICATION NUMBER: 09/021,031
; PRIOR FILING DATE: February 10, 1998
; PRIOR APPLICATION NUMBER: 60/039,325
; PRIOR FILING DATE: February 13, 1997
; PRIOR APPLICATION NUMBER: 09/035,172
; PRIOR FILING DATE: March 4, 1998
; PRIOR APPLICATION NUMBER: 60/040,431
; PRIOR FILING DATE: March 5, 1997
; PRIOR APPLICATION NUMBER: 09/041,894
; PRIOR FILING DATE: March 12, 1998
; PRIOR APPLICATION NUMBER: 60/040,199
; PRIOR FILING DATE: March 14, 1997
; PRIOR APPLICATION NUMBER: 09/050,817
; PRIOR FILING DATE: March 30, 1998
; PRIOR APPLICATION NUMBER: 60/043,792
; PRIOR FILING DATE: April 11, 1997
; PRIOR APPLICATION NUMBER: 09/074,999
; PRIOR FILING DATE: May 8, 1998
; PRIOR APPLICATION NUMBER: 60/048,431
; PRIOR FILING DATE: May 29, 1997
; PRIOR APPLICATION NUMBER: 09/107,592
; PRIOR FILING DATE: June 30, 1998
; PRIOR APPLICATION NUMBER: 60/052,751
; PRIOR FILING DATE: July 1, 1997
; PRIOR APPLICATION NUMBER: 09/094,079
; PRIOR FILING DATE: June 9, 1998
; PRIOR APPLICATION NUMBER: 60/049,975
; PRIOR FILING DATE: June 13, 1997
; NUMBER OF SEQ ID NOS: 35654
; SOFTWARE: PERL Program
; SEQ ID NO 7506
; LENGTH: 213
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; OTHER INFORMATION: Incyte ID No: hu00129794
US-09-540-210B-7506

Query Match 5.3%; Score 16; DB 5; Length 213;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 81 gggcagcagctgtgac 96
|||||
DB 195 GGCAGCAGCTGTGAC 180

RESULT 39

US-09-539-331D-26866/c
; Sequence 26866, Application US/09539331D
; GENERAL INFORMATION:
; APPLICANT: Seilhamer, Jeffrey J.
; APPLICANT: Deleageane, Angelo M.
; APPLICANT: Stuart, Susan G.
; APPLICANT: Stuve, Laura L.
; APPLICANT: Mullahy, Sara J.
; APPLICANT: Naughton, Rebecca E.
; TITLE OF INVENTION: POLYNUCLEOTIDES OF CARDIOVASCULAR SYSTEM TISSUE
; FILE REFERENCE: PD-1022 CIP
; CURRENT APPLICATION NUMBER: US/09/539,331D
; CURRENT FILING DATE: 2000-03-30
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 40961
; SOFTWARE: PERL Program
; SEQ ID NO 26866
; LENGTH: 349
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc.feature
; OTHER INFORMATION: Incyte ID No: hu00486369
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 26, 37, 75, 79, 128, 207, 250, 285, 288, 291, 308, 339
; OTHER INFORMATION: a, t, c, g, or other
US-09-539-331D-26866

Query Match 5.3%; Score 16; DB 5; Length 349;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 81 gggcagcagctgtgac 96
|||||
DB 171 GGCAGCAGCTGTGAC 156

RESULT 40

US-10-027-632-186248
; Sequence 186248, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; POLYMORPHISMS IN THE HUMAN GENOME
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28

; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 186248
; LENGTH: 468
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-186248

Query Match 5.3%; Score 16; DB 6; Length 468;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 163 ctcaagatctctcattc 178
|||||
DB 129 ctcaagatctctcattc 144

RESULT 41

US-09-918-995-37903
; Sequence 37903, Application US/09918995
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FROM VARIOUS CDNA LIBRARIES
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 37903
; LENGTH: 494
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc.feature
; LOCATION: (1)...(494)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-37903

Query Match 5.3%; Score 16; DB 5; Length 494;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 81 gggcagcagctgtgac 96
|||||
DB 82 gggcagcagctgtgac 97

RESULT 42

US-60-377-240-10518
; Sequence 10518, Application US/60377240
; GENERAL INFORMATION:
; APPLICANT: Diggans, James C.
; APPLICANT: Porter, Mark
; APPLICANT: Wei, Tao
; TITLE OF INVENTION: Canine Gene Microarrays for Molecular Toxicology Modeling
; FILE REFERENCE: 44921-5116-PR
; CURRENT APPLICATION NUMBER: US/60/377,240
; CURRENT FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 11109
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10518
; LENGTH: 533
; TYPE: DNA
; ORGANISM: Canis familiaris


```
; FEATURE:
; OTHER INFORMATION:
; NAME/KEY: misc_feature
; LOCATION: (1)...(533)
; OTHER INFORMATION: n = a or c or g or t
US-60-377-240-10518

Query Match          5.3%  Score 16;  DB 7;  Length 533;
Best Local Similarity 100.0%;  Pred. No. 1.4e+02;
Matches 16;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

Oy 227 agccgcagggccccct 242
Db 280 agccgcagggccccct 295

RESULT 43
US-10-027-632-278270/c
; Sequence 278270, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027.632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 278270
; LENGTH: 543
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-278270

Query Match          5.3%  Score 16;  DB 6;  Length 543;
Best Local Similarity 100.0%;  Pred. No. 1.4e+02;
Matches 16;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

Oy 106 gtgaaatgctgaaag 121
Db 23 GTGAAATGCTGAAAG 8

RESULT 44
US-10-027-632-89410
; Sequence 89410, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027.632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
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; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 89410
; LENGTH: 568
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(568)
; OTHER INFORMATION: n = A,T,C or G
US-10-027-632-89410

Query Match          5.3%  Score 16;  DB 6;  Length 568;
Best Local Similarity 100.0%;  Pred. No. 1.4e+02;
Matches 16;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

Oy 74 tcacaaagggcgagcag 89
Db 439 tcacaaagggcgagcag 454

RESULT 45
US-10-027-632-303937
; Sequence 303937, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027.632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 303937
; LENGTH: 568
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(568)
; OTHER INFORMATION: n = A,T,C or G
US-10-027-632-303937

Query Match          5.3%  Score 16;  DB 6;  Length 568;
Best Local Similarity 100.0%;  Pred. No. 1.4e+02;
Matches 16;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;
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Oy 74 tccacaagggcagcag 89
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Db 439 tccacaagggcagcag 454

Search completed: July 16, 2002, 02:56:48
Job time: 24546 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: July 16, 2002, 02:49:40 ; Search time 12941.8 Seconds
(without alignments)
506.528 Million cell updates/sec

Title: us-09-375-248-1_copy_2546_2848

Perfect score: 303

Sequence: 1 gagcgctgacactggggag.....acttctgcgcgaagcgg 303

Scoring table: OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 21979536 seqs, 10817449327 residues

Word size : 0

Total number of hits satisfying chosen parameters: 43959072

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Pending_Patents_NA_Main.*

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- 46: /cgn2_6/ptodata/2/pna/US6007_COMB.seq.*
- 47: /cgn2_6/ptodata/2/pna/US6008_COMB.seq.*
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- 63: /cgn2_6/ptodata/2/pna/US6024_COMB.seq.*
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- 70: /cgn2_6/ptodata/2/pna/US6031_COMB.seq.*
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- 73: /cgn2_6/ptodata/2/pna/US6034_COMB.seq.*
- 74: /cgn2_6/ptodata/2/pna/US6035_COMB.seq.*
- 75: /cgn2_6/ptodata/2/pna/US6036_COMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	303	100.0	4111	1	PCT-US99-06133-1
2	303	100.0	4111	17	US-09-375-248-1
3	303	100.0	4195	3	US-07-959-951A-1
4	303	100.0	4195	6	US-08-257-754-1
5	303	100.0	4195	15	US-09-169-079-1
6	303	100.0	4416	10	US-08-601-132-36
7	303	100.0	4416	10	US-08-671-573A-36
8	303	100.0	4416	10	US-08-671-573B-36
9	303	100.0	4416	17	US-09-355-700-1
10	303	100.0	4416	18	US-09-440-302A-1035
11	303	100.0	4416	18	US-09-442-384A-447
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14	303	100.0	4416	24	US-09-631-092-36
15	303	100.0	4425	8	US-08-446-648-31
16	303	100.0	4425	11	US-08-770-449-31
17	303	100.0	4425	14	US-09-023-653-889
18	303	100.0	4425	36	US-09-982-610-31
19	303	100.0	4795	3	US-07-959-951A-3
20	303	100.0	4795	6	US-08-257-754-3
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23	303	100.0	9108	36	US-09-982-610-45
24	252	83.2	4113	37	US-10-081-126-1
25	252	83.2	4450	1	PCT-US99-08079-1
26	252	83.2	4450	37	US-10-012-214-1
27	252	83.2	4459	71	US-60-324-185-4274
28	238	78.5	4461	55	US-60-167-943-103
29	191	63.0	3277	59	US-60-209-009-455
30	191	63.0	3277	60	US-60-213-360-951
31	191	63.0	3277	71	US-60-324-185-4300

32 191 63.0 4462 56 US-60-172-373-15763 Sequence 15763, A
33 173 57.1 244 55 US-60-164-285-7458 Sequence 7458, Ap
34 100 33.0 516 58 US-60-195-052-399 Sequence 399, Ap
c 35 74 24.4 32768 60 US-60-213-178-297 Sequence 297, Ap
c 36 73 24.1 609 58 US-60-196-711-343 Sequence 343, Ap
c 37 73 24.1 609 58 US-60-196-713-572 Sequence 572, Ap
c 38 73 24.1 609 58 US-60-196-718-2866 Sequence 2866, Ap
39 53 17.5 492 58 US-60-196-711-279 Sequence 279, Ap
40 53 17.5 492 58 US-60-196-712-469 Sequence 469, Ap
41 53 16.8 51 56 US-60-172-373-15764 Sequence 15764, A
c 42 30 9.9 30 8 US-08-472-801-1194 Sequence 1194, Ap
c 43 30 9.9 30 10 US-08-668-235-1194 Sequence 1194, Ap
c 44 29 9.6 29 8 US-08-472-801-1170 Sequence 1170, Ap
c 45 29 9.6 29 10 US-08-668-235-1170 Sequence 1170, Ap

ALIGNMENTS

RESULT 1
PCT-US99-06133-1
; Sequence 1, Application PC/TUS9906133
; GENERAL INFORMATION:
; APPLICANT: Ferrell, Robert E.
; APPLICANT: Alitalo, Kari
; APPLICANT: Finegold, David N.
; APPLICANT: Karkkainen, Marika
; TITLE OF INVENTION: SCREENING AND THERAPY FOR LYMPHATIC DISORDERS INVOLVING
; FILE OF INVENTION: THE FLT4 RECEPTOR TYROSINE KINASE (VEGFR-3)
; CURRENT APPLICATION NUMBER: PCT/US99/06133
; CURRENT FILING DATE: 1999-03-26
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 4111
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (20)..(4111)
; OTHER INFORMATION: Human FLT4 (VEGFR-3) long form cDNA
PCT-US99-06133-1

Query Match 100.0%; Score 303; DB 1; Length 4111;
Best Local Similarity 100.0%; Pred. No. 3.9e-147;
Matches 303; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 gagcgctgacacctgggagagtgctcggctacggcgcccttcgggaaggtggtgaaagcc 60
Db 2546 gagcgctgacacctgggagagtgctcggctacggcgcccttcgggaaggtggtgaaagcc 2605
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Qy 241 ctcatgtgatcgtggagttctcgaagtacggcaacacacacacacacacacacacacacacac 300
Db 2786 ctcatgtgatcgtggagttctcgaagtacggcaacacacacacacacacacacacacacacac 2845
Qy 301 cgg 303
Db 2846 cgg 2848

RESULT 2
US-09-375-248-1
; Sequence 1, Application US/09375248
; GENERAL INFORMATION:
; APPLICANT: Ferrell, Robert E.
; APPLICANT: Alitalo, Kari
; APPLICANT: Finegold, David N.
; APPLICANT: Karkkainen, Marika
; TITLE OF INVENTION: SCREENING AND THERAPY FOR LYMPHATIC DISORDERS INVOLVING
; FILE OF INVENTION: THE FLT4 RECEPTOR TYROSINE KINASE (VEGFR-3)
; FILE REFERENCE: 28967/35255A
; CURRENT APPLICATION NUMBER: US/09/375, 248
; CURRENT FILING DATE: 1999-08-16
; EARLIER APPLICATION NUMBER: PCT/US99/06133
; EARLIER FILING DATE: 1999-03-26
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 4111
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (20)..(4111)
; FEATURE:
; OTHER INFORMATION: Human FLT4 (VEGFR-3) long form cDNA
US-09-375-248-1

Query Match 100.0%; Score 303; DB 17; Length 4111;
Best Local Similarity 100.0%; Pred. No. 3.9e-147;
Matches 303; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 61 tcgcttttcggatccacaaaggcgagctgtgacacccgtggtgaaatgctgaaa 120
Db 2606 tcgcttttcggatccacaaaggcgagctgtgacacccgtggtgaaatgctgaaa 2665
Qy 121 gagggcgccacggcgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 180
Db 2666 gagggcgccacggcgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 2725
Qy 181 atcggaac 240
Db 2726 atcggaac 2785
Qy 241 ctcatgtgatcgtggagttctcgaagtacggcaacacacacacacacacacacacacacacac 300
Db 2786 ctcatgtgatcgtggagttctcgaagtacggcaacacacacacacacacacacacacacacac 2845
Qy 301 cgg 303
Db 2846 cgg 2848

RESULT 3
US-07-959-951A-1
; Sequence 1, Application US/07959951A
; GENERAL INFORMATION:
; APPLICANT: Alitalo, Kari, et al.
; TITLE OF INVENTION: FLT4, A NOVEL RECEPTOR TYROSIN KINASE
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESSES:
; ADDRESS: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States
; ZIP: 60606-6402

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICANT: US/07/959,951A
FILING DATE: 19921009
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Gruber, Lewis S.
REGISTRATION NUMBER: 30,060
REFERENCE/DOCKET NUMBER: 28113/31104
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4195 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 20..3916
US-07-959-951A-1

Query Match 100.0%; Score 303; DB 3; Length 4195;
Best Local Similarity 100.0%; Pred. No. 3.9e-147;
Matches 303; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 2606 TCCGCTTTCCGGCATCCAAAGGCGCAGCAGCTGTGACACCGTGGCGCTCAAAATGCTGAAA 2665
Oy 121 gagggcgccagccagcagcagcagcagcagcagcagcagcagcagcagcagcagc 180
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Db 2666 GAGGCGCCACCGCCAGGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 2725
Oy 181 atcggaacacctaagcagtggtgagtgagtgagtgagtgagtgagtgagtgagtgag 240
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Db 2726 ATCGGCAACCACTCAAGTGTGTAACCTCTCTGGGGGGGTGACCAAGCCGCGGCCCC 2785
Oy 241 ctcatggtgatcgtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 300
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Db 2786 CTATGTTGATCGTGGAGTTCTGCAAGTAGGCAACCTCTCCAACCTCTCTCGCGCCCAAG 2845
Oy 301 cgg 303
Db 2846 CGG 2848

RESULT 4
US-08-257-754-1
; Sequence 1, Application US/08257754
; GENERAL INFORMATION:
; APPLICANT: Alitalo, Kari
; APPLICANT: Kaipainen, Arja
; APPLICANT: Korhonen, Jaana
; APPLICANT: Mustonen, Tuija
; APPLICANT: Pajusola, Kari
; APPLICANT: Matikainen, Marja-Terttu
; APPLICANT: Karnani, Paivi
; TITLE OF INVENTION: FLT4 RECEPTOR TYROSINE KINASE AND ITS USE IN
; TITLE OF INVENTION: DIAGNOSIS AND THERAPY
; NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICANT: US/08/257,754
FILING DATE: 09-JUN-1994
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/959,951
FILING DATE: 09-OCT-1992
ATTORNEY/AGENT INFORMATION:
NAME: Gass, David A.
REGISTRATION NUMBER: 38,153
REFERENCE/DOCKET NUMBER: 28344/32133
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4195 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 20..3916
US-08-257-754-1

Query Match 100.0%; Score 303; DB 6; Length 4195;
Best Local Similarity 100.0%; Pred. No. 3.9e-147;
Matches 303; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Oy 121 gagggcgccagccagcagcagcagcagcagcagcagcagcagcagcagcagcagc 180
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Db 2666 GAGGCGCCACCGCCAGGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 2725
Oy 181 atcggaacacctaagcagtggtgagtgagtgagtgagtgagtgagtgagtgagtgag 240
|||||
Db 2726 ATCGGCAACCACTCAAGTGTGTAACCTCTCTGGGGGGGTGACCAAGCCGCGGCCCC 2785
Oy 241 ctcatggtgatcgtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 300
|||||
Db 2786 CTATGTTGATCGTGGAGTTCTGCAAGTAGGCAACCTCTCCAACCTCTCTCGCGCCCAAG 2845
Oy 301 cgg 303
Db 2846 CGG 2848

RESULT 5
US-09-169-079-1
; Sequence 1, Application US/09169079
; GENERAL INFORMATION:

```

, MEDIUM TYPE: Floppy disk
, COMPUTER: IBM PC compatible
, OPERATING SYSTEM: PC-DOS/MS-DOS
, SOFTWARE: Patent In Release #1.0, Version #1.25
, CURRENT APPLICATION DATA:
, APPLICATION NUMBER: US/08/601,132
, FILING DATE:
, CLASSIFICATION: 530
, ATTORNEY/AGENT INFORMATION:
, NAME: Gass, David A.
, REGISTRATION NUMBER: 38 153
, REFERENCE/DOCKET NUMBER: 28113/33118
, TELECOMMUNICATION INFORMATION:
, TELEPHONE: 312/474-6300
, TELEFAX: 312/474-0448
, TELEX: 25-3856
, INFORMATION FOR SEQ ID NO: 36:
, SEQUENCE CHARACTERISTICS:
, LENGTH: 4416 base pairs
, TYPE: nucleic acid
, STRANDEDNESS: single
, TOPOLOGY: linear
, MOLECULE TYPE: DNA (genomic)
, US-08-601-132-36

```

Query Match	100.0%	Score 303;	DB 10;	Length 4416;
Best Local Similarity	100.0%;	Pred. No. 3.9e-147;		
Matches 303;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

Qy	1	gaqcgctgcactggggagagtgtctggctacgcgcgcttcggaaaggttggtgaaacc	60
Db	2546	GAGCGGCTGCACCTGGGGAGAGTCTCGGCTACGGCGCTTCGGGAAGTGTGTGAAGCC	2605
Qy	61	tcgcgtcttcggcatccacaaggcgagcagctgtgacaccgtggccgtgaaaalgcgtgaaa	120
Db	2606	TCCGCTTTCGGCATCCACAAGGCGACGACCTGTGACACCGTGCCTGAAATGCTGAAA	2665
Qy	121	gaggcgccacggccagcagcacgcgcgcgtgatgtcggagactcaagatcctcaltcac	180
Db	2666	GAGGGCGCCACGGCCACGAGCAGCGCGCTGATGTCGGAGCTCAAGATCTCATTTTAC	2725
Qy	181	atcggaaccacctaactggttcaactctctcggggcggtgcaccaagccgcaggagccccc	240
Db	2726	ATCGGCAACCACTCAACCTGTGTCAACCTCTCGGGGGCGTGCACCAAGCCCGAGGGCCCC	2785
Qy	241	ctcatggtgatcgtggagtctctgcaagtacggcaacctctccaactctctgcgcgcgccaag	300
Db	2786	CTCATGGTGATCGTGAGTCTTGCAAGTACGGCAACCTCTCCAACTTCTCTGGCGCCCAAG	2845
Qy	301	cgg 303	
Db	2846	CGG 2848	

```

RESULT      7
US-08-671-573A-36
; Sequence 36, Application US/08671573A
; GENERAL INFORMATION:
; APPLICANT: Alitalo, Karl
; APPLICANT: Joukov, Vladimir
; TITLE OF INVENTION: Receptor Ligand
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

```

; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/671.573A
; FILING DATE:
; CLASSIFICATION: 435
; APPLICATION NUMBER: 08/601.132
; FILING DATE: 14-FEB-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/585.895
; FILING DATE: 77-JAN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/510.133
; FILING DATE: 01-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Gass, David A.
; REGISTRATION NUMBER: 38,153
; REFERENCE/DOCKET NUMBER: 28113/33348
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4416 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-671-573A-36

Query Match 100.0%; Score 303; DB 10; Length 4416;
Best Local Similarity 100.0%; Pred. No. 3.9e-147;
Matches 303; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gagcggtcacctggggagagtgctcggtctacggcgcttcgggaagtggtggaagcc 60
DB 2546 GAGCGGCTGCACCTGGGGAGAGTGCTCGGCTACGGCGCTTCGGGAAGTGCTGGAAGCC 2605
QY 61 tcggtttcggcatccacaaggagcagcgcgcgtgatgtcgagctcaagatctctattcac 180
DB 2606 TC CGCTTTTCGGCATCCACAAGGGCAGCAGCTGTGACACCGTGGCGCTGAAAAATGCTGAAA 2665
QY 121 gagggcgccacgcagcagcagcgcgcgtgatgtcgagctcaagatctctattcac 180
DB 2666 GAGGGCGCCACGCCACGACGACCGCGCGCTGATGTCGGAGCTCAAGATCTCTATTAC 2725
QY 181 atcggcaaccactcaactcgtggtacacctctcctcgggcggtgcaccaagcgcgagggccc 240
DB 2726 ATCGGCAACGACCTCAACGTGGTCAACCTCCCTCGGGCGGTGCACCAAGCGCAGGGCCCC 2785
QY 241 ctcatggtatcgtgaggttcgcaagtacggcaacctctcaacttctcgcgcgccaag 300
DB 2786 CTCATGGTGATCGTGAGTTCTGCAAGTACGGCAACCTCTCCAACTTCTCGCGGCCAAG 2845
QY 301 cgg 303
DB 2846 CGG 2848

RESULT 8
US-08-671-573B-36
; Sequence 36, Application US/08671573B
; GENERAL INFORMATION:
; APPLICANT: Alitalo, Kari
; APPLICANT: Joukov, Vladimir
; TITLE OF INVENTION: Receptor Ligand
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive

; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/671.573B
; FILING DATE: 28-JUN-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/601.132
; FILING DATE: 14-FEB-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/585.895
; FILING DATE: 12-JAN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/510.133
; FILING DATE: 01-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Gass, David A.
; REGISTRATION NUMBER: 38,153
; REFERENCE/DOCKET NUMBER: 28967/33348
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4416 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-671-573B-36

Query Match 100.0%; Score 303; DB 10; Length 4416;
Best Local Similarity 100.0%; Pred. No. 3.9e-147;
Matches 303; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gagcggtcacctggggagagtgctcggtctacggcgcttcgggaagtggtggaagcc 60
DB 2546 GAGCGGCTGCACCTGGGGAGAGTGCTCGGCTACGGCGCTTCGGGAAGTGCTGGAAGCC 2605
QY 61 tcggtttcggcatccacaaggagcagcgcgcgtgatgtcgagctcaagatctctattcac 120
DB 2606 TC CGCTTTTCGGCATCCACAAGGGCAGCAGCTGTGACACCGTGGCGCTGAAAAATGCTGAAA 2665
QY 121 gagggcgccacgcagcagcagcgcgcgtgatgtcgagctcaagatctctattcac 180
DB 2666 GAGGGCGCCACGCCAGGCGAGCAGCGCGCTGATGTCGGAGCTCAAGATCTCTATTAC 2725
QY 181 atcggcaaccactcaactcgtggtacacctctcctcgggcggtgcaccaagcgcgagggccc 240
DB 2726 ATCGGCAACGACCTCAACGTGGTCAACCTCCCTCGGGCGGTGCACCAAGCGCAGGGCCCC 2785
QY 241 ctcatggtatcgtgaggttcgcaagtacggcaacctctcaacttctcgcgcgccaag 300
DB 2786 CTCATGGTGATCGTGAGTTCTGCAAGTACGGCAACCTCTCCAACTTCTCGCGGCCAAG 2845
QY 301 cgg 303
DB 2846 CGG 2848

RESULT 9
US-09-355-700-1
; Sequence 1, Application US/09355700
; GENERAL INFORMATION:

APPLICANT: Ludwig Institute for Cancer Research
Helsinki University Licensing
Alltalo, Kari(U.S. only)
Joukov, Vladimir (U.S. only)
TITLE OF INVENTION: Vascular Endothelial Growth Factor C (VEGF-C)
Protein and Gene, Mutants Thereof, and Uses Thereof
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/355,700
FILING DATE: 05-NOV-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/795,430
FILING DATE: 05-FEB-1997
APPLICATION NUMBER: PCT/FI96/00427
FILING DATE: 01-AUG-1996
APPLICATION NUMBER: 08/671,573
FILING DATE: 28-JUN-1996
APPLICATION NUMBER: 08/601,132
FILING DATE: 14-FEB-1996
APPLICATION NUMBER: 08/585,895
FILING DATE: 12-JAN-1996
APPLICATION NUMBER: 08/510,133
FILING DATE: 01-AUG-1995
APPLICATION NUMBER: 08/340,011
FILING DATE: 14-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Gass, David A.
REGISTRATION NUMBER: 38,153
REFERENCE/DOCKET NUMBER: 28967/34140
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4416 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-355-700-1

Query Match 100.0%; Score 303; DB 17; Length 4416;
Best Local Similarity 100.0%; Pred. No. 3.9e-147;
Matches 303; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 gagcggtgcacctgggagagtgctcggtacgagcgtcggtggaagtggtgaaagcc 60
|||||
Db 2546 GAGCGGCTGCACCTGGGAGAGTGTCTCGGCTACGCGCTTCGGGAAGGTGTGAAAGCC 2605
Qy 61 tccgcttcggcatccacagggcagcagctgtgacacggtggcggtgaaatgctgaaa 120
|||||
Db 2606 TCCGCTTTCGGCATCCACAGGGCAGCAGCTGTGACACCGTGGCGGTGAAAATGCTGAAA 2665
Qy 121 gagggcgccagggcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 180
|||||
Db 2666 GAGGGCGCACGGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 2725

Qy 181 atcggcaaccacctcaacgtggtcaacctctcctcgggggtgcaaccaagccgagggcccc 240
|||||
Db 2726 ATCGCAACCACTCAACGCTGCTCAACCTCTCGGGGGCTGCAACAGCCGAGGGCCCC 2785
Qy 241 ctcatggtgatcgtggagttctgcaagtacggcaacctctccaacttctctgcgcgccaag 300
|||||
Db 2786 CTCATGGTGATCGTGGAGTTCTGCAAGTACGGCAACCTCTCCAACTTCTCGCGCCCAAG 2845
Qy 301 cgg 303
|||
Db 2846 CGG 2848
RESULT 10
US-09-440-302A-1035
; Sequence 1035, Application US/09440302A
; GENERAL INFORMATION:
; APPLICANT: Chenchik, Alex
; APPLICANT: Lukashov, Matvey E.
; TITLE OF INVENTION: Human Neurobiology Array
; FILE REFERENCE: CLON-006CIP11
; CURRENT APPLICATION NUMBER: US/09/440.302A
; CURRENT FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: 09/053,375
; PRIOR FILING DATE: 1998-03-31
; NUMBER OF SEQ ID NOS: 1193
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1035
; LENGTH: 4416
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 4243
; OTHER INFORMATION: n = A,T,C or G
US-09-440-302A-1035

Query Match 100.0%; Score 303; DB 18; Length 4416;
Best Local Similarity 100.0%; Pred. No. 3.9e-147;
Matches 303; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 gagcggtgcacctgggagagtgctcggtacgagcgtcggtggaagtggtgaaagcc 60
|||||
Db 2546 gagcggtgcacctgggagagtgctcggtacgagcgtcggtggaagtggtgaaagcc 2605
Qy 61 tccgcttcggcatccacagggcagcagctgtgacacggtggcggtgaaatgctgaaa 120
|||||
Db 2606 tccgcttcggcatccacagggcagcagctgtgacacggtggcggtgaaatgctgaaa 2665
Qy 121 gagggcgccagggcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 180
|||||
Db 2666 gagggcgccagggcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 2725
Qy 181 atcggcaaccacctcaacgtggtcaacctctcctcgggggtgcaaccaagccgagggcccc 240
|||||
Db 2726 atcggcaaccacctcaacgtggtcaacctctcctcgggggtgcaaccaagccgagggcccc 2785
Qy 241 ctcatggtgatcgtggagttctgcaagtacggcaacctctccaacttctctgcgcgccaag 300
|||||
Db 2786 ctcatggtgatcgtggagttctgcaagtacggcaacctctccaacttctctgcgcgccaag 2845
Qy 301 cgg 303
|||
Db 2846 cgg 2848
RESULT 11
US-09-442-384A-447
; Sequence 447, Application US/09442384A
; GENERAL INFORMATION:
; APPLICANT: Chenchik, Alex
; APPLICANT: Lukashov, Matvey


```
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0821P3PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4425 base pairs
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; US-08-446-648-31

Query Match 100.0%; Score 303; DB 8; Length 4425;
Best Local Similarity 100.0%; Pred. No. 3.9e-147;
Matches 303; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gaacggctgcacctggagagtgctcgctacggcgcccttcgggaagtggtggaagcc 60
DB 2557 GAGCGGCTGCACCTGGGAGAGTGCTCGGTACGGCCCTTCGGGAAGGTGGTGAAGCC 2616

QY 61 tcgctttcggcatcccaaggagcagcagctgtgacacccgtggcgtgaaaaatgctgaaa 120
DB 2617 TCCGCTTTCCGCATCCACAAGGCGAGCAGCTGTGACACCCGTGGCCGTGAAAATGCTGAAA 2676

QY 121 gagggcgccagccagcagcagcagcagcagcagcagcagcagcagcagcagcagc 180
DB 2677 GAGGGCGCCACGCGCCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 2736

QY 181 atcggaacacacctcaacgtgggtcaacacctcctcgggcgctgacacacccagcgcccaag 300
DB 2737 ATCGGCAACCACTCAACGTGGTCAACCTCCTCGGGCGGTGCACCAAGCCGAGGGCCCC 2796

QY 241 ctcagtgtgatcgtggagttcgtgaaatcagggcaacctctccaaacttctcgtcgcccaag 300
DB 2797 CTCATGCTGATCGTGGAGTTCTGCAACTACGGCAACCTCTCCAACCTTCTCTGCGGCCAAG 2856

QY 301 cgg 303
DB 2857 CGG 2859

RESULT 16
US-08-770-449-31
; Sequence 31, Application US/08770449
; GENERAL INFORMATION:
; APPLICANT: Bennett, Brian D.
; APPLICANT: Goeddel, David
; APPLICANT: Lee, James M.
; APPLICANT: Matthews, William
; APPLICANT: Tsai, Siao Ping
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: PROTEIN TYROSINE KINASE AGONIST ANTIBODIES
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/770,449
; FILING DATE: 20-Dec-1996
```

```
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/00586
; FILING DATE: 22-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/826935
; FILING DATE: 22-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/222616
; FILING DATE: 04-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0821P2D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4425 base pairs
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; US-08-770-449-31

Query Match 100.0%; Score 303; DB 11; Length 4425;
Best Local Similarity 100.0%; Pred. No. 3.9e-147;
Matches 303; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gaacggctgcacctggagagtgctcgctacggcgcccttcgggaagtggtggaagcc 60
DB 2557 GAGCGGCTGCACCTGGGAGAGTGCTCGGTACGGCCCTTCGGGAAGGTGGTGAAGCC 2616

QY 61 tcgctttcggcatcccaaggagcagcagctgtgacacccgtggcgtgaaaaatgctgaaa 120
DB 2617 TCCGCTTTCCGCATCCACAAGGCGAGCAGCTGTGACACCCGTGGCCGTGAAAATGCTGAAA 2676

QY 121 gagggcgccagccagcagcagcagcagcagcagcagcagcagcagcagcagcagc 180
DB 2677 GAGGGCGCCACGCGCCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 2736

QY 181 atcggaacacacctcaacgtgggtcaacacctcctcgggcgctgacacacccagcgcccaag 240
DB 2737 ATCGGCAACCACTCAACGTGGTCAACCTCCTCGGGCGGTGCACCAAGCCGAGGGCCCC 2796

QY 241 ctcagtgtgatcgtggagttcgtgaaatcagggcaacctctccaaacttctcgtcgcccaag 300
DB 2797 CTCATGCTGATCGTGGAGTTCTGCAAGTACGGCAACCTCTCCAACCTTCTCTGCGGCCAAG 2856

QY 301 cgg 303
DB 2857 CGG 2859

RESULT 17
US-09-023-655-889
; Sequence 889, Application US/09023655
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Susan G. Stuart
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
; TITLE OF INVENTION: EXPRESSION
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
```


APPLICANT: Alitalo, Kari, et al.
TITLE OF INVENTION: FLT4, A NOVEL RECEPTOR TYROSIN KINASE
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/959,951A
FILING DATE: 19921009
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Gruber, Lewis S.
REGISTRATION NUMBER: 30,060
REFERENCE/DOCKET NUMBER: 28113/31104
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 4795 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 20..4111
US-07-959-951A-3

Query Match 100.0%; Score 303; DB 3; Length 4795;
Best Local Similarity 100.0%; Pred. No. 3.9e-147;
Matches 303; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 gagcggtgcacctggggagagtgctcgctacgagcgccttcgggaaagtgtggaagcc 60
Db 2546 GAGCGGCTGCACCTGGGGAGAGTGCTCGCTACGCGCTTCGGGAAGGTGGTGAAGCC 2605
Qy 61 tcggtttcgggcatccacaaggagcagctgtgacaccgtggtggtgaaatgctgaaa 120
Db 2606 TCCGCTTTTCGGCATCCACAAGGCGAGCAGCTGTGACACCGTGGCGGTGAAATGCTGAAA 2665
Qy 121 gagggcgccacgagcagcagcgcgctgtatgctgagctcaagatcctcatcacc 180
Db 2666 GAGGGCGCCACGGCCAGCAGCAGCGCGCTGTATGTCGGAGCTCAAGATCCTCATTCAC 2725
Qy 181 atcggaaccacctcaacgttggtcaacctctcctcgggcggtgacacaaagcgcagggcccc 240
Db 2726 ATCGGCAACCACTCAACGTGGTCAACCTCTCTGGGGCGTGCACCAAGCGCGGCCCC 2785
Qy 241 ctcatgtatcgtggagttctgcaagtaagcgaacctctccaactctcgtgcgccaag 300
Db 2786 CTCATGTGATCGTGGAGTTCTGCAAGTACGGCAACCTCTCCAACTTCTCTCGCGGCAAG 2845
Qy 301 cgg 303
Db 2846 CGG 2848

RESULT 20
US-08-257-754-3
; Sequence 3, Application US/08257754
; GENERAL INFORMATION:

APPLICANT: Alitalo, Kari
APPLICANT: Kaipainen, Arja
APPLICANT: Korhonen, Jaana
APPLICANT: Mustonen, Tuija
APPLICANT: Pajusola, Kari
APPLICANT: Matikainen, Marja-Terttu
APPLICANT: Kannani, Paivi
TITLE OF INVENTION: FLT4 RECEPTOR TYROSINE KINASE AND ITS USE IN
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/257,754
FILING DATE: 09-JUN-1994
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/959,951
FILING DATE: 09-OCT-1992
ATTORNEY/AGENT INFORMATION:
NAME: Gass, David A.
REGISTRATION NUMBER: 38,153
REFERENCE/DOCKET NUMBER: 28344/32133
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 4795 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 20..4111
US-08-257-754-3

Query Match 100.0%; Score 303; DB 6; Length 4795;
Best Local Similarity 100.0%; Pred. No. 3.9e-147;
Matches 303; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 gagcggtgcacctggggagagtgctcgctacgagcgccttcgggaaagtgtggaagcc 60
Db 2546 GAGCGGCTGCACCTGGGGAGAGTGCTCGCTACGCGCTTCGGGAAGGTGGTGAAGCC 2605
Qy 61 tcggtttcgggcatccacaaggagcagctgtgacaccgtggtggtgaaatgctgaaa 120
Db 2606 TCCGCTTTTCGGCATCCACAAGGCGAGCAGCTGTGACACCGTGGCGGTGAAATGCTGAAA 2665
Qy 121 gagggcgccacgagcagcagcgcgctgtatgctgagctcaagatcctcatcacc 180
Db 2666 GAGGGCGCCACGGCCAGCAGCAGCGCGCTGTATGTCGGAGCTCAAGATCCTCATTCAC 2725
Qy 181 atcggaaccacctcaacgttggtcaacctctcctcgggcggtgacacaaagcgcagggcccc 240
Db 2726 ATCGGCAACCACTCAACGTGGTCAACCTCTCTGGGGCGTGCACCAAGCGCGGCCCC 2785
Qy 241 ctcatgtatcgtggagttctgcaagtaagcgaacctctccaactctcgtgcgccaag 300
Db 2786 CTCATGTGATCGTGGAGTTCTGCAAGTACGGCAACCTCTCCAACTTCTCTCGCGGCAAG 2845

Qy 301 cgg 303
|||
Db 2846 CGG 2848

RESULT 21

US-09-169-079-3

Sequence 3, Application US/09169079

GENERAL INFORMATION:

APPLICANT: Alitalo, Kari

APPLICANT: Kaipainen, Arja

APPLICANT: Valtola, Reijo

APPLICANT: Jussila, Lotta

TITLE OF INVENTION: Fil4 (VEGFR-3) as a Target for Tumor Imaging and Anti-Tumor Thera

FILE REFERENCE: 28113/34891

CURRENT APPLICATION NUMBER: US/09/169,079

EARLIER FILING DATE: 1998-10-09

EARLIER FILING DATE: 1997-07-28

EARLIER FILING DATE: 1997-07-28

EARLIER FILING DATE: 1994-11-14

EARLIER FILING DATE: 1994-11-14

EARLIER FILING DATE: 1994-07-09

EARLIER FILING DATE: 1992-10-09

NUMBER OF SEQ ID NOS: 22

SOFTWARE: Patent In Ver. 2.0

SEQ ID NO 3

LENGTH: 4795

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: CDS

LOCATION: (20)..(4108)

US-09-169-079-3

Query Match 100.0%; Score 303; DB 15; Length 4795;
Best Local Similarity 100.0%; Pred. No. 3.9e-147;
Matches 303; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 gagcggctcacctggggagagtgctcggtacgcgccttcgggaagtggtggaagcc 60
|||
Db 2546 gagcggctcacctggggagagtgctcggtacgcgccttcgggaagtggtggaagcc 2605
Qy 61 tcgcgttcggtacacacagggcagcagctgtgacacgtggtggaagtggtggaagcc 120
|||
Db 2606 tcgcgttcggtacacacagggcagcagctgtgacacgtggtggaagtggtggaagcc 2665
Qy 121 gagggcgccacggccagcagcagcgcgcgtgatgtcgagctcaagatcctcattcac 180
|||
Db 2666 gagggcgccacggccagcagcagcgcgcgtgatgtcgagctcaagatcctcattcac 2725
Qy 181 atcggcaaccactcaacgtggtcacccttcctcgggcggtgacacacggcggccccc 240
|||
Db 2726 atcggcaaccactcaacgtggtcacccttcctcgggcggtgacacacggcggccccc 2785
Qy 241 ctcatggtgatcgtgagttctcgaagtcaggaacacctctcgaacctctcgtcgcccaag 300
|||
Db 2786 ctcatggtgatcgtgagttctcgaagtcaggaacacctctcgaacctctcgtcgcccaag 2845
Qy 301 cgg 303
|||
Db 2846 cgg 2848

RESULT 22

US-08-446-648-45

Sequence 45, Application US/08446648

GENERAL INFORMATION:

APPLICANT: Genentech, Inc.

APPLICANT: Bennett, Brian D.

APPLICANT: Goeddel, David
APPLICANT: Lee, James M.
APPLICANT: Matthews, William
APPLICANT: Tsai, Siao Ping
APPLICANT: Wood, William I.
TITLE OF INVENTION: PROTEIN TYROSINE KINASE AGONIST ANTIBODIES
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,648
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/222616
FILING DATE: 04-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0821P3PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 9108 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
US-08-446-648-45

Query Match 100.0%; Score 303; DB 8; Length 9108;
Best Local Similarity 100.0%; Pred. No. 3.8e-147;
Matches 303; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 gagcggctgcacctggggagagtgctcggtacgcgccttcgggaagtggtggaagcc 60
|||
Db 3489 GAGCGGCTGCACCTGGGAGAGTGCTCGGCTACGGCGCTTCGGGAAGGTGTTGGAAGCC 3548
Qy 61 tcgcgttcggtacacacagggcagcagctgtgacacgtggtggaagtggtggaagcc 120
|||
Db 3549 TCCGCTTTCGGCATCCACAAAGGGCAGCAGCTGTGACACCGCTGGCGCTGAAATGCTGAAA 3608
Qy 121 gagggcgccacggcagcagcagcgcgcgtgatgtcgagctcaagatcctcattcac 180
|||
Db 3609 GAGGGCGCCAGCGGCGAGCAGCAGCGCGCTGTGTGCGAGCTCAAGATCCTCATTCAC 3668
Qy 181 atcggcaaccactcaacgtggtcacccttcctcgggcggtgacacacggcggccccc 240
|||
Db 3669 ATCGCAACCACTCAACGTGTCAACCTCTCTCGGGGGGTGACCAAGCGCAGGGCCCC 3728
Qy 241 ctcatggtgatcgtgagttctcgaagtcaggaacacctctcgaacctctcgtcgcccaag 300
|||
Db 3729 CTCATGTTGATCGTGGAGTTCTGCAAGTAGGCAACCTCTCCAACTTCTCTGCGGCCCAAG 3788
Qy 301 cgg 303
|||
Db 3789 CGG 3791

RESULT 23

US-09-982-610-45

; Sequence 45, Application US/09982610
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; Bennett, Brian D.
; Goeddel, David

; Lee, James M.
; Matthews, William
; Tsai, Siao Ping
; Wood, William I.

; TITLE OF INVENTION: PROTEIN TYROSINE KINASE AGONIST ANTIBODIES
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/982,610
; FILING DATE: 17-Oct-2001
; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/446,648
; FILING DATE: 1996-MAY-23
; APPLICATION NUMBER: 08/22616
; FILING DATE: 04-APR-1994

; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0821P3PCT

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168

; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9108 base pairs
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear

; SEQUENCE DESCRIPTION: SEQ ID NO: 45:
US-09-982-610-45

Query Match 100.0%; Score 303; DB 36; Length 9108;
Best Local Similarity 100.0%; Pred. No. 3.8e-147;
Matches 303; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gagcggtgcacgtgggagagtgctcggtctacggccttcgggaagtggtggaagcc 60
DB 3489 GAGCGGCTGCACGTGGGAGAGTGTCTGGCTACGGCGCTTCGGGAAGTGTGGAAGCC 3548

QY 61 tcggtttcggcatccacaaaggcagcagctgtgacacccgtggccgtgaaatgctgaaa 120
DB 3549 TCGGCTTTTCGGCATCCACAAAGGCGACAGCTGTGACCCGTGGCGTGAATGCTGAAA 3608

QY 121 gagggcgccacgcagcagcagcgcgcgtgatgtcgagctcaagatctctattcac 180
DB 3609 GAGGGCGCCACGCCACGAGCAGCCGCGCTGATGTGCGAGCTCAAGATCTCTATTCA 3668

QY 181 atcggaacacactcaacgttggttaacctctcgtggggcgtgaccacgagcagggccccc 240
DB 3669 ATCGGAACACACTCAACGTGTTCAACCTCTCTCGGGCGCTGCACCAAGCCGAGGGCCCC 3728

QY 241 ctcattggtgatcgtgaggttctgcaagtacggcaacctctcacaacttctcgcgcgcaag 300
|||||

DB 3729 CTCATGGTATCGTGGAGTTCTGCAAGTACGGCAACCTCTCCAACCTTCTCTGGCGCCAAG 3788

QY 301 cgg 303
|||

DB 3789 CGG 3791

RESULT 24

US-10-081-126-1

; Sequence 1, Application US/10081126
; GENERAL INFORMATION:

; APPLICANT: De Vries, Gerald W.
; TITLE OF INVENTION: Methods of Extending Corneal Graft

; TITLE OF INVENTION: Survival
; FILE REFERENCE: P-AR 4951
; CURRENT APPLICATION NUMBER: US/10/081,126
; CURRENT FILING DATE: 2002-02-22
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 4113
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (22)...(4110)
US-10-081-126-1

Query Match 83.2%; Score 252; DB 37; Length 4113;
Best Local Similarity 99.7%; Pred. No. 1.6e-120;
Matches 302; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 gagcggtgcacgtgggagagtgctcggtctacggccttcgggaagtggtggaagcc 60
DB 2548 gagcggtgcacgtgggagagtgctcggtctacggccttcgggaagtggtggaagcc 2607

QY 61 tcggtttcggcatccacaaaggcagcagctgtgacacccgtggccgtgaaatgctgaaa 120
DB 2608 tcggtttcggcatccacaaaggcagcagctgtgacacccgtggccgtgaaatgctgaaa 2667

QY 121 gagggcgccacgcagcagcgcgcgtgatgtcgagctcaagatctctattcac 180
DB 2668 gagggcgccacgcagcagcgcgcgtgatgtcgagctcaagatctctattcac 2727

QY 181 atcggaacacactcaacgttggttaacctctcgtggggcgtgaccacgagcagggccccc 240
DB 2728 atcggaacacactcaacgttggttaacctctcgtggggcgtgaccacgagcagggccccc 2787

QY 241 ctcattggtgatcgtgaggttctgcaagtacggcaacctctcacaacttctcgcgcgcaag 300
DB 2788 ctcattggtgatcgtgaggttctgcaagtacggcaacctctcacaacttctcgcgcgcaag 2847

QY 301 cgg 303
|||

DB 2848 cgg 2850

RESULT 25

PCT-US99-08079-1

; Sequence 1, Application PC/TUS9908079
; GENERAL INFORMATION:

; APPLICANT: Northwest Biotherapeutics, Inc.
; TITLE OF INVENTION: METHODS FOR THE DIAGNOSIS AND TREATMENT OF METASTATIC

; TITLE OF INVENTION: PROSTATE TUMORS
; FILE REFERENCE: 8511-025-228
; CURRENT APPLICATION NUMBER: PCT/US99/08079
; CURRENT FILING DATE: 1999-04-13
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 4450
; TYPE: DNA

RESULT 28
US-60-167-943-103
: Sequence 103, Application US/60167943
: GENERAL INFORMATION:
: APPLICANT: Hodgson, David M.
: APPLICANT: Lincoln, Stephen E.
: APPLICANT: Russo, Frank D.
: APPLICANT: Spiro, Peter A.
: APPLICANT: Bannille, Steve C.
: APPLICANT: Bratcher, Shawn R.
: APPLICANT: Dufour, Gerard E.
: APPLICANT: Cohen, Howard J.
: APPLICANT: Rosen, Bruce
: APPLICANT: Shah, Purvi
: APPLICANT: Chalup, Michael S.
: APPLICANT: Hillman, Jennifer L.
: FILE REFERENCE: PT-0093 P
: CURRENT APPLICATION NUMBER: US/60/167,943
: CURRENT FILING DATE: 1999-11-29
: NUMBER OF SEQ ID NOS: 244
: SOFTWARE: PERL Program
: SEQ ID NO 103
: LENGTH: 4461
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc_feature
: OTHER INFORMATION: Incyte ID No: 902563.1
: FEATURE:
: NAME/KEY: unsure
: LOCATION: 2402-2421
: OTHER INFORMATION: a, t, c, g, or other
US-60-167-943-103

Query Match 78.5%; Score 238; DB 55; Length 4461;
Best Local Similarity 100.0%; Pred. No. 3.2e-113;
Matches 238; Conservative 0; Mismatches 0; Indels 0; Gaps 0:

Qy 5 ggcctgcacctgggagagtgctcgctacgcgccttcgggaaagtggtggaagcctccg 64
Db 2561 ggcctgcacctgggagagtgctcgctacgcgccttcgggaaagtggtggaagcctccg 2620

Qy 65 ctttcggcatccacaaggcagcagctgtgacacccgtgcccgtgaaatgctgaaaggg 124
Db 2621 ctttcggcatccacaaggcagcagctgtgacacccgtgcccgtgaaatgctgaaaggg 2680

Qy 125 gcgcacgcccagcagcagcagcgcgcgtgatgtcggagctcaagatcctcattcacatcg 184
Db 2681 gcgcacgcccagcagcagcagcgcgcgtgatgtcggagctcaagatcctcattcacatcg 2740

Qy 185 gcaaccacctcaacgtggtcaacctctcggggcgtgacacacccagcagggcccccct 242
Db 2741 gcaaccacctcaacgtggtcaacctctcggggcgtgacacacccagcagggcccccct 2798

RESULT 29
US-60-209-009-455
: Sequence 455, Application US/60209009
: GENERAL INFORMATION:
: APPLICANT: Paris, Mary
: APPLICANT: Pearson, Cecelia I.
: TITLE OF INVENTION: GENES EXPRESSED IN PROSTATE CANCER
: FILE REFERENCE: PA-0027 P
: CURRENT APPLICATION NUMBER: US/60/209,009
: CURRENT FILING DATE: 2000-06-01
: NUMBER OF SEQ ID NOS: 501
: SOFTWARE: PERL Program
: SEQ ID NO 455
: LENGTH: 3277
: TYPE: DNA
: ORGANISM: Homo sapiens

: FEATURE:
: NAME/KEY: misc_feature
: OTHER INFORMATION: Incyte ID No: 1084493.6
US-60-209-009-455

Query Match 63.0%; Score 191; DB 59; Length 3277;
Best Local Similarity 99.6%; Pred. No. 1.1e-88;
Matches 241; Conservative 0; Mismatches 1; Indels 0; Gaps 0:

Qy 1 gagcggctgcacctggggagagtgctcgctacggcgcccttcgggaaagtggtggaagcc 60
Db 25 gagcggctgcacctggggagagtgctcgctacggcgcccttcgggaaagtggtggaagcc 84

Qy 61 tcgcgttcggcatccacaaggcagcagctgtgacacccgtgcccgtgaaaaatgctgaaa 120
Db 85 tcgcgttcggcatccacaaggcagcagctgtgacacccgtgcccgtgaaaaatgctgaaa 144

Qy 121 gaggcgccacgcccagcagcagcgcgcgtgatgtcggagctcaagatcctcattcac 180
Db 145 gaggcgccacgcccagcagcagcgcgcgtgatgtcggagctcaagatcctcattcac 204

Qy 181 atcggcaaccacctcaacgtggtcaacctctcggggcgtgacacacccagcagggccccc 240
Db 205 atcggcaaccacctcaacgtggtcaacctctcggggcgtgacacacccagcagggccccc 264

Qy 241 ct 242
Db 265 ct 266

RESULT 30
US-60-213-360-951
: Sequence 951, Application US/60213360
: GENERAL INFORMATION:
: APPLICANT: Morris, MacDonald
: APPLICANT: Lal, Preeti
: TITLE OF INVENTION: Method for the Identification of Sequence Polymorphisms Using
: TITLE OF INVENTION: Polynucleotide Sequence Databases, and Single Nucleotide Poly
: FILE REFERENCE: GX-0014 P
: CURRENT APPLICATION NUMBER: US/60/213,360
: CURRENT FILING DATE: 2000-06-21
: NUMBER OF SEQ ID NOS: 8347
: SOFTWARE: PERL Program
: SEQ ID NO 951
: LENGTH: 3277
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc_feature
: OTHER INFORMATION: Incyte ID No: 1084493.6
US-60-213-360-951

Query Match 63.0%; Score 191; DB 60; Length 3277;
Best Local Similarity 99.6%; Pred. No. 1.1e-88;
Matches 241; Conservative 0; Mismatches 1; Indels 0; Gaps 0:

Qy 1 gagcggctgcacctggggagagtgctcgctacggcgcccttcgggaaagtggtggaagcc 60
Db 25 gagcggctgcacctggggagagtgctcgctacggcgcccttcgggaaagtggtggaagcc 84

Qy 61 tcgcgttcggcatccacaaggcagcagctgtgacacccgtgcccgtgaaaaatgctgaaa 120
Db 85 tcgcgttcggcatccacaaggcagcagctgtgacacccgtgcccgtgaaaaatgctgaaa 144

Qy 121 gaggcgccacgcccagcagcagcgcgcgtgatgtcggagctcaagatcctcattcac 180
Db 145 gaggcgccacgcccagcagcagcgcgcgtgatgtcggagctcaagatcctcattcac 204

Qy 181 atcggcaaccacctcaacgtggtcaacctctcggggcgtgacacacccagcagggccccc 240

Db 205 atcggcaaccactcaacgtgtgtaacctctctcgggcggtgcaccaagccgagggcccc 264
Qy 241 ct 242
Db 265 ct 266

RESULT 31
US-60-324-185-4300
; Sequence 4300, Application US/60324185
; GENERAL INFORMATION:
; APPLICANT: Morris, MacDonald
; APPLICANT: Lal, Preeti
; TITLE OF INVENTION: POLYNUCLEOTIDE SEQUENCE DATABASES, AND SINGLE NUCLEOTIDE
; TITLE OF INVENTION: POLYNUCLEOTIDE SEQUENCE DATABASES, AND SINGLE NUCLEOTIDE
; TITLE OF INVENTION: POLYNUCLEOTIDE SEQUENCE DATABASES, AND SINGLE NUCLEOTIDE
; FILE REFERENCE: GX-0019-1 P
; CURRENT APPLICATION NUMBER: US/60/324,185
; NUMBER OF SEQ ID NOS: 2001-09-21
; SOFTWARE: PERL Program
; SEQ ID NO 4300
; LENGTH: 3277
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: 1084493.6
US-60-324-185-4300

Query Match 63.0%; Score 191; DB 71; Length 3277;
Best Local Similarity 99.6%; Pred. No. 1.le-88;
Matches 241; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 gagcgctgcacctgggagagtgctcgctacgagcgccttcgggaaagtggtgaaagcc 60
Db 25 gagcgctgcacctgggagagtgctcgctacgagcgccttcgggaaagtggtgaaagcc 84
Qy 61 tcgcgtttcggcatcccaaggcagcagctgtgacacccgtggcgtgaaaatgctgaaa 120
Db 85 tcgcgtttcggcatcccaaggcagcagctgtgacacccgtggcgtgaaaatgctgaaa 144
Qy 121 gagggcgccagggcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 180
Db 145 gagggcgccagggcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 204
Qy 181 atcggcaaccactcaacgtgtgtaacctctctcgggcggtgcaccaagccgagggcccc 240
Db 205 atcggcaaccactcaacgtgtgtaacctctctcgggcggtgcaccaagccgagggcccc 264
Qy 241 ct 242
Db 265 ct 266

RESULT 32
US-60-172-373-15763
; Sequence 15763, Application US/60172373
; GENERAL INFORMATION:
; APPLICANT: Morris, MacDonald
; APPLICANT: Lal, Preeti
; APPLICANT: Diep, Dinh
; TITLE OF INVENTION: Method for the Identification of Sequence Polymorphisms Using
; TITLE OF INVENTION: Polynucleotide Sequence Databases, and Single Nucleotide Polymor
; FILE REFERENCE: GX-0006 P
; CURRENT APPLICATION NUMBER: US/60/172,373
; CURRENT FILING DATE: 1999-12-16
; NUMBER OF SEQ ID NOS: 25,772
; SOFTWARE: PERL Program
; SEQ ID NO 15763

; LENGTH: 4462
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: 902563.2
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 2402-2421, 2907, 3602
; OTHER INFORMATION: a, t, c, g, or other
US-60-172-373-15763

Query Match 63.0%; Score 191; DB 56; Length 4462;
Best Local Similarity 99.6%; Pred. No. 1.le-88;
Matches 241; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 gagcgctgcacctgggagagtgctcgctacgagcgccttcgggaaagtggtgaaagcc 60
Db 2557 gagcgctgcacctgggagagtgctcgctacgagcgccttcgggaaagtggtgaaagcc 2616
Qy 61 tcgcgtttcggcatcccaaggcagcagcagcagcagcagcagcagcagcagcagcagc 120
Db 2617 tcgcgtttcggcatcccaaggcagcagcagcagcagcagcagcagcagcagcagc 2676
Qy 121 gagggcgccagggcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 180
Db 2677 gagggcgccagggcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 2736
Qy 181 atcggcaaccactcaacgtgtgtaacctctctcgggcggtgcaccaagccgagggcccc 240
Db 2737 atcggcaaccactcaacgtgtgtaacctctctcgggcggtgcaccaagccgagggcccc 2796
Qy 241 ct 242
Db 2797 ct 2798

RESULT 33
US-60-164-285-7458
; Sequence 7458, Application US/60164285
; GENERAL INFORMATION:
; APPLICANT: Ma, Xiao-Jun
; TITLE OF INVENTION: Tumor Associated Molecules (TAMs): Targets for diagnosis, tre
; FILE REFERENCE: 3214
; CURRENT APPLICATION NUMBER: US/60/164,285
; CURRENT FILING DATE: 1999-11-05
; NUMBER OF SEQ ID NOS: 8259
; SEQ ID NO 7458
; LENGTH: 244
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-164-285-7458

Query Match 57.1%; Score 173; DB 55; Length 244;
Best Local Similarity 100.0%; Pred. No. 2.9e-79;
Matches 173; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 120 agagggcgccagggcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 179
Db 72 agagggcgccagggcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 131
Qy 180 catcgcaaccactcaacgtgtgtaacctctctcgggcggtgcaccaagccgagggcccc 239
Db 132 catcgcaaccactcaacgtgtgtaacctctctcgggcggtgcaccaagccgagggcccc 191
Qy 240 cctcatggtgatcgtagtctgcaagtagtcgcaagtagtcgcaagtagtcgcaagtagtc 292
Db 192 cctcatggtgatcgtagtctgcaagtagtcgcaagtagtcgcaagtagtcgcaagtagtc 244

RESULT 34

; NUMBER OF SEQ ID NOS: 7494
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2866
; LENGTH: 609
; TYPE: DNA
; ORGANISM: HUMAN
US-60-196-718-2866

Query Match 24.1%; Score 73; DB 58; Length 609;
Best Local Similarity 100.0%; Pred. No. 4.3e-27;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 ggaagagtctcggtacagcccttcggaaagggtgtaagacctccgcttccgcatc 75
|||||

Db 138 GGAGAGTCTCGGTACCGGCCCTTCGGGAAGGTGGTGAAGCCCTCCGCTTCGGCATC 79
|||||

Qy 76 cacaagggcagca 88
|||||

Db 78 CACAAGGCAGCA 66
|||||

RESULT 39

US-60-196-711-279

; Sequence 279, Application US/60196711

; GENERAL INFORMATION:

; APPLICANT: Bonazzi, Vivien

; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS OF THE

; TITLE OF INVENTION: SER/THR AND TYR FAMILY OF KINASES, NUCLEIC ACID MOLECULES

; FILE REFERENCE: CL000452

; CURRENT APPLICATION NUMBER: US/60/196,711

; CURRENT FILING DATE: 2000-04-13

; NUMBER OF SEQ ID NOS: 2378

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 279

; TYPE: DNA

; ORGANISM: HUMAN

US-60-196-711-279

Query Match

Best Local Similarity 100.0%; Score 53; DB 58; Length 492;

Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 66 ttctggcatccacaagggcagcagctgtgacacccgtggccgtgaaaatgctga 118
|||||

Db 440 ttctggcatccacaagggcagcagctgtgacacccgtggccgtgaaaatgctga 492
|||||

RESULT 40

US-60-196-712-469

; Sequence 469, Application US/60196712

; GENERAL INFORMATION:

; APPLICANT: Bonazzi, Vivien

; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,

; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,

; FILE REFERENCE: CL000451

; CURRENT APPLICATION NUMBER: US/60/196,712

; CURRENT FILING DATE: 2000-04-13

; NUMBER OF SEQ ID NOS: 3846

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 469

; TYPE: DNA

; ORGANISM: HUMAN

US-60-196-712-469

Query Match

Best Local Similarity 100.0%; Score 53; DB 58; Length 492;

Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 66 ttctggcatccacaagggcagcagctgtgacacccgtggccgtgaaaatgctga 118
|||||

Db 440 ttctggcatccacaagggcagcagctgtgacacccgtggccgtgaaaatgctga 492
|||||

RESULT 41

US-60-172-373-15764

; Sequence 15764, Application US/60172373

; GENERAL INFORMATION:

; APPLICANT: Morris, MacDonald

; APPLICANT: Lal, Preeti

; APPLICANT: Diep, Dinh

; TITLE OF INVENTION: Method for the Identification of Sequence Polymorphisms Using

; TITLE OF INVENTION: Polynucleotide Sequence Databases, and Single Nucleotide Poly

; FILE REFERENCE: GX-0006 P

; CURRENT APPLICATION NUMBER: US/60/172,373

; CURRENT FILING DATE: 1999-12-16

; NUMBER OF SEQ ID NOS: 25,772

; SOFTWARE: PERL Program

; SEQ ID NO 15764

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc_feature

; OTHER INFORMATION: Incyte ID No: SNP00023212

; FEATURE:

; NAME/KEY: snp

; LOCATION: 26

; OTHER INFORMATION: 902563.2, 2700, G->C

US-60-172-373-15764

Query Match

Best Local Similarity 100.0%; Score 51; DB 56; Length 51;

Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 119 aagaggcgccacggcagcagcagccgcgcgtgatctcgagctcaaga 169
|||||

Db 1 aagaggcgccacggcagcagcagccgcgcgtgatctcgagctcaaga 51
|||||

RESULT 42

US-08-472-801-1194/c

; Sequence 1194, Application US/08472801

; GENERAL INFORMATION:

; APPLICANT: Hesse 2

; APPLICANT: Smith, Larry J.

; TITLE OF INVENTION: Method and Compositions for Cellular

; FILE REFERENCE: Hesse 2

; CURRENT APPLICATION NUMBER: US/08/472,801

; CURRENT FILING DATE: 1995-06-07

; NUMBER OF SEQ ID NOS: 3601

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 1194

; TYPE: DNA

; ORGANISM: Homo sapiens

US-08-472-801-1194

Query Match

Best Local Similarity 100.0%; Score 30; DB 8; Length 30;

Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 105 cgtgaaaatgctgaaagagggcgcacggc 134
|||||

Db 30 CCGTAAATGCTGAAAGAGGGCGCCACGGC 1
|||||

RESULT 43
US-08-668-235-1194/c
; Sequence 1194, Application US/08668235
; GENERAL INFORMATION:
; APPLICANT: Larry J. Smith
; TITLE OF INVENTION: Methods and Compositions for Cellular
; FILE REFERENCE: Hsied-1
; CURRENT APPLICATION NUMBER: US/08/668,235
; EARLIER FILING DATE: 1996-06-17
; EARLIER FILING DATE: 07/748,997
; EARLIER FILING DATE: 08/23/91
; EARLIER FILING DATE: 08/426,781
; EARLIER FILING DATE: 04/22/95
; EARLIER FILING DATE: 08/472,801
; NUMBER OF SEQ ID NOS: 3629
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1194
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Homo sapiens
US-08-668-235-1194

Query Match 9.9%; Score 30; DB 10; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.00013; Mismatches 0; Indels 0; Gaps 0;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 105 cgtgaaatgctgaaagggcgccacgcg 134
|||||
Db 30 CGTGAATGCTGAAAGAGGCGCCACGCG 1

RESULT 44
US-08-472-801-1170/c
; Sequence 1170, Application US/08472801
; GENERAL INFORMATION:
; APPLICANT: Hsied 2
; APPLICANT: Smith, Larry J.
; TITLE OF INVENTION: Method and Compositions for Cellular
; FILE REFERENCE: Hsied 2
; CURRENT APPLICATION NUMBER: US/08/472,801
; EARLIER FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 3601
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1170
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Homo sapiens
US-08-472-801-1170

Query Match 9.6%; Score 29; DB 8; Length 29;
Best Local Similarity 100.0%; Pred. No. 0.00042;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 65 ctttcggcatccacaagggcagcagctgt 93
|||||
Db 29 CTTTCGGCATCCACAAGGGCAGCAGCTGT 1

RESULT 45
US-08-668-235-1170/c
; Sequence 1170, Application US/08668235
; GENERAL INFORMATION:
; APPLICANT: Larry J. Smith
; TITLE OF INVENTION: Methods and Compositions for Cellular
; FILE REFERENCE: Hsied-1
; CURRENT APPLICATION NUMBER: US/08/668,235
; EARLIER FILING DATE: 1996-06-17

; EARLIER APPLICATION NUMBER: 07/748,997
; EARLIER FILING DATE: 08/23/91
; EARLIER APPLICATION NUMBER: 08/426,781
; EARLIER FILING DATE: 04/22/95
; EARLIER APPLICATION NUMBER: 08/472,801
; EARLIER FILING DATE: 06/07/95
; NUMBER OF SEQ ID NOS: 3629
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1170
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Homo sapiens
US-08-668-235-1170

Query Match 9.6%; Score 29; DB 10; Length 29;
Best Local Similarity 100.0%; Pred. No. 0.00042;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 65 ctttcggcatccacaagggcagcagctgt 93
|||||
Db 29 CTTTCGGCATCCACAAGGGCAGCAGCTGT 1

Search completed: July 16, 2002, 02:49:56
Job time: 31249 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: July 15, 2002, 22:53:39 ; Search time 223.79 Seconds
(without alignments)
332.575 Million cell updates/sec

Title: US-09-375-248-1_COPY_2546_2848

Perfect score: 303

Sequence: 1 gaggcgctgcacctggggag.....acttctgcgcgaagcg 303

Scoring table:

OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 383533 seqs, 122816752 residues

Word size : 0

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued Patents.NA.*

1: /cgn2_6/ptodata/2/ina/5A_COMB.seq.*

2: /cgn2_6/ptodata/2/ina/5B_COMB.seq.*

3: /cgn2_6/ptodata/2/ina/6A_COMB.seq.*

4: /cgn2_6/ptodata/2/ina/6B_COMB.seq.*

5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq.*

6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	303	100.0	4195	1	US-08-340-011-1
2	303	100.0	4195	3	US-08-901-710-1
3	303	100.0	4416	3	US-08-795-430-1
4	303	100.0	4425	1	US-08-222-616-31
5	303	100.0	4425	5	PCT-US95-04228-31
6	303	100.0	4795	1	US-08-340-011-3
7	303	100.0	4795	3	US-08-901-710-3
8	303	100.0	9108	5	PCT-US95-04228-45
9	17	5.6	17	4	US-08-584-040-4146
10	17	5.6	3120	1	US-08-456-647B-19
11	17	5.6	3120	2	US-08-237-401A-19
12	17	5.6	4071	4	US-09-098-707A-1
13	17	5.6	4071	4	US-09-483-539-1
14	17	5.6	4236	1	US-08-810-116-7
15	17	5.6	4236	2	US-07-930-548A-7
16	17	5.6	8460	1	US-08-469-005A-9
17	17	5.6	8519	4	US-09-261-907-1
18	17	5.6	4403765	4	US-09-103-840A-2
19	17	5.6	4411529	4	US-09-103-840A-1
20	16	5.3	78	6	5457037-7
21	16	5.3	850	4	US-08-998-416-314
22	16	5.3	1065	4	US-09-330-611-15
23	16	5.3	1320	1	US-07-681-704A-1
24	16	5.3	1522	3	US-08-993-359-25
25	16	5.3	2185	1	US-08-173-508-3
26	16	5.3	2185	2	US-08-265-310-3
27	16	5.3	2185	3	US-08-951-742-3

28	16	5.3	2514	4	US-09-144-914-3	Sequence 3, Appli
c 29	16	5.3	2625	6	5457037-4	Patent No. 5457037
c 30	16	5.3	3336	6	5457037-1	Patent No. 5457037
c 31	16	5.3	6122	1	US-08-403-545-1	Sequence 1, Appli
c 32	16	5.3	6122	4	US-08-404-381-1	Sequence 1, Appli
c 33	16	5.3	28958	1	US-08-258-261B-6	Sequence 6, Appli
c 34	16	5.3	28958	1	US-08-456-837-6	Sequence 6, Appli
c 35	16	5.3	28958	1	US-08-457-342-6	Sequence 6, Appli
c 36	16	5.3	28958	1	US-08-457-646A-6	Sequence 6, Appli
c 37	16	5.3	28958	1	US-08-458-076A-6	Sequence 6, Appli
c 38	16	5.3	28958	1	US-08-764-233A-4	Sequence 4, Appli
c 39	16	5.3	28958	1	US-08-457-335A-6	Sequence 6, Appli
c 40	16	5.3	28958	1	US-08-729-214-6	Sequence 6, Appli
c 41	16	5.3	28958	3	US-09-028-934-6	Sequence 6, Appli
c 42	16	5.3	49377	1	US-08-764-233A-1	Sequence 99, Appli
c 43	15	5.0	171	4	US-09-020-956-99	Sequence 99, Appli
c 44	15	5.0	171	4	US-09-030-607-99	Sequence 99, Appli
c 45	15	5.0	171	4	US-09-439-313-99	Sequence 99, Appli

ALIGNMENTS

RESULT 1
US-08-340-011-1
: Sequence 1, Application US/08340011
: Patent No. 5776755
: GENERAL INFORMATION:
: APPLICANT: Alitalo, et al.
: TITLE OF INVENTION: FLT4, A NOVEL RECEPTOR TYROSIN KINASE
: NUMBER OF SEQUENCES: 20
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
: STREET: 6300 Sears Tower, 233 South Wacker Drive
: CITY: Chicago
: STATE: Illinois
: COUNTRY: United States of America
: ZIP: 60606-6402
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/340,011
: FILING DATE:
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 07/959,951
: FILING DATE: 09-OCT-1992
: ATTORNEY/AGENT INFORMATION:
: NAME: Meyers, Thomas C.
: REGISTRATION NUMBER: 36,989
: REFERENCE/DOCKET NUMBER: 32267
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 312/474-6300
: TELEFAX: 312/474-0448
: TELEX: 25-3856
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 4195 base pairs
: TYPE: nucleic acid
: TOPOLOGY: linear
: MOLECULE TYPE: CDNA
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 20..3916
: US-08-340-011-1

Query Match 100.0%; Score 303; DB 1; Length 4195;
Best Local Similarity 100.0%; Pred. No. 2.2e-140;

;; PRIORITY APPLICATION DATA:
;; APPLICATION NUMBER: 08/671,573
;; FILING DATE: 28-JUN-1996
;; PRIORITY APPLICATION DATA:
;; APPLICATION NUMBER: 08/601,132
;; FILING DATE: 14-FEB-1996
;; PRIORITY APPLICATION DATA:
;; APPLICATION NUMBER: 08/585,895
;; FILING DATE: 12-JAN-1996
;; PRIORITY APPLICATION DATA:
;; APPLICATION NUMBER: 08/510,133
;; FILING DATE: 01-AUG-1995
;; PRIORITY APPLICATION DATA:
;; APPLICATION NUMBER: 08/340,011
;; FILING DATE: 14-NOV-1994
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Gass, David A.
;; REGISTRATION NUMBER: 38,153
;; REFERENCE/DOCKET NUMBER: 28967/33691
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 312/474-6300
;; TELEFAX: 312/474-0448
;; TELEX: 25-3856
;; INFORMATION FOR SEQ ID NO: 1:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 4416 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: cDNA
US-08-795-430-1

Query Match 100.0%; Score 303; DB 3; Length 4416;
Best Local Similarity 100.0%; Pred. No. 2.2e-140;
Matches 303; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gagggctcacctgggagagtgctcggtacggcgcttcggaagtggtgaagcc 60
DB 2546 GAGCGGCTGCACCTGGGGAGAGTGTCTGGCTACGGCGCCTTCGGGAAGTGTGTGAAGCC 2605

QY 61 tcggtttcggcatccacaaggagcagcagctgtgacacgcgtggcggtgaaatgctgaaa 120
DB 2606 TCCGCTTTCGGCATCCACAAGGCGCAGCTGTGACACCGTGGCGCTGAAATGCTGAAA 2665

QY 121 gagggcgacagcgagcagcagcgcgcgtgattcggagctcaagatctcttacc 180
DB 2666 GAGGGCGCCACGCCGACGAGCACCAGCGCGCTGATGTCGGAGCTCAAGATCTCTATTCAC 2725

QY 181 atcggaacacacctcaacgttggtcaacacctcctcgggcgctgacccaagcgcgagggcccc 240
DB 2726 ATCGGAACACACCTCAACGTGGTCAACCTCTCTGGGGCGTGCACCAAGCGCAGGGCCCC 2785

QY 241 ctcatggtatcgtgagttctgcaagtcagcagtcgcaaacctctcctgagcgcgaag 300
DB 2786 CTCATGGTATCGTGGAGTCTGCAAGTACGGCAACCTCTCCAACCTCTCTGCGCGCAAG 2845

QY 301 cgg 303
DB 2846 CGG 2848

RESULT 4
US-08-222-616-31
; Sequence 31, Application US/08222616
; Patent No. 5635177
; GENERAL INFORMATION:
; APPLICANT: Bennett, Brian D.
; APPLICANT: Goeddel, David
; APPLICANT: Lee, James M.
; APPLICANT: Matthews, William
; APPLICANT: Tsai, Siao Ping
; APPLICANT: Wood, William I.

;; TITLE OF INVENTION: PROTEIN TYROSINE KINASE AGONIST
;; TITLE OF INVENTION: ANTIBODIES
;; NUMBER OF SEQUENCES: 42
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Genentech, Inc.
;; STREET: 460 Point San Bruno Blvd
;; CITY: South San Francisco
;; STATE: California
;; COUNTRY: USA
;; ZIP: 94080
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: 5.25 inch, 360 kb floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: patin (Genentech)
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/222,616
;; FILING DATE: 4-APR-1994
;; CLASSIFICATION: 530
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: PCT/US93/00586
;; FILING DATE: 22-JAN-1993
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 07/826935
;; FILING DATE: 22-JAN-1992
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Lee, Wendy M.
;; REGISTRATION NUMBER:
;; REFERENCE/DOCKET NUMBER: 821P2
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 415/225-1994
;; TELEFAX: 415/952-9881
;; TELEX: 910/371-7168
;; INFORMATION FOR SEQ ID NO: 31:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 4425 bases
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
US-08-222-616-31

Query Match 100.0%; Score 303; DB 1; Length 4425;
Best Local Similarity 100.0%; Pred. No. 2.2e-140;
Matches 303; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gagggctgcacctgggagagtgctcggtacggcgcttcggaagtggtgaaagcc 60
DB 2557 GAGCGGCTGCACCTGGGGAGAGTGTCTGGCTACGGCGCCTTCGGGAAGTGTGTGAAGCC 2616

QY 61 tcggtttcggcatccacaaggagcagcagctgtgacacgcgtggcggtgaaatgctgaaa 120
DB 2617 TCCGCTTTCGGCATCCACAAGGCGCAGCTGTGACACCGTGGCGCTGAAATGCTGAAA 2676

QY 121 gagggcgacagcgacagcagcgcgcgtgattcggagctcaagatctcttacc 180
DB 2677 GAGGGCGCCACGCCGACGAGCACCAGCGCTGATGTCGGAGCTCAAGATCTCTATTCAC 2736

QY 181 atcggaacacacctcaacgttggtcaacacctcctcgggcgctgacccaagcgcgagggcccc 240
DB 2737 ATCGGAACACACCTCAACGTGGTCAACCTCTCTGGGGCGTGCACCAAGCGCAGGGCCCC 2796

QY 241 ctcatggtatcgtgagttctgcaagtcagcagtcgcaaacctctcctgagcgcgaag 300
DB 2797 CTCATGGTATCGTGGAGTCTGCAAGTACGGCAACCTCTCCAACCTCTCTGCGCGCAAG 2856

QY 301 cgg 303
DB 2857 CGG 2859

RESULT 5
PCT-US95-04228-31

Sequence 31, Application PC/TUS9504228
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Bennett, Brian D.
APPLICANT: Goeddel, David
APPLICANT: Lee, James M.
APPLICANT: Matthews, William
APPLICANT: Tsai, Siao Ping
APPLICANT: Wood, William I.
TITLE OF INVENTION: PROTEIN TYROSINE KINASE AGONIST ANTIBODIES
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04228
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/222616
FILING DATE: 04-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Wendy M. Lee
REGISTRATION NUMBER: 00,000
REFERENCE/DOCKET NUMBER: 821P3PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 4425 bases
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
PCT-US95-04228-31
Query Match 100.0%; Score 303; DB 5; Length 4425;
Best Local Similarity 100.0%; Pred. No. 2.2e-140;
Matches 303; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 gagcggctgcacctggggagagtgctcggctacggcgcccttcgggaagtggtggaagcc 60
DB 2557 GAGCGGCTGCACCTGGGGAGAGTGTCTGGCTACGGCGCTTCGGGAAGGTGTGGAAGCC 2616
QY 61 tcgcgtttcggcatccacaaaggcagcagctgtgacacccgtgcccgtgaaaaatcgtgaaa 120
DB 2617 TCCGCTTTCGGCATCCACAAAGGCAGCAGCTGTGACACCGTGGCGCTGAAAATGCTGAAA 2676
QY 121 gagggcgccacggcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 180
DB 2677 GAGGGCGCCACGGCCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 2736
QY 181 atcggcaaccacctcaacgtgtgtcaacctctcggggcggtgcacaaagccgagggccccc 240
DB 2737 ATCGGCAACCACCTCAACGTGTGTCAACCTCTCTCGGGGGGTGCACCAAGCCGAGGGCCCC 2796
QY 241 ctcatggtgatcgtggagttcttgcaagtacggcaacctctcaacctctcgtcgccccaag 300
DB 2797 CTCATGGTGATGCTGGAGTTCCTGCAAGTACGGCAACCTCTTCCAACTTCTCTGGGCCCAAG 2856
QY 301 cgg 303
|||

Db 2857 CGG 2859

RESULT 6

US-08-340-011-3
Sequence 3, Application US/08340011
Patent No. 5776755
GENERAL INFORMATION:
APPLICANT: Alitalo, et al.
TITLE OF INVENTION: FLT4, A NOVEL RECEPTOR TYROSIN KINASE
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/340,011
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/959,951
FILING DATE: 09-OCT-1992
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Thomas C.
REGISTRATION NUMBER: 36,989
REFERENCE/DOCKET NUMBER: 32267
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 4795 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 20..4111
US-08-340-011-3

Query Match 100.0%; Score 303; DB 1; Length 4795;
Best Local Similarity 100.0%; Pred. No. 2.2e-140;
Matches 303; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 gagcggctgcacctggggagagtgctcggcgcccttcgggaagtggtggaagcc 60
DB 2546 GAGCGGCTGCACCTGGGGAGAGTGTCTGGCTACGGCGCTTCGGGAAGGTGTGGAAGCC 2605
QY 61 tcgcgtttcggcatccacaaaggcagcagctgtgacacccgtgcccgtgaaaaatcgtgaaa 120
DB 2606 TCCGCTTTCGGCATCCACAAAGGCAGCAGCTGTGACACCGTGGCGCTGAAAATGCTGAAA 2665
QY 121 gagggcgccacggcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 180
DB 2666 GAGGGCGCCACGGCCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 2725
QY 181 atcggcaaccacctcaacgtgtgtcaacctctcggggcggtgcacaaagccgagggccccc 240
DB 2726 ATCGGCAACCACCTCAACGTGTGTCAACCTCTCTCGGGGGGTGCACCAAGCCGAGGGCCCC 2785
QY 241 ctcatggtgatcgtggagttcttgcaagtacggcaacctctcaacctctcgtcgccccaag 300
|||

Db 2786 CTCATGGTGCACCTTCTGCAAGTACGGCAACCTCTCCAACCTCTCTCGCGCCCAAG 2845

QY 301 cgg 303
|||

Db 2846 CGG 2848

RESULT 7

US-08-901-710-3

; Sequence 3, Application US/08901710

; Patent No. 6107046

; GENERAL INFORMATION:

; APPLICANT: Alitalo, Kari

; APPLICANT: Aprelikova, Olga

; APPLICANT: Pajusola, Katri

; APPLICANT: Armstrong, Elna

; APPLICANT: Korhonen, Jaana

; APPLICANT: Kalpainen, Arja

; APPLICANT: Matikainen, Marja-Terttu

; TITLE OF INVENTION: FLT4, A RECEPTOR TYROSINE KINASE, AND USES

; NUMBER OF SEQUENCES: 20

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun

; STREET: 6300 Sears Tower, 233 South Wacker Drive

; CITY: Chicago

; STATE: Illinois

; COUNTRY: United States of America

; ZIP: 60606-6402

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/901.710

; FILING DATE:

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/340.011

; FILING DATE: 14-NOV-1994

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/257.754

; FILING DATE: 09-JUL-1994

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/959.951

; FILING DATE: 09-OCT-1992

; ATTORNEY/AGENT INFORMATION:

; NAME: Goss, David A.

; REGISTRATION NUMBER: 38,153

; REFERENCE/DOCKET NUMBER: 28113/33824

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 312/474-6300

; TELEFAX: 312/474-0448

; TELEX: 25-3856

; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 4795 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 20..4111

US-08-901-710-3

Query Match 100.0%; Score 303; DB 3; Length 4795;

Best Local Similarity 100.0%; Pred. No. 2.2e-140;

Matches 303; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 2546 GAGCGGCTGCACCTTGGGGAGAGTGTCTCGGCTACGGCGCTTTCGGGAAGGTGGTGAAGCC 2605

QY 61 tccgcttttcggcatccacaaagggcagcgtgtgacacccgtggccgtgaaatgctgaaa 120
|||||

Db 2606 TCCGCTTTTCGGCATCCACAAGGCGACGAGCTGTGACACCGTGGCGGTGAAATGCTGAAA 2665

QY 121 gagggcgccacggccagcgagcacgcgcgctgatgtcgaggctcaagatcctcattcac 180
|||||

Db 2666 GAGGCGCCACGGCCAGCGAGCACCGCGCGCTGATGTGCGAGCTCAAGATCCTCATTTAC 2725

QY 181 atcggcaaccacctcaacgtggtcaacctcctcggggcgtgcacaaagccagggcccc 240
|||||

Db 2726 ATCGGCAACCACTCAACGTGTCAACCTCTCGGGGCGTGCACCAACCCCGAGGGCCCC 2785

QY 241 ctcatggtgatcgtggagttcttcaagtacggcaacctctccaaacttctcgcgcgcaag 300
|||||

Db 2786 CTCATGGTGCATGGTGGAGTTCTGCAAGTACGGCAACCTCTCCAACCTCTCGCGCCCAAG 2845

QY 301 cgg 303
|||

Db 2846 CGG 2848

RESULT 8

PCT-US95-04228-45

; Sequence 45, Application PC/TUS9504228

; GENERAL INFORMATION:

; APPLICANT: Genentech, Inc.

; APPLICANT: Bennett, Brian D.

; APPLICANT: Goeddel, David

; APPLICANT: Lee James M.

; APPLICANT: Matthews, William

; APPLICANT: Tsai, Siao Ping

; APPLICANT: Wood, William I.

; TITLE OF INVENTION: PROTEIN TYROSINE KINASE AGONIST ANTIBODIES

; NUMBER OF SEQUENCES: 45

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Genentech, Inc.

; STREET: 460 Point San Bruno Blvd

; CITY: South San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94080

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: patin (Genentech)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US95/04228

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/222616

; FILING DATE: 04-APR-1994

; ATTORNEY/AGENT INFORMATION:

; NAME: Wendy M. Lee

; REGISTRATION NUMBER: 00,000

; REFERENCE/DOCKET NUMBER: 8213PCT

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415/225-1994

; TELEFAX: 415/952-9881

; TELEX: 910/371-7168

; INFORMATION FOR SEQ ID NO: 45:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 9108 bases

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

PCT-US95-04228-45

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Query Match      100.0%: Score 303; DB 5; Length 9108;
Best Local Similarity 100.0%: Pred. No. 2.1e-140; Indels 0; Gaps 0;
Matches 303; Conservative 0; Mismatches 0;

Qy 1 gagcggtgcacctggggagagtgtcgggtactcgcgccttcgggaagtggtggaagcc 60
    |||||
Db 3489 GAGCGGCTGCACCTGGGGAGAGTGTCTCGGCTACGGCGCCTTCGGGAAGTGTGGAAGCC 3548

Qy 61 tccgctttcggcatccacaaggcgagcagctgtgacaccgtggccgtgaaaatgctgaaa 120
    |||||
Db 3549 TCCGCTTTTCGGCATCCACCAAGGCGACAGCTGTGACACCGTGCCTGCGCGTGAATGCTGAAA 3608

Qy 121 gaggggcacacggcagcagcagcgcgcgtgctgagtctcgagactcaagatctcttccac 180
    |||||
Db 3609 GAGGGCGCCACCGCCAGCAGCAGCAGCCGCGCTGTATGTCGGAGCTCAAGATCTCATTTAC 3668

Qy 181 atcggcaaccactcaacgttgctcaacctcttcgggcgctgacccaagcgcagggccccc 240
    |||||
Db 3669 ATCGGCAACCACCTCAACCTGTGTCAACCTTCCTCGGGCGTGCACCAAGCCGAGGGCCCC 3728

Qy 241 ctcatgtgtagtggaggtctgcaagtacgagtcaggaacctctccaacttctgcgcgccaag 300
    |||||
Db 3729 CTCATGGTGATCGTGGAGTTCGTCAAGTACGGCAACCTTCCAACTTCTCGCGGCCAAG 3788

Qy 301 cgg 303
    |||
Db 3789 CGG 3791

RESULT 9
US-08-584-040-4146
; Sequence 4146, Application US/08584040
; Patent No. 6346398
; GENERAL INFORMATION:
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: TREATMENT OF DISEASES OR
; TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
; TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
; NUMBER OF SEQUENCES: 8502
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Suite 4700
; STATE: Los Angeles
; COUNTRY: California
; ZIP: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/584,040
; FILING DATE: January 11, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/005,974
; FILING DATE: October 26, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 218/064
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEX: (213) 955-0440
; TELEX: 67-3510
```

```
; INFORMATION FOR SEQ ID NO: 4146:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-584-040-4146

Query Match      5.6%: Score 17; DB 4; Length 17;
Best Local Similarity 70.6%: Pred. No. 19;
Matches 12; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 163 ctcaagatctctcatcca 179
    |||||
Db 1 CUCAAGAUCCUCAUCA 17

RESULT 10
US-08-456-647B-19
; Sequence 19, Application US/08456647B
; Patent No. 5811516
; GENERAL INFORMATION:
; APPLICANT: Lemke Ph.D. et al., Greg E.
; TITLE OF INVENTION: PROTEIN-TYROSINE KINASE GENES
; NUMBER OF SEQUENCES: 54
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: US
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/456,647B
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/237,401
; FILING DATE: 02-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/884,486
; FILING DATE: 15-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Wetherell Ph.D., John R.
; REGISTRATION NUMBER: 31,678
; REFERENCE/DOCKET NUMBER: 07251/007002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 678-5070
; TELEFAX: (619) 678-5099
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3120 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; IMMEDIATE SOURCE:
; CLONE: Tyro-10
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 485...3047
US-08-456-647B-19

Query Match      5.6%: Score 17; DB 1; Length 3120;
Best Local Similarity 100.0%: Pred. No. 15;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```


NAME: Hand, J. Mark
REGISTRATION NUMBER: 36,545
REFERENCE/DOCKET NUMBER: 19963PV
TELECOMMUNICATION INFORMATION:
TELEPHONE: 732/594-3905
TELEFAX: 732/594-4720
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4071 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-09-483-539-1

Query Match 5.6%; Score 17; DB 4; Length 4071;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 163 ctcaagatcctcatcca 179
|||||
Db 2656 CTCAAGATCCTCATTC A 2672

RESULT 14
US-08-810-116-7
Sequence 7, Application US/08810116
Patent No. 5766860
GENERAL INFORMATION:
APPLICANT: Terman, Bruce I.
APPLICANT: Carrion, Miguel E.
TITLE OF INVENTION: Identification of a No. 5766860el Human Growth
TITLE OF INVENTION: Factor Receptor
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: American Cyanamid Company
STREET: One Cyanamid Plaza
CITY: Wayne
STATE: New Jersey
COUNTRY: U.S.A.
ZIP: 07470

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/810,116
FILING DATE: 25-FEB-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/930,548
FILING DATE: 23-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Gordon, Alan M.
REGISTRATION NUMBER: 30,637
REFERENCE/DOCKET NUMBER: 31,298-01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-831-3244
TELEFAX: 201-831-3305

INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 4236 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..4068
US-08-810-116-7

Query Match 5.6%; Score 17; DB 1; Length 4236;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 163 ctcaagatcctcatcca 179
|||||
Db 2656 CTCAAGATCCTCATTC A 2672

RESULT 15
US-07-930-548A-7
Sequence 7, Application US/07930548A
Patent No. 5861301
GENERAL INFORMATION:
APPLICANT: Terman, Bruce I.
APPLICANT: Carrion, Miguel E.
TITLE OF INVENTION: Identification of a No. 5861301el Human Growth
TITLE OF INVENTION: Factor Receptor
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: American Cyanamid Company
STREET: One Cyanamid Plaza
CITY: Wayne
STATE: New Jersey
COUNTRY: U.S.A.
ZIP: 07470

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/930,548A
FILING DATE: 23-NOV-1992
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Gordon, Alan M.
REGISTRATION NUMBER: 30,637
REFERENCE/DOCKET NUMBER: 31,298-01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-831-3244
TELEFAX: 201-831-3305
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 4236 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..4068
US-07-930-548A-7

Query Match 5.6%; Score 17; DB 2; Length 4236;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 163 ctcaagatcctcatcca 179
|||||
Db 2656 CTCAAGATCCTCATTC A 2672

RESULT 16
US-08-469-005A-9/c
Sequence 9, Application US/08469005A
Patent No. 5663874
GENERAL INFORMATION:
APPLICANT: KUHAJDA, FRANCIS P.
APPLICANT: PASTERNAK, GARY A.
TITLE OF INVENTION: CANCER RELATED ANTIGEN

```
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BAKER & BOTTS, L.L.P.
; STREET: 1299 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20004-2400
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,005A
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/188,426
; FILING DATE: 24-JAN-1994
; APPLICATION NUMBER: 08/096,908
; FILING DATE: 26-JUL-1993
; APPLICATION NUMBER: 07/917,716
; FILING DATE: 24-JUL-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Posotske, Laurence H
; REGISTRATION NUMBER: 34,698
; REFERENCE/DOCKET NUMBER: 062482-0113
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-639-7700
; TELEFAX: 202-639-7890
; TELEX:
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8460 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 124...7650
; OTHER INFORMATION:
;
; US-08-469-005A-9

Query Match 5.6%; Score 17; DB 1; Length 8460;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 83 gcagcagctgtgacacc 99
|||||
Db 1738 GCAGCAGCTGTGACACC 1722

RESULT 17
US-09-261-907-1/c
; Sequence 1, Application US/09261907A
; Patent No. 6294364
; GENERAL INFORMATION:
; APPLICANT: ELLIS, CATHERINE
; APPLICANT: LONSDALE, JOHN
; APPLICANT: BERGSMAN, DEK J.
; APPLICANT: MOONEY, JEFFREY L.
; APPLICANT: DEPIERA, MEGAN E.
; APPLICANT: CHAPMAN, CONRAD
; TITLE OF INVENTION: HUMAN FAS
; FILE REFERENCE: GP-70603
; CURRENT APPLICATION NUMBER: US/09/261,907A
```

```
; CURRENT FILING DATE: 1999-03-03
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 8519
; TYPE: DNA
; ORGANISM: HOMO SAPIENS
; US-09-261-907-1

Query Match 5.6%; Score 17; DB 4; Length 8519;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 83 gcagcagctgtgacacc 99
|||||
Db 1770 GCAGCAGCTGTGACACC 1754

RESULT 18
US-09-103-840A-2/c
; Sequence 2, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; TITLE OF INVENTION: TUBERCULOSIS
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 4403765
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; OTHER INFORMATION: CDC 1551
; OTHER INFORMATION: "n" bases at various positions throughout the sequence
; OTHER INFORMATION: represent a, t, c or g
; US-09-103-840A-2

Query Match 5.6%; Score 17; DB 4; Length 4403765;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 29 gctacggcgcttcggg 45
|||||
Db 3179438 GCTACGGCGCTTCGGG 3179422

RESULT 19
US-09-103-840A-1/c
; Sequence 1, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; TITLE OF INVENTION: TUBERCULOSIS
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 4411529
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; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37Rv
US-09-103-840A-1

Query Match      5.6%; Score 17; DB 4; Length 4411529;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 29 gctacggcgcccttcggg 45
|||||
Db 3185328 GCTACGGCGCCCTTCGGG 3185312

RESULT 20
5457037-7/c
; Patent No. 5457037
; APPLICANT: TOGMONT, ANGELO;CARRERA, PAOLO;CAMERINI, BARBARA;
; GALLI, GIULIANO;LUCHESE, GIUSEPPE;GRANDI, GUIDO;DI GENNARO, CARLO
; TITLE OF INVENTION: CLONING OF THE GENE CODING THE ISOAMYLASE
; ENZYME AND ITS USE IN THE PRODUCTION OF SAID ENZYME
; NUMBER OF SEQUENCES: 7
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/1,797
; FILING DATE: 08-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 749,621
; FILING DATE: 19-AUG-1991
; APPLICATION NUMBER: 224,114
; FILING DATE: 25-JUL-1988
; SEQ ID NO:7:
; LENGTH: 78
5457037-7

Query Match      5.3%; Score 16; DB 6; Length 78;
Best Local Similarity 100.0%; Pred. No. 55;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 134 ccagcgagcaccgcgc 149
|||||
Db 53 CCAGCGAGCACC GC GC 38

RESULT 21
US-08-998-416-314/c
; Sequence 314, Application US/08998416
; Patent No. 6239264
; GENERAL INFORMATION:
; APPLICANT: Philippsen, Peter
; APPLICANT: Pohlmann, Rainer
; APPLICANT: Steinert, Sabine
; APPLICANT: Mohr, Christine
; APPLICANT: Wendland, Jurgene
; APPLICANT: Knechtie, Philipp
; APPLICANT: Rebschung, Corinne
; TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPIL
; AND USES THEREOF
; NUMBER OF SEQUENCES: 1152
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NO. 6239264artis Corporation
; STREET: 3054 Cornwallis Road
; CITY: Research Triangle Park
; STATE: No.6239264th Carolina
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/998.416
; FILING DATE: 24-DEC-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: CH 0016/97
; FILING DATE: 31-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: PF/5-30306/A/COC1976
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8587
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 314:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 850 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: PAG1254UP
US-08-998-416-314

Query Match      5.3%; Score 16; DB 4; Length 850;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 88 agctgtgacaccgtg 103
|||||
Db 493 AGCTGTGACACCGTGG 478

RESULT 22
US-09-330-611-15/c
; Sequence 15, Application US/09330611
; Patent No. 6248874
; GENERAL INFORMATION:
; APPLICANT: FREY, Perry A.
; APPLICANT: RUZICKA, Frank J.
; TITLE OF INVENTION: DNA MOLECULES ENCODING BACTERIAL LYSINE 2,3-AMINOMUTASE
; FILE REFERENCE: 032026/0476
; CURRENT APPLICATION NUMBER: US/09/330,611
; CURRENT FILING DATE: 1999-06-11
; EARLIER APPLICATION NUMBER: US 09/198,942
; EARLIER FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 15
; TYPE: DNA
; ORGANISM: Treponema pallidum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1065)
US-09-330-611-15

Query Match      5.3%; Score 16; DB 4; Length 1065;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 138 cgagcaccgcgcgctg 153
|||||
Db 685 CGAGCACC GC GC GTG 670

RESULT 23
US-07-681-704A-1/c
; Sequence 1, Application US/07681704A
; Patent No. 527965
; GENERAL INFORMATION:
```


REFERENCE/DOCKET NUMBER: 18740/125/CACO
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202 672 5300
TELEFAX: 202 672 5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2185 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 531..2069
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 531..902
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 903..2069
FEATURE:
NAME/KEY: misc_feature
LOCATION: 531..533
OTHER INFORMATION: /note= "Met at position -124"
OTHER INFORMATION: represents fMet"
US-08-173-508-3

Query Match 5.3%; Score 16; DB 1; Length 2185;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 216 ggcgtgacccaagccg 231
|||||
DB 1943 GCGGTGCACCAAGCCG 1958

RESULT 26
US-08-265-310-3
Sequence 3, Application US/08265310
Patent No. 5856166
GENERAL INFORMATION:
APPLICANT: Bartfeld, Daniel
APPLICANT: Butler, Michael J.
APPLICANT: Hadary, Dany
APPLICANT: Jenish, David
APPLICANT: Krieger, Timothy
APPLICANT: Malek, Lawrence T.
APPLICANT: Soostmeyer, Gisela
APPLICANT: Walczyk, Eva
APPLICANT: Krygsman, Phyllis
APPLICANT: Garven, Shella
TITLE OF INVENTION: STREPTOMYCES PROTEASES AND IMPROVED
TITLE OF INVENTION: STREPTOMYCES STRAINS FOR EXPRESSION OF PEPTIDES AND
TITLE OF INVENTION: POLYPEPTIDES
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W.
CITY: Washington, D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/265.310
FILING DATE: 24-JUN-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,508

FILING DATE: 23-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 18740/133/CACO
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202 672 5300
TELEFAX: 202 672 5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2185 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 531..2069
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 531..902
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 903..2069
FEATURE:
NAME/KEY: misc_feature
LOCATION: 531..533
OTHER INFORMATION: /note= "Met at position -124"
OTHER INFORMATION: represents fMet"
US-08-265-310-3

Query Match 5.3%; Score 16; DB 2; Length 2185;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 216 ggcgtgacccaagccg 231
|||||
DB 1943 GCGGTGCACCAAGCCG 1958

RESULT 27
US-08-951-742-3
Sequence 3, Application US/08951742
Patent No. 6127144
GENERAL INFORMATION:
APPLICANT: Bartfeld, Daniel
APPLICANT: Michael J. Butler
APPLICANT: Dany Hadary
APPLICANT: David Jenish
APPLICANT: Tim Krieger
APPLICANT: Lawrence T. Malek
APPLICANT: Gisela Soostmeyer
APPLICANT: Eva Walczyk
APPLICANT: Phyllis Krygsman
APPLICANT: Shella Garven
TITLE OF INVENTION: METHOD FOR EXPRESSION OF PROTEINS IN
TITLE OF INVENTION: BACTERIAL HOST CELLS
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/951,742

; FILING DATE: 16-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Bent, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 0189740/0140
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LEN:TH: 2185 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 531..2066
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 531..902
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 903..2066
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 531..533
; OTHER INFORMATION: /product= "Met at position -124
; OTHER INFORMATION: represents fmet"
; US-08-951-742-3

Query Match 5.3%; Score 16; DB 3; Length 2185;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 216 ggcgtgaccacgcgcg 231
|||||
Db 1943 GCGGTGCACCAAGCGG 1958

RESULT 28
US-09-144-914-3
; Sequence 3, Application US/09144914
; Patent No. 6309855
; GENERAL INFORMATION:
; APPLICANT: Duprat, Fabrice
; APPLICANT: Lesage, Florian
; APPLICANT: Fink, Michel
; APPLICANT: Lazdunski, Michel
; TITLE OF INVENTION: FAMILY OF MAMMALIAN POTASSIUM CHANNELS, THEIR CLONING
; ENZYME AND ITS USE IN THE PRODUCTION OF SAID ENZYME
; FILE REFERENCE: 989.6705CIP
; CURRENT APPLICATION NUMBER: US/09/144,914
; CURRENT FILING DATE: 1998-09-01
; EARLIER APPLICATION NUMBER: 08/749,816
; EARLIER FILING DATE: 1996-11-15
; EARLIER APPLICATION NUMBER: 60/095,234
; EARLIER FILING DATE: 1998-08-04
; EARLIER APPLICATION NUMBER: FR 96/01565
; EARLIER FILING DATE: 1996-02-08
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 2514
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (126)..(1307)
; FEATURE:
; OTHER INFORMATION: TASK

US-09-144-914-3

Query Match 5.3%; Score 16; DB 4; Length 2514;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 138 cgagcaccgcgcgcgctg 153
|||||
Db 899 cgagcaccgcgcgcgctg 914

RESULT 29
5457037-4/c
; Patent No. 5457037
; APPLICANT: TOGNONI, ANGELO;CARRERA, PAOLO;CAMERINI, BARBARA;
; GALLI, GIULIANO;LUCCHESI, GIUSEPPE;GRANDI, GUIDO;DI GENNARO, CARLO
; TITLE OF INVENTION: CLONING OF THE GENE CODING THE ISOAMYLASE
; ENZYME AND ITS USE IN THE PRODUCTION OF SAID ENZYME
; NUMBER OF SEQUENCES: 7
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/1,797
; FILING DATE: 08-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 749,621
; FILING DATE: 19-AUG-1991
; APPLICATION NUMBER: 224,114
; FILING DATE: 25-JUL-1988
; SEQ ID NO:4:
; LENGTH: 2625
; 5457037-4

Query Match 5.3%; Score 16; DB 6; Length 2625;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 134 ccagcgagcaccgcgcgc 149
|||||
Db 281 CCAGCGAGCACCGCGC 266

RESULT 30
5457037-1/c
; Patent No. 5457037
; APPLICANT: TOGNONI, ANGELO;CARRERA, PAOLO;CAMERINI, BARBARA;
; GALLI, GIULIANO;LUCCHESI, GIUSEPPE;GRANDI, GUIDO;DI GENNARO, CARLO
; TITLE OF INVENTION: CLONING OF THE GENE CODING THE ISOAMYLASE
; ENZYME AND ITS USE IN THE PRODUCTION OF SAID ENZYME
; NUMBER OF SEQUENCES: 7
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/1,797
; FILING DATE: 08-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 749,621
; FILING DATE: 19-AUG-1991
; APPLICATION NUMBER: 224,114
; FILING DATE: 25-JUL-1988
; SEQ ID NO:1:
; LENGTH: 3336
; 5457037-1

Query Match 5.3%; Score 16; DB 6; Length 3336;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 134 ccagcgagcaccgcgcgc 149
|||||
Db 993 CCAGCGAGCACCGCGC 978

RESULT 31

US-08-403-545-1

Sequence 1, Application US/08403545
Patent No. 5656483
GENERAL INFORMATION:
APPLICANT: Sokatch, John R.
APPLICANT: Sykes, Pamela Joy
APPLICANT: Madhusudhan, K.T.
TITLE OF INVENTION: Genes Encoding Operon and Promoter for
TITLE OF INVENTION: Branched Chain Keto Acid Dehydrogenase of Pseudomonas putida
TITLE OF INVENTION: and Methods
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Carolyn D. Moon
ADDRESSEE: Dunlap, Coddling, Perterson and Lee
STREET: 9400 N Broadway, Suite 420
CITY: Oklahoma City
STATE: Oklahoma
COUNTRY: USA
ZIP: 73114
COMPUTER TYPE: Diskette 5.25 inch, 360 Kb Storage
COMPUTER: IBM AT
OPERATING SYSTEM: MS-DOS Version 3.3
SOFTWARE: Professional Write 2.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/403,545
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 7/603/781
APPLICATION NUMBER: 07/172,148
FILING DATE: 23-003-1988
ATTORNEY/AGENT INFORMATION:
NAME: Carolyn D. Moon
REGISTRATION NUMBER: 33,022
REFERENCE/DOCKET NUMBER: 5820.101
TELECOMMUNICATION INFORMATION:
TELEPHONE: Attorney, (405) 478-5344
TELEFAX: Attorney, (405) 478-5349
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 6122 base pairs
TYPE: Nucleic acid
STRANDEDNESS: Double stranded
TOPOLOGY: Circular
MOLECULE TYPE: Genomic DNA
DESCRIPTION: Seq ID No. 56564831 is genomic DNA from P. putida
DESCRIPTION: strain Pg2 which contains the control region regulating
DESCRIPTION: expression of the bkd operon and the four structural genes
DESCRIPTION: of the bkd operon, bkdA1, bkdA2, bkdB and lpdV.
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: No. 5656483 applicable
ORIGINAL SOURCE:
ORGANISM: Pseudomonas putida
STRAIN: Pg2
INDIVIDUAL ISOLATE: No. 5656483 applicable
DEVELOPMENTAL STAGE: No. 5656483 applicable
HAPLOTYPE: No. 5656483 applicable
TISSUE TYPE: No. 5656483 applicable
CELL TYPE: Gram negative, aerobic bacilli
CELL LINE: No. 5656483 applicable
ORGANELLE: No. 5656483 applicable
IMMEDIATE SOURCE:
LIBRARY: Genomic DNA from Pseudomonas putida
CLONE: pJRS54
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION: 35 Minutes
UNITS:
FEATURE:
NAME/KEY: Promoter plus leader

LOCATION: 1-792
IDENTIFICATION METHOD: By experiment
OTHER INFORMATION: The promoter plus leader are responsible
OTHER INFORMATION: for expression of the bkd operon in Pseudomonas putida
FEATURE:
NAME/KEY: bkdA1, Gene encoding branched-chain keto acid
NAME/KEY: dehydrogenase-decarboxylase E1 alpha subunit.
LOCATION: 805-2031. Initiating methionine codon is at
LOCATION: position 802, however mature peptide does not contain N-
LOCATION: terminal methionine.
IDENTIFICATION METHOD: By experiment
OTHER INFORMATION: The E1 component of branched chain keto
OTHER INFORMATION: acid dehydrogenase catalyzes the oxidative decarboxylation.
OTHER INFORMATION: of the keto acid substrate. E1 is composed of two subunit.
OTHER INFORMATION: E1 alpha and E1 beta.
FEATURE:
NAME/KEY: bkdA2, Gene encoding branched-chain keto acid
NAME/KEY: dehydrogenase-decarboxylase E1 beta subunit.
LOCATION: 2078-3091. Initiating methionine codon is position
LOCATION: 2075, however mature peptide does not contain N-terminal
LOCATION: methionine.
IDENTIFICATION METHOD: By experiment
OTHER INFORMATION: See description for Feature 2 above.
FEATURE:
NAME/KEY: bkdB Gene encoding the E2 component of branched
NAME/KEY: chain keto acid dehydrogenase
LOCATION: 3098-4363 Initiating methionine codon is position
LOCATION: 3095, however mature peptide does not contain N-terminal
LOCATION: methionine.
IDENTIFICATION METHOD: By experiment
OTHER INFORMATION: E2 catalyzes the transacylation of the
OTHER INFORMATION: fatty acyl group from the lipoyl residue of E2 to coenzym
OTHER INFORMATION: A. E2 is the core of the complex and binds E1 and E3
OTHER INFORMATION: components.
FEATURE:
NAME/KEY: lpdV, Gene encoding the E3 component of branched
NAME/KEY: chain keto acid dehydrogenase
LOCATION: 4369-5745. N-terminal methionine is present on
LOCATION: mature peptide.
IDENTIFICATION METHOD: By experiment
OTHER INFORMATION: E3 is LPD-val, the specific lipoaamide
OTHER INFORMATION: dehydrogenase which catalyzes oxidation of the
OTHER INFORMATION: dihydrolipoyl residue of the E2 component of branched cha
OTHER INFORMATION: keto acid dehydrogenase and the reduction of NAD+.
PUBLICATION INFORMATION:
AUTHORS: Sokatch, John R.
AUTHORS: McCully, Vicki
AUTHORS: Gebrosky, Janet
AUTHORS: Sokatch, David, J.
TITLE: Isolation of a specific lipoaamide dehydrogenase
TITLE: for a branched-chain keto acid dehydrogenase
TITLE: from Pseudomonas putida
JOURNAL: Journal of Bacteriology
VOLUME: 148
ISSUE:
PAGES: 639-646
DATE: 1981
AUTHORS: Sokatch, John R.
AUTHORS: McCully, Vicki
AUTHORS: Roberts, C.M.
TITLE: Purification of a branched-chain keto acid
TITLE: dehydrogenase from Pseudomonas putida
JOURNAL: Journal of Bacteriology
VOLUME: 148
ISSUE:
PAGES: 647-652
DATE: 1981
AUTHORS: Sykes, Pamela
AUTHORS: Burns, Gayle
AUTHORS: Menard, Joan
AUTHORS: Hatter, Kenneth
AUTHORS: Sokatch, John R.
TITLE: Molecular cloning of genes encoding branched-chain

TITLE: keto acid dehydrogenase of Pseudomonas putida
JOURNAL: Journal of Bacteriology
VOLUME: 169
ISSUE: 1619-1625
PAGES: 1987
DATE: 1987
AUTHORS: Burns, Gayle
AUTHORS: Brown, Tracy
AUTHORS: Hatter, Kenneth
AUTHORS: Sokatch, John R.
TITLE: Comparison of the amino acid sequences of the
TITLE: transacylase components of branched-chain oxoacid
TITLE: dehydrogenase of Pseudomonas putida, and the pyruvate and 2-
TITLE: oxoglutarate dehydrogenases of Escherichia coli
JOURNAL: European Journal of Biochemistry
VOLUME: 176
ISSUE: 165-169
PAGES: 1988
DATE: 1988
AUTHORS: Burns, Gayle
AUTHORS: Brown, Tracy
AUTHORS: Hatter, Kenneth
AUTHORS: Idriss, John M.
AUTHORS: Sokatch, John R.
TITLE: Similarity of the E1 subunits of branched-chain-
TITLE: oxoacid dehydrogenase from Pseudomonas putida to the
TITLE: corresponding subunits of mammalian branched-chain-oxoacid
TITLE: and pyruvate dehydrogenases
JOURNAL: European Journal of Biochemistry
VOLUME: 176
PAGES: 311-317
DATE: 1988
AUTHORS: Burns, Gayle
AUTHORS: Brown, Tracy
AUTHORS: Hatter, Kenneth
AUTHORS: Sokatch, John R.
TITLE: Sequence analysis of the lpdV gene for lipoamide
Patent No. 5656483
TITLE: dehydrogenase of Pseudomonas putida
JOURNAL: European Journal of Biochemistry
VOLUME: 179
ISSUE: 61-69
PAGES: 1989
DATE: 1989
AUTHORS: Madhusudhan, K.T.
AUTHORS: Huang, G.
AUTHORS: Burns, Gayle
AUTHORS: Sokatch, J.R.
TITLE: Transcriptional analysis of the promoter region of
TITLE: the branched chain keto acid dehydrogenase operon of
TITLE: Pseudomonas putida
JOURNAL: Journal of Bacteriology
VOLUME: 172
ISSUE: October, 1990
Query Match 5.3%; Score 16; DB 1; Length 6122;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 192 cctcaacgtgtggtcaac 207
Db 1509 CCTCAACGTGTGTCAC 1524
RESULT 32
US-08-404-381-1
Sequence 1, Application US/08404381
Patent No. 6168945
GENERAL INFORMATION:
APPLICANT: Sokatch, John R.
APPLICANT: Sykes, Pamela Joy
APPLICANT: Madhusudhan, K.T.

TITLE OF INVENTION: Genes Encoding Operon and Promoter for
TITLE OF INVENTION: Branched Chain Keto Acid Dehydrogenase of Pseudomonas putid
TITLE OF INVENTION: and Methods
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Carolyn D. Moon
ADDRESSEE: Dunlap, Coddling, Perterson and Lee
STREET: 9400 N. Broadway, Suite 420
CITY: Oklahoma City
STATE: Oklahoma
COUNTRY: USA
ZIP: 73114
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette 5.25 inch, 360 kb Storage
COMPUTER: IBM AT
OPERATING SYSTEM: MS-DOS Version 3.3
SOFTWARE: Professional Write 2.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/404,381
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/603,781
FILING DATE:
APPLICATION NUMBER: 07/172,148
FILING DATE: 23-003-1988
ATTORNEY/AGENT INFORMATION:
NAME: Carolyn D. Moon
REGISTRATION NUMBER: 33, 022
REFERENCE/DOCKET NUMBER: 5820.101
TELECOMMUNICATION INFORMATION: 478-5344
TELEPHONE: Attorney, (405) 478-5344
TELEFAX: Attorney, (405) 478-5349
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 6122 base pairs
TYPE: Nucleic acid
STRANDEDNESS: Double stranded
TOPOLOGY: Circular
MOLECULE TYPE: Genomic DNA
DESCRIPTION: Seq ID No. 61689451 is genomic DNA from P. putida
DESCRIPTION: strain ppg2 which contains the control region regulating
DESCRIPTION: expression of the bkd operon and the four structural genes
DESCRIPTION: of the bkd operon, bkdA1, bkdA2, bkdB and lpdV.
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: No. 6168945 applicable
ORIGINAL SOURCE:
ORGANISM: Pseudomonas putida
STRAIN: Ppg2
INDIVIDUAL ISOLATE: No. 6168945 applicable
DEVELOPMENTAL STAGE: No. 6168945 applicable
HAPLOTYPE: No. 6168945 applicable
TISSUE TYPE: No. 6168945 applicable
CELL TYPE: Gram negative, aerobic bacilli
CELL LINE: No. 6168945 applicable
ORGANELLE: No. 6168945 applicable
IMMEDIATE SOURCE:
LIBRARY: Genomic DNA from Pseudomonas putida
CLONE: pJRS54
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION: 35 Minutes
UNITS:
FEATURE:
NAME/KEY: Promoter plus leader
LOCATION: 1-792
IDENTIFICATION METHOD: By experiment
OTHER INFORMATION: The promoter plus leader are responsible
OTHER INFORMATION: for expression of the bkd operon in Pseudomonas putida
FEATURE:
NAME/KEY: bkdA1, Gene encoding branched-chain keto acid

NAME/KEY: dehydrogenase-decarboxylase E1 alpha subunit.
LOCATION: 805-2031. Initiating methionine codon is at
LOCATION: position 802, however mature peptide does not contain N-
IDENTIFICATION METHOD: terminal methionine.
IDENTIFICATION METHOD: By experiment
OTHER INFORMATION: The E1 component of branched chain keto
OTHER INFORMATION: acid dehydrogenase catalyzes the oxidative decarboxylation
OTHER INFORMATION: of the keto acid substrate. E1 is composed of two subunits,
OTHER INFORMATION: E1 alpha and E1 beta.
FEATURE:
NAME/KEY: bkdA2, Gene encoding branched-chain keto acid
LOCATION: dehydrogenase-decarboxylase E1 beta subunit.
LOCATION: 2078-3091. Initiating methionine codon is position
LOCATION: 2075, however mature peptide does not contain N-terminal
LOCATION: methionine.
IDENTIFICATION METHOD: By experiment
OTHER INFORMATION: See description for Feature 2 above.
FEATURE:
NAME/KEY: bkdB Gene encoding the E2 component of branched
LOCATION: chain keto acid dehydrogenase
LOCATION: 3098-4363 Initiating methionine codon is position
LOCATION: 3095, however mature peptide does not contain N-terminal
LOCATION: methionine.
IDENTIFICATION METHOD: By experiment
OTHER INFORMATION: E2 catalyzes the transacylation of the
OTHER INFORMATION: fatty acyl group from the lipoyl residue of E2 to coenzyme
OTHER INFORMATION: A. E2 is the core of the complex and binds E1 and E3
OTHER INFORMATION: components.
FEATURE:
NAME/KEY: lpdV, Gene encoding the E3 component of branched
LOCATION: chain keto acid dehydrogenase.
LOCATION: 4369-5745. N-terminal methionine is present on
LOCATION: mature peptide.
IDENTIFICATION METHOD: By experiment
OTHER INFORMATION: E3 is lpd-val, the specific lipamide
OTHER INFORMATION: dehydrogenase which catalyzes oxidation of the
OTHER INFORMATION: dihydrolipoyl residue of the E2 component of branched chain
OTHER INFORMATION: keto acid dehydrogenase and the reduction of NAD+.
PUBLICATION INFORMATION:
AUTHORS: Sokatch, John R.
AUTHORS: McCully, Vicki
AUTHORS: Gebrosky, Janet
AUTHORS: Sokatch, David, J.
TITLE: Isolation of a specific lipamide dehydrogenase
TITLE: for a branched-chain keto acid dehydrogenase
TITLE: from Pseudomonas putida
JOURNAL: Journal of Bacteriology
VOLUME: 148
ISSUE:
PAGES: 639-646
DATE: 1981
AUTHORS: Sokatch, John R.
AUTHORS: McCully, Vicki
AUTHORS: Roberts, C.M.
TITLE: Purification of a branched-chain keto acid
TITLE: dehydrogenase from Pseudomonas putida
JOURNAL: Journal of Bacteriology
VOLUME: 148
ISSUE:
PAGES: 647-652
DATE: 1981
AUTHORS: Sykes, Pamela
AUTHORS: Burns, Gayle
AUTHORS: Menard, Joan
AUTHORS: Hatter, Kenneth
AUTHORS: Sokatch, John R.
TITLE: Molecular cloning of genes encoding branched-chain
TITLE: keto acid dehydrogenase of Pseudomonas putida
JOURNAL: Journal of Bacteriology
VOLUME: 169
ISSUE:
PAGES: 1619-1625
DATE: 1987

AUTHORS: Burns, Gayle
AUTHORS: Brown, Tracy
AUTHORS: Hatter, Kenneth
AUTHORS: Sokatch, John R.
TITLE: Comparison of the amino acid sequences of the
TITLE: transacylase components of branched-chain oxoacid
TITLE: dehydrogenase of Pseudomonas putida, and the pyruvate and 2-
TITLE: oxoglutarate dehydrogenases of Escherichia coli
JOURNAL: European Journal of Biochemistry
VOLUME: 176
ISSUE:
PAGES: 165-169
DATE: 1988
AUTHORS: Burns, Gayle
AUTHORS: Brown, Tracy
AUTHORS: Hatter, Kenneth
AUTHORS: Idriss, John M.
AUTHORS: Sokatch, John R.
TITLE: Similarity of the E1 subunits of branched-chain-
TITLE: oxoacid dehydrogenase from Pseudomonas putida to the
TITLE: corresponding subunits of mammalian branched-chain-oxoacid
TITLE: and pyruvate dehydrogenases
JOURNAL: European Journal of Biochemistry
VOLUME: 176
ISSUE:
PAGES: 311-317
DATE: 1988
AUTHORS: Burns, Gayle
AUTHORS: Brown, Tracy
AUTHORS: Hatter, Kenneth
AUTHORS: Sokatch, John R.
TITLE: Sequence analysis of the lpdV gene for lipamide
TITLE: Patent No. 6168945
TITLE: dehydrogenase of Pseudomonas putida
JOURNAL: European Journal of Biochemistry
VOLUME: 179
ISSUE:
PAGES: 61-69
DATE: 1989
AUTHORS: Madhusudhan, K.T.
AUTHORS: Huang, G.
AUTHORS: Burns, Gayle
AUTHORS: Sokatch, J.R.
TITLE: Transcriptional analysis of the promoter region of
TITLE: the branched chain keto acid dehydrogenase operon of
TITLE: Pseudomonas putida
JOURNAL: Journal of Bacteriology
VOLUME: 172

Query Match 5.3%; Score 16; DB 4; Length 6122;
Best Local Similarity 100.0%; Pred. No. 46;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Caps 0;

QY 192 cctcaacgtgtgctaac 207
|||||

Db 1509 CCTCAACGTGTGTCAC 1524

RESULT 33

US-08-258-261B-6/c

; Sequence 6, Application US/08258261B

; Patent No. 5635949

; GENERAL INFORMATION:

; APPLICANT: Schupp, Thomas

; APPLICANT: Ligon, James M.

; APPLICANT: Beck, James Joseph

; APPLICANT: Hill, Dwight Steven

; APPLICANT: Ryals, John Andrew

; APPLICANT: Gaffney, Thomas Deane

; APPLICANT: Lam, Stephen Ting

; APPLICANT: Hammer, Phillip E.

; APPLICANT: Ukner, Scott Joseph

; TITLE OF INVENTION: Genes for the synthesis of

; FILING DATE: 01-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/457,205
; FILING DATE: 01-JUN-1995
; APPLICATION NUMBER: 08/258,261
; FILING DATE: 08-Jun-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Elmer, James Scott
; REGISTRATION NUMBER: 36,129
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8614
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28958 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-457-342-6

Query Match 5.3%; Score 16; DB 1; Length 28958;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 126 cgccacgcccagcgag 141
|||||

Db 18696 CGCCACGCCAGCGAG 18681

RESULT 36
US-08-457-646A-6/c
; Sequence 6, Application US/08457646A
; Patent No. 5679560
; GENERAL INFORMATION:
; APPLICANT: Schupp, Thomas
; APPLICANT: Ligon, James M.
; APPLICANT: Beck, James Joseph
; APPLICANT: Hill, Dwight Steven
; APPLICANT: Ryals, John Andrew
; APPLICANT: Gaffney, Thomas Deane
; APPLICANT: Lam, Stephen Ting
; APPLICANT: Hammer, Phillip E.
; APPLICANT: Uknes, Scott Joseph
; TITLE OF INVENTION: Genes for the synthesis of
; TITLE OF INVENTION: antipathogenic substances
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ciba-Geigy Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: NY
; COUNTRY: USA
; ZIP: 10532
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/457,646A
; FILING DATE: 01-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/457,205
; FILING DATE: 01-JUN-1995
; APPLICATION NUMBER: 08/258,261
; FILING DATE: 08-Jun-1994

; ATTORNEY/AGENT INFORMATION:
; NAME: Elmer, James Scott
; REGISTRATION NUMBER: 36,129
; REFERENCE/DOCKET NUMBER: CGC 1506/CIP3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8614
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28958 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-457-646A-6

Query Match 5.3%; Score 16; DB 1; Length 28958;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 126 cgccacgcccagcgag 141
|||||

Db 18696 CGCCACGCCAGCGAG 18681

RESULT 37
US-08-458-076A-6/c
; Sequence 6, Application US/08458076A
; Patent No. 5698425
; GENERAL INFORMATION:
; APPLICANT: Schupp, Thomas
; APPLICANT: Ligon, James M.
; APPLICANT: Beck, James Joseph
; APPLICANT: Hill, Dwight Steven
; APPLICANT: Ryals, John Andrew
; APPLICANT: Gaffney, Thomas Deane
; APPLICANT: Lam, Stephen Ting
; APPLICANT: Hammer, Phillip E.
; APPLICANT: Uknes, Scott Joseph
; TITLE OF INVENTION: Genes for the synthesis of
; TITLE OF INVENTION: antipathogenic substances
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ciba-Geigy Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: NY
; COUNTRY: USA
; ZIP: 10532
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/458,076A
; FILING DATE: 01-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/457,205
; FILING DATE: 01-JUN-1995
; APPLICATION NUMBER: 08/258,261
; FILING DATE: 08-Jun-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Elmer, James Scott
; REGISTRATION NUMBER: 36,129
; REFERENCE/DOCKET NUMBER: CGC 1506/CIP3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8614
; TELEFAX: 919-541-8689

; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28958 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-08-458-076A-6

Query Match 5.3%; Score 16; DB 1; Length 28958;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 126 cgcacgcccagcgag 141
Db 18696 CCCACGCCACGCGAG 18681

RESULT 38
US-08-764-233A-4/c
; Sequence 4, Application US/08764233A
; Patent No. 5716849
; GENERAL INFORMATION:
; APPLICANT: Ligon, James M.
; APPLICANT: Schupp, Thomas
; APPLICANT: Beck, James J.
; APPLICANT: Hill, Dwight S.
; APPLICANT: Neff, Snezana
; APPLICANT: Ryals, John A.
; TITLE OF INVENTION: Genes For The Biosynthesis Of Soraphen
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ciba-Geigy Corporation
; STREET: 520 White Plains Road, P.O. Box 2005
; CITY: Tarrytown
; STATE: NY
; COUNTRY: USA
; ZIP: 10591
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/08/764,233A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/729,214
; FILING DATE: 09-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/258,261
; FILING DATE: 08-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: 1506/CIP6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919) 541-8587
; TELEFAX: (919) 541-8689
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28958 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: Sorangium cellulosum
; IMMEDIATE SOURCE:

; CLONE: p98/1
; US-08-764-233A-4

Query Match 5.3%; Score 16; DB 1; Length 28958;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 126 cgcacgcccagcgag 141
Db 18696 CCCACGCCACGCGAG 18681

RESULT 39
US-08-457-335A-6/c
; Sequence 6, Application US/08457335A
; Patent No. 5723759
; GENERAL INFORMATION:
; APPLICANT: Schupp, Thomas
; APPLICANT: Ligon, James M.
; APPLICANT: Beck, James Joseph
; APPLICANT: Hill, Dwight Steven
; APPLICANT: Ryals, John Andrew
; APPLICANT: Gaffney, Thomas Deane
; APPLICANT: Lam, Stephen Ting
; APPLICANT: Hammer, Phillip E.
; APPLICANT: Uknes, Scott Joseph
; TITLE OF INVENTION: Genes for the synthesis of
; TITLE OF INVENTION: antipathogenic substances
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ciba-Geigy Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: NY
; COUNTRY: USA
; ZIP: 10532
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/457,335A
; FILING DATE: 01-JUN-1995
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/457,205
; FILING DATE: 01-JUN-1995
; APPLICATION NUMBER: 08/258,261
; FILING DATE: 08-Jun-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Elmer, James Scott
; REGISTRATION NUMBER: 36,129
; REFERENCE/DOCKET NUMBER: CGC 1506/CIP3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8614
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28958 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-08-457-335A-6

Query Match 5.3%; Score 16; DB 1; Length 28958;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 126 cgcacggccgcgag 141
|||||
Db 18696 CGCCACGCCGCGAG 18681

RESULT 40
US-08-729-214-6/C
; Sequence 6, Application US/08729214
; Patent No. 5817502
; GENERAL INFORMATION:
; APPLICANT: Ligon, James M.
; APPLICANT: Hill, Dwight Steven
; APPLICANT: Ryals, John Andrew
; APPLICANT: Hammer, Phillip E.
; APPLICANT: van Pee, Karl-Heinz
; TITLE OF INVENTION: Genes for the synthesis of
; TITLE OF INVENTION: antipathogenic substances
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ciba-Geigy Corporation
; STREET: 520 White Plains Road
; CITY: Tarrytown
; STATE: NY
; COUNTRY: USA
; ZIP: 10591
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/729,214
; FILING DATE: TBA
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: CGC 1506/CIP5
; TELEPHONE: 919-541-8587
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28958 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-729-214-6

Query Match 5.3%; Score 16; DB 1; Length 28958;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 126 cgcacggccgcgag 141
|||||
Db 18696 CGCCACGCCGCGAG 18681

RESULT 41
US-08-934-6/c
; Sequence 6, Application US/09028934
; Patent No. 6117670
; GENERAL INFORMATION:
; APPLICANT: Ligon, James M.
; APPLICANT: Hill, Dwight S.
; APPLICANT: Lam, Steven T.
; APPLICANT: Hammer, Phillip E.

; APPLICANT: van Pee, Karl-Heinz
; APPLICANT: Kirner, Sabine
; APPLICANT: Young, Thomas R.
; TITLE OF INVENTION: Pyrrolnitrin Biosynthesis Genes and Uses
; TITLE OF INVENTION: Thereof
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NO. 6117670artis Corporation
; STREET: 3054 Cornwalls Road
; CITY: Research Triangle Park
; STATE: NC
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/028,934
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/729,214
; FILING DATE: 09-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/258,261
; FILING DATE: 08-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: CGC1506/CIP7
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8587
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28958 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-09-028-934-6

Query Match 5.3%; Score 16; DB 3; Length 28958;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 126 cgcacggccgcgag 141
|||||
Db 18696 CGCCACGCCGCGAG 18681

RESULT 42
US-08-764-233A-1/c
; Sequence 1, Application US/08764233A
; Patent No. 5716849
; GENERAL INFORMATION:
; APPLICANT: Ligon, James M.
; APPLICANT: Schupp, Thomas
; APPLICANT: Beck, James J.
; APPLICANT: Hill, Dwight S.
; APPLICANT: Neff, Snezana
; APPLICANT: Ryals, John A.
; TITLE OF INVENTION: Genes For The Biosynthesis Of Soraphen
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ciba-Geigy Corporation
; STREET: 520 White Plains Road, P.O. Box 2005
; CITY: Tarrytown

; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
US-09-020-956-99

Query Match 5.0%; Score 15; DB 4; Length 171;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 229 ccgcaggggccccctc 243
|||||
DB 28 CCGCAGGGCCCCCTC 42

RESULT 44

US-09-030-607-99
; Sequence 99, Application US/09030607
; Patent No. 6262245
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FO
; NUMBER OF SEQUENCES: 224
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/030,607
; FILING DATE: 25-FEB-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.427C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 99:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 171 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
US-09-030-607-99

Query Match 5.0%; Score 15; DB 4; Length 171;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 229 ccgcaggggccccctc 243
|||||
DB 28 CCGCAGGGCCCCCTC 42

RESULT 45

US-09-439-313-99
; Sequence 99, Application US/09439313
; Patent No. 6329505
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun

; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang Yuqui
; APPLICANT: Reed, Steven G.
; APPLICANT: Kalos, Michael
; APPLICANT: Fanger, Gary
; APPLICANT: Retter, Mark
; APPLICANT: Solk, John
; APPLICANT: Day, Craig
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; FILE REFERENCE: DIAGNOSIS OF PROSTATE CANCER
; CURRENT APPLICATION NUMBER: US/09/439,313
; CURRENT FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 575
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 99
; LENGTH: 171
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-439-313-99

Query Match 5.0%; Score 15; DB 4; Length 171;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 229 ccgcaggggccccctc 243
|||||
DB 28 ccgcaggggccccctc 42

Search completed: July 15, 2002, 23:07:17
Job time: 22970 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: July 15, 2002, 23:09:35 ; Search time 932.4 Seconds
(without alignments)
557.942 Million cell updates/sec

Title: US-09-375-248-1_COPY_2546_2848
Perfect score: 303
Sequence: 1 gagcggctgcacctggggag.....acttctgcgcgccaagcgg 303

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 1736436 seqs, 858457221 residues

Word size : 0

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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5:	/SIDSI/gcgdata/geneseq/geneseq-emb1/NA1984.DAT.*
6:	/SIDSI/gcgdata/geneseq/geneseq-emb1/NA1985.DAT.*
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22:	/SIDSI/gcgdata/geneseq/geneseq-emb1/NA2001A.DAT.*
23:	/SIDSI/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT.*
24:	/SIDSI/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	303	100.0	4111	21 AAC62405	Human Flt4/VEGFR-3
2	303	100.0	4111	22 AAC62405	Human Flt4/VEGFR-3
3	303	100.0	4195	17 AAT12068	FLT4 receptor tyro
4	303	100.0	4195	21 AA337815	Human Flt4 recepto
5	303	100.0	4195	21 AA252333	Human tyrosine kin
6	303	100.0	4425	16 AAT03090	Protein tyrosine-k
7	303	100.0	4795	21 AA337816	Human Flt4 recepto
8	303	100.0	4795	21 AA252334	Human tyrosine kin
9	303	100.0	9108	16 AAT03104	Plasmid PRK5.tkl-1

10	252	83.2	4450	21 AAC62210	Nucleotide sequenc
11	20	6.6	7680	23 AAS70286	DNA encoding novel
12	18	5.9	3351	20 AA231552	S. rochei strain E
13	17	5.6	17	18 AAX71396	Human KDR VEGF rec
14	17	5.6	218	17 AAT14887	Thermus thermophil
15	17	5.6	272	22 ABA11580	Human nervous syst
16	17	5.6	768	22 ABA103972	Human cDNA clone (
17	17	5.6	813	22 AAH06553	Human cDNA clone (
18	17	5.6	1101	22 AAS22655	DNA encoding novel
19	17	5.6	1116	23 AAS85415	DNA encoding novel
20	17	5.6	1116	23 AAS91079	DNA encoding novel
21	17	5.6	1233	23 AAS85413	DNA encoding novel
22	17	5.6	1302	23 AAS83501	Human polynucleoti
23	17	5.6	1406	22 AAG91319	Nucleotide sequenc
24	17	5.6	1417	22 AAH75162	Human cDNA sequenc
25	17	5.6	1767	22 AAH15398	Human cDNA sequenc
26	17	5.6	1824	22 AAL03231	Human reproductive
27	17	5.6	1901	22 ABA15613	Human nervous syst
28	17	5.6	2484	23 AAS83500	Human cDNA sequenc
29	17	5.6	2624	22 AAH14499	Human cDNA sequenc
30	17	5.6	2863	22 AAS22891	Receptor protein t
31	17	5.6	3120	19 AAV53895	Receptor protein t
32	17	5.6	3120	20 AAV65317	DNA encoding novel
33	17	5.6	4008	22 AAS22909	A novel type III R
34	17	5.6	4071	13 AAQ28272	Human receptor tyr
35	17	5.6	4071	20 AAV99829	Human VEGFR-2 enco
36	17	5.6	4225	22 AAF83308	Human KDR genomic
37	17	5.6	4236	19 AAV34763	Human immune/haema
38	17	5.6	5414	22 AAK78291	Drosophila melanog
39	17	5.6	5656	23 ABL10071	Mouse ischaemic co
40	17	5.6	6730	24 ABI99504	cDNA for protein (
41	17	5.6	8460	18 AAT88206	Cancer specific ge
42	17	5.6	8470	21 AAZ95007	Human fatty acid s
43	17	5.6	8519	21 AAZ37760	Human immune/haema
44	17	5.6	8864	22 AAK79882	Drosophila melanog
45	17	5.6	9889	23 ABL10070	

ALIGNMENTS

RESULT 1	
AAC62405	
ID AAC62405 standard; cDNA: 4111 BP.	
XX	
AC AAC62405;	
XX	
DT 31-JAN-2001 (first entry)	
DE Human Flt4/VEGFR-3 coding sequence.	
DE	
XX	
XX Human: Flt4; fms-like tyrosine kinase 4; lymphoedema;	
XX vascular endothelial growth factor receptor 3; VEGFR-3;	
XX Mliroy-Nonne syndrome; lymphoedema praecox; ss.	
XX	
OS Homo sapiens.	
XX	
PN WO200058511-A1.	
XX	
PD 05-OCT-2000.	
XX	
PF 26-MAR-1999; 99WO-US06133.	
XX	
PR 26-MAR-1999; 99WO-US06133.	
XX	
PA (LUDW-) LUDWIG INST CANCER RES.	
PA (UYHE-) UNIV HELSINKI LICENSING LTD OY.	
PA (UYPI-) UNIV PITTSBURGH.	
PI Ferrell RE, Alitalo K, Finegold DN, Karkkainen M;	
XX	
DR WPI; 2000-679298/66.	
DR P-PSDB; AAB29047.	


```

XX      Sequence 4195 BP; 889 A; 1279 C; 1305 G; 722 T; 0 other;
SQ
      Query Match      100.0%;      Score 303;      DB 21;      Length 4195;
      Best Local Similarity 100.0%;      Pred. No. 1.6e-141;
      Matches 303;      Conservative 0;      Mismatches 0;      Indels 0;      Gaps 0;

Qy 1 gagcggctgcacctggggagagtgctcggctcacgcgcttcgcggaaagtggtggaagcc 60
Db 2546 gagcggctgcacctggggagagtgctcggctcacgcgcttcgcggaaagtggtggaagcc 2605
Qy 61 tccgctttcgcattccacaaaggcagcagctgtgacaccgtggccgtgaaatgctgaaa 120
Db 2606 tccgctttcggcatccacaaaggcagcagctgtgacaccgtggccgtgaaatgctgaaa 2665
Qy 121 gagggcgccacggcgacgagcagcgcgcgctgctgagtcgagagctcaagatcctcatcac 180
Db 2666 gagggcgccacggcgacgagcagcgcgcgctgctgagtcgagagctcaagatcctcatcac 2725
Qy 181 atcggcaaccactcaacgtggtgtaacctctcctcggggtgacacagcgagggcccc 240
Db 2726 atcggcaaccactcaacgtggtgtaacctctcctcggggtgacacagcgagggcccc 2785
Qy 241 cteatggtgactggtggagttctcgaagtacggcaacctctccaacttctcgcgccaag 300
Db 2786 cteatggtgactggtggagttctcgaagtacggcaacctctccaacttctcgcgccaag 2845
Qy 301 cgg 303
Db 2846 cgg 2848

RESULT 5
AAZ52333
ID AAZ52333 standard; cDNA; 4195 BP.
XX
XX AAZ52333;
XX
XX 17-AUG-2000 (first entry)
XX
XX Human tyrosine kinase receptor Flt4-short form cDNA.
XX
XX Human; receptor tyrosine kinase; RTK; Flt4; fms-like tyrosine kinase 4;
KW VEGFR-3; vascular endothelial growth factor receptor-3; chromosome 5q35;
KW cytotastic; tumour imaging; anti-tumour therapy; treatment; diagnosis;
KW neoplastic disease; lymphoma; carcinoma; breast; squamous cell; melanoma;
KW sarcoma; malignancy; ss.
XX
XX Homo sapiens.
XX
XX Key      Location/Qualifiers
FH CDS      20..3916
FT FT      /*tag= a
FT FT      /product= "Flt4 receptor-short form"
FT FT      /note= "The start codon is surrounded by typical
FT FT      consensus kozak sequence"
FT FT      20..79
FT FT      sig_peptide
FT FT      /*tag= b
FT FT      /note= "Directs protein to endoplasmic reticulum"
FT FT      mat_peptide
FT FT      80..3913
FT FT      /*tag= c
FT FT      /product= "Mature Flt4 receptor-short form"
XX
XX WO200021560-A1.
XX
XX 20-APR-2000.
XX
XX 08-OCT-1999;      99WO-US23525.
XX
XX 09-OCT-1998;      98US-0169079.
XX
XX {LUDWIG INST CANCER RES.
XX

```

(UYHE-) UNIV HELSINKI LICENSING LTD OY.

Alitalo K, Kaipainen A, Valtola R, Jussila L;
WPI: 2000-317850/27.
P-PSDB: AAY70746.

Treating neoplastic diseases such as lymphoma, carcinomas, melanomas and sarcomas, involves administering a compound capable of inhibiting binding of ligand proteins to fms-like tyrosine kinase-4 receptor .

Example 14; Page 109-115; 148pp; English.

The patent discloses a method to treat neoplastic disease characterised by expression of fms-like tyrosine kinase 4 (Flt4) receptor (also referred as vascular endothelial growth factor receptor-3, VEGFR-3) in endothelial cells of blood vessels adjacent to malignant neoplasm. The method involves administering a compound that inhibits binding of a ligand to Flt4 thereby inhibiting Flt4 mediated proliferation of vascular endothelial cells. The compound is useful for treating neoplastic disease such as breast carcinomas, squamous cell carcinomas, lymphomas, melanomas and sarcomas. Flt4 receptor tyrosine kinase binding compounds can be used for manufacturing medicament useful for diagnostic screening, imaging and treatment of malignancies characterised by Flt4-expressing blood cells. The present sequence is a cDNA encoding the short form of Flt4 receptor from an oligo-dr primed human erythroleukaemia cell line (HEL) cDNA library in bacteriophage lambda gt10. The Flt4 gene maps to chromosomal region 5q95 and is expressed as 5.8 kb and 4.5 kb mRNAs which differ in their 3' sequences and are differentially expressed in HEL and DAMI cell lines. Flt4 belongs to a subfamily of class III receptor tyrosine kinases (RTKs). It is used as a target for tumour imaging and anti-tumour therapy.

Sequence 4195 BP: 889 A; 1279 C; 1305 G; 722 T; 0 other;

Query Match	100.0%	Score	303	DB	21	Length	4195
Best Local Similarity	100.0%	Pred.	No. 1.6e-141				
Matches	303	Conservative	0	Mismatches	0	Indels	0
							Gaps
Qy	1	gagcggtgcacctggggagagtgctcggtctacggcgctctcggaagagtggtggaagcc	60				
Db	2546	gagcggtgcacctggggagagtgctcggtctacggcgctctcggaagagtggtggaagcc	2605				
Qy	61	tccgctttcggcatccacaaaggcagcagctgtgcacacgtggccgtgaaaatgctgaaa	120				
Db	2606	tccgctttcggcatccacaaaggcagcagctgtgcacacgtggccgtgaaaatgctgaaa	2665				
Qy	121	gaggggcgccacgcgcagcgacacgcgcgtgatgtcgaggctcaagatcctcattcac	180				
Db	2666	gaggggcgccacgcgcagcgacacgcgcgtgatgtcgaggctcaagatcctcattcac	2725				
Qy	181	atcgggcaaccacctcaacgctggtcaacctctcggggcgctgcaccaagccgagggcccc	240				
Db	2726	atcgggcaaccacctcaacgctggtcaacctctcggggcgctgcaccaagccgagggcccc	2785				
Qy	241	ctcatgtgatcgtggagttctgcaagtacaggcaacctctcacaacttctgcgcgcacaag	300				
Db	2786	ctcatggtgatcgtggagttctgcaagtacaggcaacctctcacaacttctgcgcgcacaag	2845				
Qy	301	cgg 303					
Db	2846	cgg 2848					
RESULT	6						
AAAT03090							
ID	AAAT03090	standard; DNA;	4425	BP.			
XX							
XX	AAAT03090;						
XX							
DT	14-FEB-1996	(first entry)					
XX							

DE Protein tyrosine-kinase SAL-S1 gene.
XX
KW Protein tyrosine-kinase; pTK; SAL-S1; agonist; cell growth;
KW differentiation; ss.

OS Homo sapiens.

XX Key Location/Qualifiers
FH CDS 30..3927
FT /*tag= a
FT sig_peptide 30..102
FT /*tag= b
FT mat_peptide 103..3924
FT /*tag= c

XX W09527061-A1.

PN 12-OCT-1995.

XX 04-APR-1995; 95WO-US04228.

XX 04-APR-1994; 94US-0222616.

XX (GETH) GENENTECH INC.

XX Bennett BD, Goeddel D, Lee JM, Matthews W, Tsai SP;
PI Wood WI;

XX WPI: 1995-366160/47.

XX P-PSDB: AAR85937.

XX Agonist antibodies which activate specific protein tyrosine
PT kinase(s) - also activate chimeric proteins of kinase extracellular
PT domain and Ig constant domain, useful for studying, and therapeutic
PT modulation of, cell growth and differentiation
XX
PS Disclosure: Fig 15A-F; 125pp; English.

XX DNA probes based on protein tyrosine-kinase (pTK) sequences were used
CC to screen cDNA libraries to identify novel pTK genes. The SAL-S1
CC gene (see also AAT03101) was isolated from several megakaryocytic cell
CC libraries. The gene can be used to produce recombinant SAL-S1 or its
CC fragments, to detect related genes, and to design drugs, peptides
CC or antisense nucleotides that modulate pTK activity.

XX Sequence 4425 BP; 939 A; 1348 C; 1361 G; 777 T; 0 other;

Query Match 100.0%; Score 303; DB 16; Length 4425;
Best Local Similarity 100.0%; Pred. No. 1.6e-141;
Matches 303; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gaggcgtcacctgggagagtgctcggtacggcgcttcgggaagggtggaagcc 60
DB 2557 gaggcgtcacctgggagagtgctcggtacggcgcttcgggaagggtggaagcc 2616
QY 61 tccgctttcgcatcaccaaggcagcagctgtgacacgtgcccgtgaaatgctgaaa 120
DB 2617 tccgctttcgcatcaccaaggcagcagctgtgacacgtgcccgtgaaatgctgaaa 2676
QY 121 gaggcgccacgcccagcagcagcgcgctgatgtcgaggctcaaatctcttcac 180
DB 2677 gaggcgccacgcccagcagcagcgcgctgatgtcgaggctcaaatctcttcac 2736
QY 181 atcggaaccactcaacggtgacactctctcgggcgctgacacagccgagggccc 240
DB 2737 atcggaaccactcaacggtgacactctctcgggcgctgacacagccgagggccc 2796
QY 241 ctcatggtgatcgtgagttctgcaagtacgcgcaacctctcaactctctcgcccaag 300
DB 2797 ctcatggtgatcgtgagttctgcaagtacgcgcaacctctcaactctctcgcccaag 2856
QY 301 cgg 303

DB 2857 cgg 2859
III
RESULT 7
AAA37816
XX AAA37816 standard; cDNA; 4795 BP.
AC AAA37816;
XX
DT 15-JAN-2001 (first entry)
XX
DE Human Flt4 receptor tyrosine kinase long form coding sequence.

XX Human; Flt4 receptor tyrosine kinase; antibody; extracellular domain;
KW lymphatic vessel detection; lymphatic tissue; lymph node tissue;
KW endothelial venule; diagnosis; lymphoma; long form; ss.
XX
OS Homo sapiens.

XX Key Location/Qualifiers
FH CDS 20..4111
FT /*tag= a
FT /product= Flt4 receptor tyrosine kinase long form

XX US6107046-A.

XX 22-AUG-2000.

XX 28-JUL-1997; 97US-0901710.

XX 09-OCT-1992; 92US-0959951.

XX 09-JUN-1994; 94US-0257754.

XX 14-NOV-1994; 94US-0340011.

XX (ORIN) ORION CORP.

XX (LUDW-) LUDWIG INST CANCER RES.

XX Alitalo K, Aprelikova O, Armstrong E, Korhonen J, Kaipainen A;
XX Matikainen M, Pajusola K;

XX WPI: 2000-571323/53.

XX P-PSDB: AAY90366.

XX Antibody to extracellular domain of or to an epitope unique to a
PT vertebrate Flt4 receptor tyrosine kinase protein useful for diagnosing
PT lymphoma and imaging lymphatic vessels or high endothelial venules in
PT tissue

XX Disclosure: Column 55-66; 66pp; English.

XX This sequence encodes the human Flt4 receptor tyrosine kinase long
CC form protein. The invention relates to an antibody (i) specific to the
CC extracellular domain of or to an epitope unique to a vertebrate Flt4
CC receptor tyrosine kinase protein (ii). A composition comprising (i) is
CC useful for detecting lymphatic vessels, lymphatic tissue comprising lymph
CC node tissue or high endothelial venules in an organism preferably mammal
CC especially human. The method comprises administering the composition and
CC detecting (i) bound to lymphatic vessels, lymphatic tissue or high
CC endothelial venules. (i) is also useful for screening a biological sample
CC for the presence of (ii) or diagnosing a disease state. The diagnosing
CC method of the disease state preferably lymphoma comprises obtaining a
CC tissue sample on a vertebrate organism suspected of being in a diseased
CC state characterised by in Flt4 expression in lymphatic cells or high
CC endothelial venules and screening the diseased state utilising (i).
CC (i) is also useful for imaging lymphatic vessels or high endothelial
CC venules in a tissue by contacting the tissue with (i) and imaging the
CC vessels by detecting (i) bound to the tissues.

XX Sequence 4795 BP; 977 A; 1490 C; 1494 G; 834 T; 0 other;

Query Match 100.0%; Score 303; DB 21; Length 4795;

```
Best Local Similarity 100.0%; Pred. No. 1.6e-141;
Matches 303; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gagcgctgcacctggggagtgctcggtacggcgcttcggggaagtgtggaagcc 60
   |||
Db 2546 gagcgctgcacctggggagtgctcggtacggcgcttcggggaagtgtggaagcc 2605

QY 61 tcgccttcggcatccacagggcagcagctgtgacacgctgcccgtgaaatgctgaaa 120
   |||
Db 2606 tcgccttcggcatccacagggcagcagctgtgacacgctgcccgtgaaatgctgaaa 2665

QY 121 gagggcgccacgcgagcagccgcgcgtgagctgagctcaagatcctcattcac 180
   |||
Db 2666 gagggcgccacgcgagcagccgcgcgtgagctgagctcaagatcctcattcac 2725

QY 181 atcggaacacacctaactggtgtcaacctctcctgggctgacccaagcgcagggcccc 240
   |||
Db 2726 atcggaacacacctaactggtgtcaacctctcctgggctgacccaagcgcagggcccc 2785

QY 241 ctcatggtgatcgtgagttctgcaagtacggcaacctctccaacttctcgcgccaag 300
   |||
Db 2786 ctcatggtgatcgtgagttctgcaagtacggcaacctctccaacttctcgcgccaag 2845

QY 301 cgg 303
   |||
Db 2846 cgg 2848

RESULT 8
AAZ52334
ID AAZ52334 standard; cDNA; 4795 BP.
AC
XX
XX
Df 17-AUG-2000 (first entry)
XX
DE Human tyrosine kinase receptor Flt4-long form cDNA.
XX
KW Human: receptor tyrosine kinase; RTK; Flt4; fms-like tyrosine kinase 4;
KW VEGFR-3; vascular endothelial growth factor receptor-3; chromosome 5q35;
KW cytotatic; tumour imaging; anti-tumour therapy; treatment; diagnosis;
KW neoplastic disease; lymphoma; carcinoma; breast; squamous cell; melanoma;
KW sarcoma; malignancy; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 20..4111
FT FT /*tag= a
FT FT /product= "Flt4 receptor-long form"
XX
PN WO200021560-A1.
XX
XX 20-APR-2000.
XX
PF 08-OCT-1999; 99WO-US23525.
XX
PR 09-OCT-1998; 98US-0169079.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
PA (UYHE-) UNIV HELSINKI LICENSING LTD OY.
XX
PI Alltalo K, Kaipainen A, Valtola R, Jussila L;
XX
XX WPI; 2000-317850/27.
DR P-PSDB; AAY70747.
XX
XX Treating neoplastic diseases such as lymphoma, carcinomas, melanomas
PT and sarcomas, involves administering a compound capable of inhibiting
PT binding of ligand proteins to fms-like tyrosine kinase-4 receptor .
XX
PS Disclosure; Page 120-127; 148pp; English.
XX
```

```
CC The patent discloses a method to treat neoplastic disease characterised
CC by expression of fms-like tyrosine kinase 4 (Flt4) receptor (also
CC referred as vascular endothelial growth factor receptor-3, VEGFR-3) in
CC endothelial cells of blood vessels adjacent to malignant neoplasm. The
CC method involves administering a compound that inhibits binding of a
CC ligand to Flt4 thereby inhibiting Flt4 mediated proliferation of vascular
CC endothelial cells. The compound is useful for treating neoplastic disease
CC such as breast carcinomas, squamous cell carcinomas, lymphomas, melanomas
CC and sarcomas. Flt4 receptor tyrosine kinase binding compounds can be used
CC for manufacturing medicament useful for diagnostic screening, imaging and
CC treatment of malignancies characterised by Flt4-expressing blood cells.
CC The present sequence is a cDNA encoding the long form of Flt4 receptor
CC from an oligo-dT primed human erythroleukaemia cell line (HEL) cDNA
CC library in bacteriophage lambda gt11. The Flt4 gene maps to chromosomal
CC region 5q35 and is expressed as 5.8 kb and 4.5 kb mRNAs which differ in
CC their 3' sequences and are differentially expressed in HEL and DAMI cell
CC lines. Flt4 belongs to a subfamily of class III receptor tyrosine kinases
CC (RTKs). It is used as a target for tumour imaging and anti-tumour
CC therapy.
XX
SQ Sequence 4795 BP; 977 A; 1490 C; 1494 G; 834 T; 0 other;

Query Match 100.0%; Score 303; DB 21; Length 4795;
Best Local Similarity 100.0%; Pred. No. 1.6e-141;
Matches 303; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gagcgctgcacctggggagtgctcggtacggcgcttcggggaagtgtggaagcc 60
   |||
Db 2546 gagcgctgcacctggggagtgctcggtacggcgcttcggggaagtgtggaagcc 2605

QY 61 tcgccttcggcatccacagggcagcagctgtgacacgctgcccgtgaaatgctgaaa 120
   |||
Db 2606 tcgccttcggcatccacagggcagcagctgtgacacgctgcccgtgaaatgctgaaa 2665

QY 121 gagggcgccacgcgagcagccgcgcgtgagctgagctcaagatcctcattcac 180
   |||
Db 2666 gagggcgccacgcgagcagccgcgcgtgagctgagctcaagatcctcattcac 2725

QY 181 atcggaacacacctaactggtgtcaacctctcctgggctgacccaagcgcagggcccc 240
   |||
Db 2726 atcggaacacacctaactggtgtcaacctctcctgggctgacccaagcgcagggcccc 2785

QY 241 ctcatggtgatcgtgagttctgcaagtacggcaacctctccaacttctcgcgccaag 300
   |||
Db 2786 ctcatggtgatcgtgagttctgcaagtacggcaacctctccaacttctcgcgccaag 2845

QY 301 cgg 303
   |||
Db 2846 cgg 2848

RESULT 9
AAZ03104
ID AAT03104 standard; DNA; 9108 BP.
XX
XX AAT03104;
XX
XX 14-FEB-1996 (first entry)
XX
XX Plasmid pRK5.tk1-1.1 encoding Sal S-1.
XX
XX Protein tyrosine-kinase; pTK; SAL-S1; agonist; cell growth;
XX differentiation; pRK5.tk1-1.1; ss.
XX
XX Chimeric synthetic;
XX OS Chimeric Homo sapiens.
XX
XX WO9527061-A1.
XX
XX 12-OCT-1995.
XX
XX 04-APR-1995; 95WO-US04228.
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XX PR 04-APR-1994; 94US-0222616.
XX PA (GETH ) GENENTECH INC.
XX PT Bennett BD, Goeddel D, Lee JM, Matthews W, Tsai SP;
XX PI Wood WT;
XX DR WPI; 1995-366160/47.
XX PT Agonist antibodies which activate specific protein tyrosine
XX PT kinases) ; also activate chimeric proteins of kinase extracellular
XX PT domain and Ig constant domain, useful for studying, and therapeutic
XX PT modulation of, cell growth and differentiation
XX PS Example 7; Page 102-111; 125pp; English.
XX CC PCR primers given in AAT03102-03 were used to amplify plasmid
XX CC PRK5.tkl1-1.1 (AAT03104) incorporating SAL-SI (see AAT03090) DNA.
XX CC The product was used to construct a fusion of the SAL-SI
XX CC extracellular domain and human IgG1 Fc domain, which was expressed
XX CC in 293 and COS7 cells and used to raise antibodies having
XX CC protein tyrosine-kinase agonist activity.
XX SQ Sequence 9108 BP; 2086 A; 2554 C; 2491 G; 1977 T; 0 other;

Query Match 100.0%; Score 303; DB 16; Length 9108;
Best Local Similarity 100.0%; Pred. No. 1.5e-141;
Matches 303; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gagcggtgcacctgggagagtgctcgctacggcgcttcgggaagtggtggaagcc 60
DB 3489 gagcggtgcacctgggagagtgctcgctacggcgcttcgggaagtggtggaagcc 3548
QY 61 tcgcgttcggcatccacaaaggagagctgtgacacccgtgacacccgtgacacccgtgacac 120
DB 3549 tcgcgttcggcatccacaaaggagagctgtgacacccgtgacacccgtgacacccgtgacac 3608
QY 121 gagggcgccagcgccagcagcagcagcgctgctgctgctgctgctgctgctgctgctgctgct 180
DB 3609 gagggcgccagcgccagcagcagcagcgctgctgctgctgctgctgctgctgctgctgctgct 3668
QY 181 atcggcaaccacctcaactgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgct 240
DB 3669 atcggcaaccacctcaactgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgct 3728
QY 241 ctcatggtgatcgtgagttcttctgcaagtacggcaacctctcaactctctcgcgcgccaag 300
DB 3729 ctcatggtgatcgtgagttcttctgcaagtacggcaacctctcaactctctcgcgcgccaag 3788
QY 301 cgg 303
DB 3789 cgg 3791

RESULT 10
AAC62210
ID AAC62210 standard; DNA; 4450 BP.
XX AC AAC62210;
XX DT 06-MAR-2001 (first entry)
XX DE Nucleotide sequence of the human flt-4 gene.
XX KW Antisense oligonucleotide; flt-4; receptor type tyrosine kinase;
XX KW lymphangiogenesis; prostate cancer; prostate cell; ss.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX FT CDS 22..3918
```

```
FT FT /*tag= a *flt-4*
FT FT /product=
FT FT /transl_except= (pos: 55..57, aa: Trp)
FT FT /transl_except= (pos: 58..60, aa: Leu)
FT FT /transl_except= (pos: 61..63, aa: Cys)
FT FT /transl_except= (pos: 64..66, aa: Leu)
FT FT /transl_except= (pos: 67..69, aa: Gly)
FT FT /transl_except= (pos: 70..72, aa: Leu)
FT FT /transl_except= (pos: 73..75, aa: Leu)
FT FT /transl_except= (pos: 76..78, aa: Asp)
FT FT /transl_except= (pos: 79..81, aa: Gly)
FT FT /transl_except= (pos: 82..84, aa: Leu)
FT FT /transl_except= (pos: 85..87, aa: Val)
FT FT /transl_except= (pos: 88..90, aa: Ser)
FT FT /transl_except= (pos: 91..93, aa: Asp)
FT FT /transl_except= (pos: 94..96, aa: Tyr)
FT FT /transl_except= (pos: 97..99, aa: Ser)
FT FT /transl_except= (pos: 1639..1641, aa: Lys)
FT FT /transl_except= (pos: 2236..2238, aa: Arg)
FT FT /transl_except= (pos: 3508..3510, aa: Ser)
FT FT /transl_except= (pos: 3598..3600, aa: Ser)
FT FT /transl_except= (pos: 3796..3798, aa: Phe)
XX XX
XX PN WO200062063-A1.
XX XX 19-OCT-2000.
XX XX
XX PF 13-APR-1999; 99WO-US08079.
XX XX
XX PR 13-APR-1999; 99WO-US08079.
XX XX (NMBI-) NORTHWEST BIOTHEAPEUTICS INC.
XX XX Su SL;
XX XX WPI; 2000-687067/67.
XX DR P-PSDB; AAB30542.
XX XX
XX PT Detecting metastatic potential, diagnosing metastatic prostate cancer
XX PT or determining the prognosis of a subject with prostate cancer
XX XX comprises detecting the expression of flt-4 in a prostate cell -
XX PS Claim 6; Fig 1A-F; 78pp; English.
XX XX
XX CC The present sequence encodes human flt-4. Flt-4 is a receptor type
XX CC tyrosine kinase with 7 Ig-like domains similar to other VEGF receptors.
XX CC Flt-4 may play a role in lymphangiogenesis. Antisense oligonucleotides
XX CC can be used for detecting the metastatic potential, diagnosing
XX CC metastatic prostate cancer or determining the prognosis of a subject
XX CC with prostate cancer. The method comprises identifying the prostate
XX CC cell in a body fluid sample and detecting the expression of flt-4 in
XX CC the cell. Expression of flt-4 in a prostate cell indicates that the
XX CC cell is a cancerous prostate cell that has metastatic potential or is
XX CC a secondary tumour metastasis of a primary prostate tumour.
XX SQ Sequence 4450 BP; 968 A; 1352 C; 1349 G; 781 T; 0 other;

Query Match 83.2%; Score 252; DB 21; Length 4450;
Best Local Similarity 99.7%; Pred. No. 4.4e-116;
Matches 302; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 gagcggtgcacctgggagagtgctcgctacggcgcttcgggaagtggtggaagcc 60
DB 2548 gagcggtgcacctgggagagtgctcgctacggcgcttcgggaagtggtggaagcc 2607
QY 61 tcgcgttcggcatccacaaaggagagctgtgacacccgtgacacccgtgacacccgtgacacccgtgacac 120
DB 2608 tcgcgttcggcatccacaaaggagagctgtgacacccgtgacacccgtgacacccgtgacacccgtgacac 2667
QY 121 gagggcgccagcgccagcagcagcgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgct 180
DB 2668 gagggcgccagcgccagcagcagcgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgct 2727
```

Oy 181 atcggcaaccctcaacgtggtcaacctctcgtggcggtgcaccacaagcgagggccccc 240
|||||
Db 2728 atcggcaaccctcaacgtggtcaacctctcgtggcggtgcaccacaagcgagggccccc 2787

Oy 241 ctcatggtgatcgtggagttctgcaagtacaggcaacctctccaaacttccctgctgcgcgccaag 300
|||||
Db 2788 ctcatggtgatcgtggagttctgcaagtacaggcaacctctccaaacttccctgctgcgcgccaag 2847

Oy 301 cgg 303
|||
Db 2848 cgg 2850

RESULT 11
AAS70286
ID AAS70286 standard; cDNA; 7680 BP.
XX
AC AAS70286;
XX
DT 13-FEB-2002 (first entry)
XX
DE DNA encoding novel human diagnostic protein #6090.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX
OS Homo sapiens.
XX
PN W0200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US08631.
XX
PR 31-MAR-2000; 2000US-0540217.
PR 23-AUG-2000; 2000US-0649167.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
DR WPI: 2001-639362/73.
DR P-PSDB; ABC06099.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity -
XX
PS Claim 1: SEQ ID NO 6090; 103pp; English.
XX
CC The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AAS64197-AAS94564 represent novel human
CC diagnostic coding sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.

XX
SQ Sequence 7680 BP; 2279 A; 1661 C; 1739 G; 2001 T; 0 other;

Query Match 6.6%; Score 20; DB 23; Length 7680;
Best Local Similarity 100.0%; Pred. No. 2.6; Mismatches 0; Indels 0; Gaps 0;
Matches 20; Conservative 0;

Oy 106 gtgaaaatgctgaagagg 125
|||||
Db 2827 gtgaaaatgctgaagagg 2846

RESULT 12
AAZ31552
ID AAZ31552 standard; DNA; 3351 BP.
XX
AC AAZ31552;
XX
DT 10-JAN-2000 (first entry)
XX
DE S. rochei strain E87 inulin-degrading enzyme coding sequence.
XX
KW Inulin-degrading enzyme; IDE; inulotetraose production;
KW inulotriose preparation; raffinose purification; ketose decomposition;
KW ss.
XX
OS Streptomyces rochei.
XX
PN JP11243962-A.
XX
PD 14-SEP-1999.
XX
PF 27-FEB-1998; 98JP-0061957.
XX
PR 27-FEB-1998; 98JP-0061957.
XX
PA (NIPT) NIPPON TENSAI SEITO KK.
XX
DR WPI: 1999-603711/52.
DR P-PSDB; AAY43179.
XX
PT New inulin-degrading enzyme gene - useful for preparation of
PT inulotetraose and/or inulotriose
XX
PS Claim 1; Page 9-12; 15pp; Japanese.
XX
CC This sequence encodes the Streptomyces rochei strain E87 inulin-degrading
CC enzyme (IDE) of the invention. The IDE is useful for the preparation of
CC inulotetraose and/or inulotriose by treating inulin with the IDE. The IDE
CC can also be used in a method for the purification of raffinose in which
CC ketoses contained in a raffinose solution is selectively decomposed by
CC using the IDE and raffinose is maintained as it is.
XX
SQ Sequence 3351 BP; 619 A; 1309 C; 1003 G; 420 T; 0 other;

Query Match 5.9%; Score 18; DB 20; Length 3351;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 67 ttccggcatccacaaggc 84
|||||
Db 3133 ttccggcatccacaaggc 3150

RESULT 13
AAX71396
ID AAX71396 standard; RNA; 17 BP.
XX
AC AAX71396;
XX
DT 28-JUL-1999 (first entry)

XX DE Human KDR VEGF receptor hammerhead ribozyme substrate #408.
XX KW flk-1; KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
KW tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
KW fms-like tyrosine kinase 1; kinase insert domain containing receptor;
KW foetal liver kinase 1; ss.
XX OS Homo sapiens.
XX PN WO9715662-A2.
XX PD 01-MAY-1997.
XX PF 25-OCT-1996; 96WO-US17480.
XX PR 11-JAN-1996; 96US-0584040.
XX PR 26-OCT-1995; 95US-0005974.
XX PA (CHIR) CHIRON CORP.
XX PA (RIBO-) RIBOZYME PHARM INC.
XX PI Escobedo J, McSwiggen J, Pavco P, Stinchcomb D;
XX WPI; 1997-259017/23.
XX Nucleic acid molecule modulating VEGF receptor(s) gene expression or
PT mRNA stability - useful for treating e.g. tumour angiogenesis,
PT psoriasis, rheumatoid arthritis, etc., in a human patient
XX Claim 4; Page 109; 218pp; English.
XX The present invention describes nucleic acid molecules which modulate
CC the synthesis, expression and/or stability of a mRNA encoding 1 or more
CC receptors of vascular endothelial growth factor (VEGF). A patient
CC (preferably human) having a condition associated with the level of the
CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
CC receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can
CC be treated by administering the nucleic acid molecule or the expression
CC vector to the patient. AAX7275 to AAX7572 represent specific examples
CC of nucleic acid molecules from the present invention.
XX SQ Sequence 17 BP; 5 A; 6 C; 1 G; 5 U; 0 other;
SQ Query Match 5.6%; Score 17; DB 18; Length 17;
Best Local Similarity 70.6%; Pred. No. 95;
Matches 12; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
OY 163 ctcaagatcctcattca 179
DB 1 cucaagaucuccauca 17
1:|||||:|:|:|:|
RESULT 14
AAT14887/c
ID AAT14887 standard; DNA; 218 BP.
XX AC AAT14887;
XX DT 17-SEP-1996 (first entry)
XX DE Thermus thermophilus HB27 218 bp DNA fragment with promoter function.
KW Base pair; bp; promoter; thermostable; Thermus sp.; ds.
XX OS Thermus thermophilus HB27.
XX PN JP08070868-A.
XX PD 19-MAR-1996.

XX PF 02-SEP-1994; 94JP-0210153.
XX PR 02-SEP-1994; 94JP-0210153.
XX PA (MITU) MITSUBISHI CHEM CORP.
XX DR WPI; 1996-203149/21.
XX DNA fragment with promoter function derived from Thermus sp.
PT bacteria - useful in the prodn. of thermostable enzymes and
PT proteins
XX PS Claim 1; Page 8; 9pp; Japanese.
XX CC AAT14881-T14888 are DNA fragments derived from Thermus thermophilus
CC HB27. The fragments all have a promoter function and are useful for
CC the prodn. of DNA with a thermostable promoter. The DNA improves
CC Thermus bacteria stability and hence improves the prodn. process for
CC thermostable enzymes and proteins.
XX SQ Sequence 218 BP; 41 A; 59 C; 80 G; 38 T; 0 other;
SQ Query Match 5.6%; Score 17; DB 17; Length 218;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 33 cggcgccttcgggaagg 49
|||||:|:|:|:|
DB 182 CGGCGCCTTCGGGAAGG 166
RESULT 15
ABAI1580
ID ABAI1580 standard; cDNA; 272 BP.
XX AC ABAI1580;
XX DT 23-JAN-2002 (first entry)
XX DE Human nervous system related polynucleotide SEQ ID NO 587.
XX KW Human; nootropic; neuroprotective; cytostatic; dermatological; virucide;
KW immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary;
KW antiparkinsonian; antisickling; antianaemic; antiarthritic; cancer;
KW antirheumatic; hepatotropic; cerebroprotective; antiinflammatory;
KW antiallergic; antidiabetic; antiulcer; anticonvulsant; antifungal;
KW antiparasitic; cardiant; immune disorder; cardiovascular disorder;
KW neurological disease; infection; nephrotropic; gene therapy; vaccine; ss.
XX OS Homo sapiens.
XX PN WO200159063-A2.
XX PD 16-AUG-2001.
XX PF 17-JAN-2001; 2001WO-US01334.
XX PR 31-JAN-2000; 2000US-0179065.
XX PR 04-FEB-2000; 2000US-0180628.
XX PR 24-FEB-2000; 2000US-0184664.
XX PR 02-MAR-2000; 2000US-0186350.
XX PR 16-MAR-2000; 2000US-0189874.
XX PR 17-MAR-2000; 2000US-0190076.
XX PR 18-APR-2000; 2000US-0198123.
XX PR 19-MAY-2000; 2000US-0205515.
XX PR 07-JUN-2000; 2000US-0209467.
XX PR 28-JUN-2000; 2000US-0214886.
XX PR 30-JUN-2000; 2000US-0215135.
XX PR 07-JUL-2000; 2000US-0216647.
XX PR 07-JUL-2000; 2000US-0216880.
XX PR 11-JUL-2000; 2000US-0217487.

CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative
 CC colitis; (c) cardiovascular disorders such as myocardial ischaemias;
 CC (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and
 CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
 CC and parasitic infections.
 CC Note: The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.

SV Sequence 272 BP; 58 A; 79 C; 87 G; 47 T; 1 other;

Query Match 5.6%; Score 17; DB 22; Length 272;
 Best Local Similarity 100.0%; Pred. No. 89;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 276 cctctcccaactctctgc 292
 Db 190 cctctcccaactctctgc 206
 |||||

RESULT 16

AAH03972
 ID AAH03972 standard; cDNA; 768 BP.

AC AAH03972;

DT 26-JUN-2001 (first entry)

XX Human cDNA clone (5'-primer) SEQ ID NO:807.

DE Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.

KW Homo sapiens.

OS Homo sapiens.

PN EP1074617-A2.

XX 07-FEB-2001.

XX 28-JUL-2000; 2000EP-0116126.

PR 29-JUL-1999; 99JP-0248036.

PR 27-AUG-1999; 99JP-0300253.

PR 11-JAN-2000; 2000JP-0118776.

PR 02-MAY-2000; 2000JP-0183767.

PR 09-JUN-2000; 2000JP-0241899.

XX (HELI-) HELIX RES INST.

PI Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;

PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;

XX WPI; 2001-318749/34.

XX Claim 1; SEQ ID 807; 2537pp + CD ROM; English.

CC The present invention describes primer sets for synthesising 5602
 CC full-length cDNAs defined in the specification. Where a primer set
 CC comprises: (a) an oligo-dr primer and an oligonucleotide complementary
 CC to the complementary strand of a polynucleotide which comprises one of
 CC the 5602 nucleotide sequences defined in the specification, where the
 CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
 CC of an oligonucleotide comprising a sequence complementary to the
 CC complementary strand of a polynucleotide which comprises a 5'-end
 CC sequence and an oligonucleotide comprising a sequence complementary to a
 CC polynucleotide which comprises a 3'-end sequence, where the
 CC oligonucleotide comprises at least 15 nucleotides and the combination of
 CC the 5'-end sequence/3'-end sequence is selected from those defined in

CC the specification. The primer sets can be used in antisense therapy and
 CC in gene therapy. The primers are useful for synthesising polynucleotides,
 CC particularly full-length cDNAs. The primers are also useful for the
 CC detection and/or diagnosis of the abnormality of the proteins encoded by
 CC the full-length cDNAs. The primers allow obtaining of the full-length
 CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
 CC AAH13633 to AAH18742 represent human cDNA sequences. AAB92446 to
 CC AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632
 CC represent oligonucleotides, all of which are used in the exemplification
 CC of the present invention.

XX Sequence 768 BP; 175 A; 222 C; 207 G; 161 T; 3 other;

Query Match 5.6%; Score 17; DB 22; Length 768;
 Best Local Similarity 100.0%; Pred. No. 87;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 72 catccacaaggcgacga 88
 Db 221 catccacaaggcgacga 237
 |||||

RESULT 17

AAH06553
 ID AAH06553 standard; cDNA; 813 BP.

XX AAH06553;

XX 26-JUN-2001 (first entry)

DE Human cDNA clone (5'-primer) SEQ ID NO:3388.

XX Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.

XX Homo sapiens.

XX EP1074617-A2.

XX 07-FEB-2001.

XX 28-JUL-2000; 2000EP-0116126.

PR 29-JUL-1999; 99JP-0248036.

PR 27-AUG-1999; 99JP-0300253.

PR 11-JAN-2000; 2000JP-0118776.

PR 02-MAY-2000; 2000JP-0183767.

PR 09-JUN-2000; 2000JP-0241899.

XX (HELI-) HELIX RES INST.

PI Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;

PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;

XX WPI; 2001-318749/34.

XX Claim 1; SEQ ID 3388; 2537pp + CD ROM; English.

CC The present invention describes primer sets for synthesising 5602
 CC full-length cDNAs defined in the specification. Where a primer set
 CC comprises: (a) an oligo-dr primer and an oligonucleotide complementary
 CC to the complementary strand of a polynucleotide which comprises one of
 CC the 5602 nucleotide sequences defined in the specification, where the
 CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
 CC of an oligonucleotide comprising a sequence complementary to the
 CC complementary strand of a polynucleotide which comprises a 5'-end
 CC sequence and an oligonucleotide comprising a sequence complementary to a
 CC polynucleotide which comprises a 3'-end sequence, where the

CC oligonucleotide comprises at least 15 nucleotides and the combination of
CC the 5'-end sequence/3'-end sequence is selected from those defined in
CC the specification. The primer sets can be used in antisense therapy and
CC in gene therapy. The primers are useful for synthesising polynucleotides,
CC particularly full-length cDNAs. The primers are also useful for the
CC detection and/or diagnosis of the abnormality of the proteins encoded by
CC the full-length cDNAs. The primers allow obtaining of the full-length
CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
CC AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to
CC AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632
CC represent oligonucleotides, all of which are used in the exemplification
CC of the present invention.
XX
XX
SQ Sequence 813 BP; 209 A; 188 C; 203 G; 209 T; 4 other;

Query Match 5.6%; Score 17; DB 22; Length 813;
Best Local Similarity 100.0%; Pred. No. 87;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 ctgcacctggggagagt 23
|||||
Db 27 ctgcacctggggagagt 43

RESULT 18
AAS22655
ID AAS22655 standard; cDNA: 1101 BP.
XX
AC AAS22655;
DT 24-OCT-2001 (first entry)
XX
DE Human cDNA encoding a novel human protein #221.
XX
KW Human: novel protein; ss: Antianaemic; osteopathic; antiinflammatory;
KW immunomodulatory; cytostatic; neuroprotective; vulnery; nootropic;
KW anticonvulsant; antiarthritic; cerebroprotective; antifungal; antiviral;
KW antibacterial; antiallergic; dermatological; haemostatic; antiasthmatic;
KW thrombolytic; immunogen; antibody; gene therapy; neurological disorder;
KW Parkinson's disease; inflammatory disorder; cancer; asthma; osteoporosis;
KW tissue regeneration; immune disorder.
XX
OS Homo sapiens.
XX
PN WO200155437-A2.
XX
PD 02-AUG-2001.
XX
PF 25-JAN-2001; 2001WO-US02623.
XX
PR 25-JAN-2000; 2000US-0491404.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Drmanac RT;
XX
DR WPI: 2001-451939/48.
DR P-PSDB; AAU14350.
XX
PT Isolated polypeptides useful for treating anti-inflammatory diseases,
PT nervous system disorders, and for regenerating bone and cartilage.
XX
PS Claim 1: Page 493-494; 894pp; English.
XX

CC The invention relates to polynucleotides encoding novel human
CC proteins or their active domains. The polypeptides, polynucleotides and
CC antibodies raised against the polypeptides are used in a method of
CC treatment of a mammal and prevention of disorders caused by the aberrant
CC protein expression or activity. The polypeptides can be used as
CC molecular weight markers, food supplements, and in antibody production.
CC The polypeptides are used to identify compounds which bind to the
CC polypeptides. Polynucleotides of the invention are used as probes and

CC primers, for sequencing, for chromosome or gene mapping, in the
CC production of recombinant proteins, and in generating anti-sense DNA or
CC RNA and in gene therapy. Polypeptides of the invention can be used to
CC target drugs to a tumour, in assays to determine biological activity, to
CC raise antibodies/elicite an immune response, to determine quantitative
CC protein levels, as tissue markers, and to isolate receptors or ligands.
CC Polypeptides of the invention may also be useful in treating platelet
CC disorders, stem cell disorders, regenerating bone, cartilage, tendon,
CC ligament and/or nerve tissue, wound healing, treating burns, promoting
CC the proliferation, differentiation and survival of stem cells, as a
CC contraceptive, treating osteoporosis and osteoarthritis, anaemia,
CC Alzheimer's, Parkinson's and Huntington's diseases, amyotrophic lateral
CC sclerosis, stroke, immune deficiencies resulting from bacterial, viral or
CC fungal infection or from autoimmunity, cancer, allergy, asthma,
CC graft-versus-host disease, eczema, haemophilia, thrombosis,
CC anti-inflammatory diseases, nervous system disorders, and infection.
XX
XX The present sequence encodes a protein of the invention.

SQ Sequence 1101 BP; 286 A; 266 C; 335 G; 214 T; 0 other;

Query Match 5.6%; Score 17; DB 22; Length 1101;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 197 acgtggtcaacctctc 213
|||||
Db 311 acgtggtcaacctctc 327

RESULT 19
AAS85415
ID AAS85415 standard; cDNA: 1116 BP.
XX
AC AAS85415;
DT 13-FEB-2002 (first entry)
XX
DE DNA encoding novel human diagnostic protein #21219.
KW Human: chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US08631.
XX
PR 31-MAR-2000; 2000US-0540217.
PR 23-AUG-2000; 2000US-0649167.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
XX
DR WPI: 2001-639362/73.
DR P-PSDB; ABG21228.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.
XX
PS Claim 1: SEQ ID No 21219; 103pp; English.

CC The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags

CC for identifying expressed genes. (I) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving
 CC (II). (II) is useful for generating antibodies against it, detecting or
 CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (II) and its binding partners are useful in medical
 CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. AAS64197-AAS94564 represent novel human
 CC diagnostic coding sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.

SQ Sequence 1116 BP; 272 A; 340 C; 299 G; 205 T; 0 other;

Query Match 5.6%; Score 17; DB 23; Length 1116;
 Best Local Similarity 100.0%; Pred. No. 86;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 274 aacctctccaacttct 290
 ||||| ||||| ||||| |||||
 Db 626 aacctctccaacttct 642

RESULT 20

AAS91079
 ID AAS91079 standard; cDNA; 1116 BP.

XX
 AC AAS91079;

DT 13-FEB-2002 (first entry)

DE DNA encoding novel human diagnostic protein #26883.

XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
 XX Homo sapiens.

XX WO200175067-A2.
 XX 11-OCT-2001.

XX 30-MAR-2001; 2001WO-US08631.

XX 31-MAR-2000; 2000US-0540217.

XX 23-AUG-2000; 2000US-0649167.

XX (HYSE-) HYSEQ INC.

XX Drmanac RT, Liu C, Tang YT;

XX WPI; 2001-639362/73.

XX P-PSDB; ABG26892.

XX New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity -

XX Claim 1; SEQ ID No 26883; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags.
 CC for identifying expressed genes. (I) is useful in gene therapy techniques

CC to restore normal activity of (II) or to treat disease states involving
 CC (II). (II) is useful for generating antibodies against it, detecting or
 CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (II) and its binding partners are useful in medical
 CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. AAS64197-AAS94564 represent novel human
 CC diagnostic coding sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.

SQ Sequence 1116 BP; 272 A; 340 C; 299 G; 205 T; 0 other;

Query Match 5.6%; Score 17; DB 23; Length 1116;
 Best Local Similarity 100.0%; Pred. No. 86;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 274 aacctctccaacttct 290
 ||||| ||||| ||||| |||||
 Db 626 aacctctccaacttct 642

RESULT 21

AAS85413

ID AAS85413 standard; cDNA; 1233 BP.

XX
 AC AAS85413;

DT 13-FEB-2002 (first entry)

DE DNA encoding novel human diagnostic protein #21217.

XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
 XX Homo sapiens.

XX WO200175067-A2.
 XX 11-OCT-2001.

XX 30-MAR-2001; 2001WO-US08631.

XX 31-MAR-2000; 2000US-0540217.

XX 23-AUG-2000; 2000US-0649167.

XX (HYSE-) HYSEQ INC.

XX Drmanac RT, Liu C, Tang YT;

XX WPI; 2001-639362/73.

XX P-PSDB; ABG21226.

XX New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity -

XX Claim 1; SEQ ID No 21217; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving

CC (II). (II) is useful for generating antibodies against it, detecting or
 CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (II) and its binding partners are useful in medical
 CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. AAS64197-AAS94564 represent novel human
 CC diagnostic coding sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 1233 BP; 316 A; 373 C; 317 G; 227 T; 0 other;

Query Match 5.6%; Score 17; DB 23; Length 1233;
 Best Local Similarity 100.0%; Pred. No. 86;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 274 aacctctccaacttct 290
 |||||
 Db 680 aacctctccaacttct 696

RESULT 22

AAS83501
 ID AAS83501 standard; cDNA; 1302 BP.

AC AAS83501;

DT 13-FEB-2002 (first entry)

DE DNA encoding novel human diagnostic protein #19305.

KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder; ss.

OS Homo sapiens.

PN WO200175067-A2.

PD 11-OCT-2001.

PF 30-MAR-2001; 2001WO-US08631.

PR 31-MAR-2000; 2000US-0540217.

PR 23-AUG-2000; 2000US-0649167.

XX (HYSE-) HYSEQ INC.

XX Drmanac RT, Liu C, Tang YT;

XX WPI; 2001-639362/73.

DR P-PSDB; ABG19314.

XX New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity -

XX Claim 1; SEQ ID No 19305; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving
 CC (II). (II) is useful for generating antibodies against it, detecting or

CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (II) and its binding partners are useful in medical
 CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. AAS64197-AAS94564 represent novel human
 CC diagnostic coding sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX

SQ Sequence 1302 BP; 324 A; 402 C; 343 G; 233 T; 0 other;

Query Match 5.6%; Score 17; DB 23; Length 1302;
 Best Local Similarity 100.0%; Pred. No. 86;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 274 aacctctccaacttct 290
 |||||
 Db 680 aacctctccaacttct 696

RESULT 23

AAC91319

ID AAC91319 standard; cDNA; 1406 BP.

AC AAC91319;

DT 16-MAR-2001 (first entry)

DE Human polynucleotide for diagnostics and therapeutics, SEQ ID NO: 19.

KW Human; diagnostics and therapeutics; dithp; cytostatic;
 KW immunosuppressive; nootropic; neuroprotective; antiviral; antiallergic;
 KW hepatotropic; antidiabetic; antiinflammatory; antitumor; vulnary;
 KW anticonvulsant; antibacterial; antifungal; antiparasitic; cardiac;
 KW cancer; immune disorder; cardiovascular disorder; neurological disease;
 KW infection; endocrine disorder; metabolic disorder; ss.

OS Homo sapiens.

PN WO200073509-A2.

PD 07-DEC-2000.

PF 31-MAY-2000; 2000WO-US15404.

XX 01-JUN-1999; 99US-0137161.

PR 02-JUN-1999; 99US-0137109.

PR 02-JUN-1999; 99US-0137113.

PR 02-JUN-1999; 99US-0137114.

PR 02-JUN-1999; 99US-0137173.

PR 02-JUN-1999; 99US-0137258.

PR 02-JUN-1999; 99US-0137259.

PR 02-JUN-1999; 99US-0137260.

PR 03-JUN-1999; 99US-0137337.

PR 03-JUN-1999; 99US-0137396.

PR 03-JUN-1999; 99US-0137411.

PR 03-JUN-1999; 99US-0137417.

PR 04-AUG-1999; 99US-0137377.

PR 04-AUG-1999; 99US-0137436.

PR 05-AUG-1999; 99US-0137500.

PR 05-AUG-1999; 99US-0137520.

PR 05-AUG-1999; 99US-0137527.

PR 05-AUG-1999; 99US-0137530.

PR 05-AUG-1999; 99US-0137536.

PR 05-AUG-1999; 99US-0137541.

PR 05-AUG-1999; 99US-0137542.

PR 05-AUG-1999; 99US-0137547.

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PR 05-AUG-1999; 99US-0137549.
PR 05-AUG-1999; 99US-0137824.
XX
XX
PA (INCY-) INCYTE GENOMICS INC.
XX
XX Hodgson DM, Lincoln SE, Russo FD, Spiro PA, Banville SC;
PI Bratcher SR, Dufour GE, Cohen HJ, Rosen BH, Hillman JL;
PI Jones AL, Yu JY, Greenawalt LB, Panzer SR, Roseberry AM;
PI Wright RJ, Daniels SE;
XX
XX WPI; 2001-016511/02.
XX
XX Fifty two human polynucleotides, referred to as DITHP polynucleotides,
PT useful in the diagnosis and treatment of cancer, immune disorders and
PT neurological diseases -
XX
XX Claim 1: Page 245-246; 263pp; English.
XX
XX The present sequence is one of fifty-two human polynucleotides for
CC diagnostics and therapeutics. The polynucleotides are referred to as
CC DITHP polynucleotides. The DITHP polynucleotides and polypeptides are
CC useful for diagnosing and treating diseases such as cancer, particularly
CC breast and ovarian cancer, and other cancers of the adrenal gland, bone,
CC bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital;
CC immune disorders such as Addison's disease, allergies, autoimmune
CC haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative
CC colitis; cardiovascular disorders such as myocardial ischaemias;
CC neurological diseases such as cerebral palsy and epilepsy; infectious
CC diseases such as viral, bacterial, fungal and parasitic infections; and
CC endocrine disorders (e.g. disorders of hypothalamus), disorders
CC associated with hypothyroidism and hyperthyroidism, pancreatic
CC disorders (e.g. diabetes mellitus) and metabolic disorders.
CC The DITHP polynucleotides are useful for screening for molecules that
CC bind to or are bound by the encoded polypeptides. The anti-DITHP
CC antibodies are useful in diagnostic assays.
XX
XX Sequence 1406 BP: 278 A; 481 C; 395 G; 251 T; 1 other;
SQ

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Query Match 5.6%; Score 17; DB 22; Length 1406;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 276 cctctccaaacttcctgc 292
    |||||
Db 227 cctctccaaacttcctgc 243

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RESULT 24
AAH75162
ID AAH75162 standard; cDNA; 1417 BP.
XX
XX
AC AAH75162;
XX
XX
DT 13-NOV-2001 (first entry)
XX
XX
DE Nucleotide sequence of a human enzyme.
XX

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KW Human; enzyme; cancer; neurological disorder; epilepsy; stroke;
KW Alzheimer's disease; Pick's disease; Huntington's disease; dementia;
KW multiple sclerosis; Parkinson's disease; amyotrophic lateral sclerosis;
KW meningitis; schizophrenia; neuroskeletal disorder; allergy;
KW addison's disease; autoimmune disease; anemia; asthma; Crohn's disease;
KW adult respiratory distress syndrome; atopic dermatitis; psoriasis;
KW diabetes mellitus; osteoporosis; pancreatitis; rheumatoid arthritis;
KW infection; genetic disorder; muscular dystrophy; Gaucher's disease;
KW Huntington's chorea; sickle cell anemia; thalassemia; atherosclerosis;
KW Von Willebrand's disease; Wilms' tumour; cell proliferative disorder;
KW leukemia; hepatitis; cirrhosis; arteriosclerosis; gene therapy; ss.
XX
XX Homo sapiens.
OS
XX

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FH Key Location/Qualifiers
FT CDS 250..1359
FT /*tag= a
FT /product= "enzyme"
XX
XX WO200164896-A2.
XX
XX 07-SEP-2001.
XX
XX 01-MAR-2001; 2001WO-US06806.
XX
XX 01-MAR-2000; 2000US-0186307.
XX 28-MAR-2000; 2000US-0192532.
XX 30-MAR-2000; 2000US-0193578.
XX
XX (INCY-) INCYTE GENOMICS INC.
XX
XX Tang YF, Lu DAM, Bandman O, Yue H, Azimzai Y, Lal P, Burford N;
PI Baughn MR;
XX
XX WPI; 2001-550184/61.
XX P-PSDB; AAG67134.
XX
XX Novel human enzyme molecule useful for treating and preventing, e.g.,
PT cancer, genetic disorders, neurological disorders, autoimmune and
PT inflammatory disorders -
XX
XX Claim 5; Page 144; 154pp; English.
XX
XX The present sequence encodes a human enzyme. The enzyme polynucleotide
CC and polypeptide are useful for diagnosis, treatment and prevention of
CC cancers, neurological disorders (e.g. epilepsy, stroke, Alzheimer's
CC disease, Pick's disease, Huntington's disease, dementia, multiple
CC sclerosis, Parkinson's disease, amyotrophic lateral sclerosis, bacterial
CC and viral meningitis, schizophrenic disorders and neuroskeletal
CC disorders), autoimmune/inflammatory disorders (e.g. allergies,
CC addison's disease, autoimmune diseases, adult respiratory distress
CC syndrome, anemia, asthma, Crohn's disease, atopic dermatitis, diabetes
CC mellitus, osteoporosis, pancreatitis, psoriasis, rheumatoid arthritis,
CC and viral, bacterial, fungal, parasitic, protozoal and helminthic
CC infections), genetic disorder (e.g. Duchenne and Becker muscular
CC dystrophy, Gaucher's disease, Huntington's chorea, sickle cell anemia,
CC thalassemia, Von Willebrand's disease and Wilms' tumour), and cell
CC proliferative disorder (e.g. atherosclerosis, leukemia, hepatitis,
CC cirrhosis, and arteriosclerosis). The polynucleotide is also useful in
CC somatic or germline gene therapy.
XX
XX Sequence 1417 BP: 292 A; 479 C; 396 G; 250 T; 0 other;
SQ

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Query Match 5.6%; Score 17; DB 22; Length 1417;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 276 cctctccaaacttcctgc 292
    |||||
Db 227 cctctccaaacttcctgc 243

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RESULT 25
AAH15398
ID AAH15398 standard; cDNA; 1767 BP.
XX
XX AAH15398;
XX
XX 26-JUN-2001 (first entry)
XX
XX Human cDNA sequence SEQ ID NO:13599.
XX
XX Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
XX
XX Homo sapiens.
OS
XX

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PN  EPI074617-A2.
XX
PD
XX
XX  07-FEB-2001.
XX
XX  28-JUL-2000; 2000EP-0116126.
XX
XX  29-JUL-1999; 99JP-0248036.
PR
XX  27-AUG-1999; 99JP-0300253.
PR
XX  11-JAN-2000; 2000JP-0118776.
PR
XX  02-MAY-2000; 2000JP-0183767.
PR
XX  09-JUN-2000; 2000JP-0241899.
XX
XX  (HELI-) HELIX RES INST.
XX
XX  Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
PI  Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
XX  WPI: 2001-318749/34.
XX
XX  Primer sets for synthesizing polynucleotides, particularly the 5602
PT  full-length cDNAs defined in the specification, and for the detection
PT  and/or diagnosis of the abnormality of the proteins encoded by the
PT  full-length cDNAs.
XX
XX  Claim 8; SEQ ID 13599; 2537pp + CD ROM; English.
XX
XX  The present invention describes primer sets for synthesizing 5602
CC  full-length cDNAs defined in the specification. Where a primer set
CC  comprises: (a) an oligo-dr primer and an oligonucleotide complementary
CC  to the complementary strand of a polynucleotide which comprises one of
CC  the 5602 nucleotide sequences defined in the specification, where the
CC  oligonucleotide comprises at least 15 nucleotides; or (b) a combination
CC  of an oligonucleotide comprising a sequence complementary to the
CC  complementary strand of a polynucleotide which comprises a 5'-end
CC  sequence and an oligonucleotide comprising a sequence complementary to a
CC  polynucleotide which comprises a 3'-end sequence, where the
CC  oligonucleotide comprises at least 15 nucleotides, and the combination
CC  of the 5'-end sequence and the 3'-end sequence is selected from those defined in
CC  the specification. The primer sets can be used in antisense therapy and
CC  in gene therapy. The primers are useful for synthesizing polynucleotides,
CC  particularly full-length cDNAs. The primers are also useful for the
CC  detection and/or diagnosis of the abnormality of the proteins encoded by
CC  the full-length cDNAs. The primers allow obtaining of the full-length
CC  cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
CC  AAH13633 to AAH18742 represent human cDNA sequences; AAH92446 to
CC  AAH95893 represent human amino acid sequences; and AAH13629 to AAH13632
CC  represent oligonucleotides, all of which are used in the exemplification
CC  of the present invention.
XX
XX  Sequence 1767 BP; 461 A; 446 C; 431 G; 429 T; 0 other;
SQ

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XX  OS
XX  Homo sapiens.
XX  WO200155320-A2.
XX
XX  PD
XX  02-AUG-2001.
XX
XX  17-JAN-2001; 2001WO-US01339.
XX
XX  31-JAN-2000; 2000US-0179065.
PR
XX  04-FEB-2000; 2000US-0180628.
PR
XX  24-FEB-2000; 2000US-0184664.
PR
XX  02-MAR-2000; 2000US-0186350.
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XX  16-MAR-2000; 2000US-0189874.
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XX  17-MAR-2000; 2000US-0190076.
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XX  18-APR-2000; 2000US-0198123.
PR
XX  19-MAY-2000; 2000US-0205515.
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XX  07-JUN-2000; 2000US-0209467.
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XX  28-JUN-2000; 2000US-0214886.
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XX  30-JUN-2000; 2000US-0215135.
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XX  07-JUL-2000; 2000US-0216647.
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XX  07-JUL-2000; 2000US-0216880.
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XX  11-JUL-2000; 2000US-0217487.
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XX  11-JUL-2000; 2000US-0217496.
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XX  14-JUL-2000; 2000US-0218290.
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XX  26-JUL-2000; 2000US-0220963.
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XX  26-JUL-2000; 2000US-0220964.
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XX  14-AUG-2000; 2000US-0224518.
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XX  14-AUG-2000; 2000US-0224519.
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XX  14-AUG-2000; 2000US-0225213.
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XX  14-AUG-2000; 2000US-0225214.
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XX  14-AUG-2000; 2000US-0225266.
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XX  14-AUG-2000; 2000US-0225267.
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XX  14-AUG-2000; 2000US-0225288.
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XX  14-AUG-2000; 2000US-0225270.
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XX  14-AUG-2000; 2000US-0225447.
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XX  14-AUG-2000; 2000US-0225757.
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XX  14-AUG-2000; 2000US-0225758.
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XX  14-AUG-2000; 2000US-0225759.
PR
XX  18-AUG-2000; 2000US-0226279.
PR
XX  22-AUG-2000; 2000US-0226681.
PR
XX  22-AUG-2000; 2000US-0226688.
PR
XX  22-AUG-2000; 2000US-0227182.
PR
XX  23-AUG-2000; 2000US-0227009.
PR
XX  30-AUG-2000; 2000US-0228924.
PR
XX  01-SEP-2000; 2000US-0229287.
PR
XX  01-SEP-2000; 2000US-0229343.
PR
XX  01-SEP-2000; 2000US-0229344.
PR
XX  01-SEP-2000; 2000US-0229345.
PR
XX  05-SEP-2000; 2000US-0229509.
PR
XX  05-SEP-2000; 2000US-0229513.
PR
XX  06-SEP-2000; 2000US-0230437.
PR
XX  06-SEP-2000; 2000US-0230438.
PR
XX  08-SEP-2000; 2000US-0231242.
PR
XX  08-SEP-2000; 2000US-0231243.
PR
XX  08-SEP-2000; 2000US-0231244.
PR
XX  08-SEP-2000; 2000US-0231413.
PR
XX  08-SEP-2000; 2000US-0231414.
PR
XX  08-SEP-2000; 2000US-0232081.
PR
XX  12-SEP-2000; 2000US-0231968.
PR
XX  14-SEP-2000; 2000US-0232397.
PR
XX  14-SEP-2000; 2000US-0232398.
PR
XX  14-SEP-2000; 2000US-0232399.
PR
XX  14-SEP-2000; 2000US-0232400.
PR
XX  14-SEP-2000; 2000US-0232401.
PR
XX  14-SEP-2000; 2000US-0233063.
PR
XX  14-SEP-2000; 2000US-0233064.
PR
XX  21-SEP-2000; 2000US-0233065.
PR
XX  21-SEP-2000; 2000US-0234223.
PR
XX  21-SEP-2000; 2000US-0234274.
PR
XX  25-SEP-2000; 2000US-0234997.
PR
XX  25-SEP-2000; 2000US-0234998.
PR

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Query Match      5.6%; Score 17; DB 22; Length 1767;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY  72 catccacaaggcgagca 88
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Db   221 catccacaaggcgagca 237

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RESULT 26
AAL03231/C
ID  AAL03231 standard; DNA; 1824 BP.
XX
XX  AAL03231;
XX
XX  21-NOV-2001 (first entry)
XX
XX  Human reproductive system related antigen DNA SEQ ID NO: 5919.
XX
XX  Human; reproductive system related antigen; reproductive system disorder;
KW  cancer; gene therapy; ds.
KW

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PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
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PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
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PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
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PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
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PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
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PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.

(HUMA-) HUMAN GENOME SCI INC.
XX Rosen CA, Barash SC, Ruben SM;
XX WPI; 2001-465570/50.
XX Isolated nucleic acid molecule encoding a reproductive system antigen
XX is used in preventing, treating or ameliorating a medical condition -
XX Disclosure; SEQ ID NO 5919; 1297pp + Sequence Listing; English.
XX The present invention provides the protein and coding sequences of a
XX number of human reproductive system related antigens. These can be used
XX in the prevention and treatment of reproductive system disorders,
XX including cancer. The present sequence is a genomic sequence encoding a
XX protein of the invention.
SQ Sequence 1824 BP; 380 A; 499 C; 488 G; 457 T; 0 other;
Query Match 5.6%; Score 17; DB 22; Length 1824;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 33 cggcgcccttcgggaagg 49
|||||
Db 1442 CGCGCCTTCGGGAAGG 1426
RESULT 27
ABAI5613
ID ABAI5613 standard; DNA; 1901 BP.
XX ABAI5613;
AC ABAI5613;
XX 23-JAN-2002 (first entry)
XX Human nervous system related polynucleotide SEQ ID NO 7944.
XX Human; nootropic; neuroprotective; cytostatic; dermatological; virucide;
XX immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary;
XX antiparkinsonian; antispasmodic; antianemic; antithrombotic; cancer;
XX antirheumatic; hepatotropic; cerebroprotective; antiinflammatory;
XX antiallergic; antidiabetic; antiulcer; anticonvulsant; antifungal;
XX antiparasitic; cardiant; immune disorder; cardiovascular disorder;
XX neurological disease; infection; nephrotropic; gene therapy; vaccine; ds.
OS Homo sapiens.
XX WO200159063-A2.
XX 16-AUG-2001.
PD 17-JAN-2001; 2001WO-US01334.
XX 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-MAR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 07-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.
PR 11-JUL-2000; 2000US-0217496.
PR 14-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
PR 26-JUL-2000; 2000US-0220964.

PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226686.
PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0242221.
PR 08-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250391.
PR 01-DEC-2000; 2000US-0251160.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 06-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
PA
XX
PI Rosen CA, Barash SC, Ruben SM;
XX
XX WPT; 2001-541565/60.
XX
XX Nucleic acids encoding 3224 human nervous system antigen polypeptides,
PT useful for preventing, diagnosing and/or treating nervous system
PT cancers and metastases -
XX
XX Disclosure; SEQ ID NO 7944; 1701pp + Sequence Listing; English.
PS
XX The invention relates to novel genes (AB11004-ABA21534) and proteins
CC (AB114678-AB18001) useful for preventing, treating or ameliorating
CC medical conditions e.g. by protein or gene therapy. The genes are
CC isolated from a range of human tissues disclosed in the specification.
CC The nucleic acids, proteins, antibodies and (ant)agonists are useful
CC in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast
CC and ovarian cancer and other cancers of the adrenal gland, bone, bone
CC marrow, breast, gastrointestinal tract, liver, lung, or urogenital;
CC (b) immune disorders e.g. Addison's disease, allergies, autoimmune
CC haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative
CC colitis; (c) cardiovascular disorders such as myocardial ischaemia;
CC (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and
CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
CC and parasitic infections.

CC Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.

XX
SQ Sequence 1901 BP; 373 A; 619 C; 573 G; 336 T; 0 other;

Query Match 5.68; Score 17; DB 22; Length 1901;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 276 cctctcccaacttcctgc 292
|||||
Db 620 cctctcccaacttcctgc 636

RESULT 28
AAS83500
ID AAS83500 standard; cDNA: 2484 BP.

XX
AC AAS83500;

XX
DT 13-FEB-2002 (first entry)

XX
DE DNA encoding novel human diagnostic protein #19304.

XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder; ss.

XX
OS Homo sapiens.

XX
PN WO200175067-A2.

XX
PD 11-OCT-2001.

XX
PF 30-MAR-2001; 2001WO-US08631.

XX
PR 31-MAR-2000; 2000US-0540217.

XX
PR 23-AUG-2000; 2000US-0649167.

XX
PA (HYSE-) HYSEQ INC.

XX
PI Drmanac RT, Liu C, Tang YT;

XX
WPI; 2001-639362/73.

XX
DR P-PSDB; ABG19313.

XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity -

XX
PS Claim 1; SEQ ID No 19304; 103pp; English.

XX
CC The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AAS64197-AAS94564 represent novel human
CC diagnostic coding sequences of the invention.

CC Note: The sequence data for this patent did not appear in the printed

CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.

XX
SQ Sequence 2484 BP; 611 A; 686 C; 672 G; 515 T; 0 other;

Query Match 5.68; Score 17; DB 23; Length 2484;
Best Local Similarity 100.0%; Pred. No. 84;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 274 aacctctcccaacttcct 290
|||||
Db 1994 aacctctcccaacttcct 2010

RESULT 29
AAH14499
ID AAH14499 standard; cDNA: 2624 BP.

XX
AC AAH14499;

XX
DT 26-JUN-2001 (first entry)

XX
DE Human cDNA sequence SEQ ID NO:12018.

XX
KW Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.

XX
OS Homo sapiens.

XX
PN EP1074617-A2.

XX
PD 07-FEB-2001.

XX
PF 28-JUL-2000; 2000EP-0116126.

XX
PR 29-JUL-1999; 99JP-0248036.

XX
PR 27-AUG-1999; 99JP-0300253.

XX
PR 11-JAN-2000; 2000JP-0118776.

XX
PR 02-MAY-2000; 2000JP-0183767.

XX
PR 09-JUN-2000; 2000JP-0241899.

XX
(HELI-) HELIX RES INST.

XX
PI Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;

XX
PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;

XX
WPI; 2001-318749/34.

XX
PT Primer sets for synthesizing polynucleotides, particularly the 5602
PT full-length cDNAs defined in the specification, and for the detection
PT and/or diagnosis of the abnormality of the proteins encoded by the
PT full-length cDNAs -

XX
PS Claim 8; SEQ ID 12018; 2537pp + CD ROM; English.

XX
CC The present invention describes primer sets for synthesising 5602
CC full-length cDNAs defined in the specification. Where a primer set
CC comprises: (a) an oligo-dT primer and an oligonucleotide complementary
CC to the complementary strand of a polynucleotide which comprises one of
CC the 5602 nucleotide sequences defined in the specification, where the
CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
CC of an oligonucleotide comprising a sequence complementary to the
CC complementary strand of a polynucleotide which comprises a 5'-end
CC sequence and an oligonucleotide comprising a sequence complementary to a
CC polynucleotide which comprises a 3'-end sequence, where the
CC oligonucleotide comprises at least 15 nucleotides and the combination of
CC the 5'-end sequence/3'-end sequence is selected from those defined in
CC the specification. The primer sets can be used in antisense therapy and
CC in gene therapy. The primers are useful for synthesising polynucleotides,
CC particularly full-length cDNAs. The primers are also useful for the
CC detection and/or diagnosis of the abnormality of the proteins encoded by
CC the full-length cDNAs. The primers allow obtaining of the full-length
CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and

CC AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to
CC AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632
CC represent oligonucleotides, all of which are used in the exemplification
CC of the present invention.

XX Sequence 2624 BP; 662 A; 684 C; 654 G; 624 T; 0 other;

Query Match 5.6%; Score 17; DB 22; Length 2624;
Best Local Similarity 100.0%; Pred. No. 84;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 ctgcacctggggagagt 23
|||||
Db 27 ctgcacctggggagagt 43

RESULT 30
AAS22891/c
ID AAS22891 standard; cDNA; 2663 BP.

AC AAS22891;

DT 24-OCT-2001 (first entry)

DE Human cDNA encoding a novel human protein #457.

XX Human: novel protein; ss: Antianaemic; osteopathic; antiinflammatory;
KW immunomodulatory; cytostatic; neuroprotective; vulnery; nootropic;
KW anticonvulsant; antiarthritic; cerebroprotective; antifungal; antiviral;
KW antibacterial; antiallergic; dermatoprotective; haemostatic; antiasthmatic;
KW thrombolytic; immunogen; antibody; gene therapy; neurological disorder;
KW Parkinson's disease; inflammatory disorder; cancer; asthma; osteoporosis;
KW tissue regeneration; immune disorder.

OS Homo sapiens.

XX WO200155437-A2.

PN 02-AUG-2001.

XX 25-JAN-2001; 2001WO-US02623.

XX 25-JAN-2000; 2000US-0491404.

PA (HYSE-) HYSEQ INC.

XX Tang YT, Liu C, Drmanac RT;

PI WPI; 2001-451939/48.

DR P-PSDB; AAU14586.

XX Isolated polypeptides useful for treating anti-inflammatory diseases,
PT nervous system disorders, and for regenerating bone and cartilage -

XX Claim 1; Page 776-777; 894pp; English.

PS The invention relates to polynucleotides encoding novel human
XX proteins or their active domains. The polypeptides, polynucleotides and
CC antibodies raised against the polypeptides are used in a method of
CC treatment of a mammal and prevention of disorders caused by the aberrant
CC protein expression or activity. The polypeptides can be used as
CC molecular weight markers, food supplements, and in antibody production.
CC The polypeptides are used to identify compounds which bind to the
CC polypeptides. Polynucleotides of the invention are used as probes and
CC primers, for sequencing, for chromosome or gene mapping, in the
CC production of recombinant proteins, and in generating anti-sense DNA or
CC RNA and in gene therapy. Polypeptides of the invention can be used to
CC target drugs to a tumour, in assays to determine biological activity, to
CC raise antibodies/elicite an immune response, to determine quantitative
CC protein levels, as tissue markers, and to isolate receptors or ligands.
CC Polypeptides of the invention may also be useful in treating platelet
CC disorders, stem cell disorders, regenerating bone, cartilage, tendon,

CC ligament and/or nerve tissue, wound healing, treating burns, promoting
CC the proliferation, differentiation and survival of stem cells, as a
CC contraceptive, treating osteoporosis and osteoarthritis, anaemia,
CC Alzheimer's, Parkinson's and Huntington's diseases, amyotrophic lateral
CC sclerosis, stroke, immune deficiencies resulting from bacterial, viral or
CC fungal infection or from autoimmunity, cancer, allergy, asthma,
CC graft-versus-host disease, eczema, haemophilia, thrombosis,
CC anti-inflammatory diseases, nervous system disorders, and infection.
CC The present sequence encodes a protein of the invention.

XX Sequence 2663 BP; 510 A; 805 C; 667 G; 681 T; 0 other;

Query Match 5.6%; Score 17; DB 22; Length 2663;
Best Local Similarity 100.0%; Pred. No. 84;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 197 acgtggtcaacctctc 213
|||||
Db 1013 ACGTGGTCAACTCCTC 997

RESULT 31
AAV55895
ID AAV55895 standard; DNA; 3120 BP.

XX AAV55895;

AC 19-NOV-1998 (first entry)

DT Receptor protein tyrosine kinase (PTK) subtype tyro-10 encoding DNA.

DE PTK; receptor; protein tyrosine kinase; brain tissue; ss.

XX Rattus sp.

OS Key Location/Qualifiers

XX CDS 485..3049

FT /*tag= a

XX US5811516-A.

XX 22-SEP-1998.

XX 02-JUN-1995; 95US-0456647.

XX 15-MAY-1992; 92US-0884486.

XX 02-MAY-1994; 94US-0237401.

XX 02-JUN-1995; 95US-0456647.

XX (SALK) SALK INST BIOLOGICAL STUDIES.

XX Lai CHC, Lemke GE;

XX WPI; 1998-530939/45.

XX P-PSDB; AAW79152.

XX Receptor protein tyrosine kinase polypeptide, tyro-3 - preferably

XX expressed in brain tissue

XX Example 2; Columns 53-60; 46pp; English.

XX This DNA encodes a novel receptor protein tyrosine kinase (PTK)
CC polypeptide subtype tyro-10. The invention provides polynucleotide
CC sequences encoding novel PTK polypeptide subtypes tyro-1 to tyro-13.
CC The PTK subtypes are found expressed predominantly in the brain tissue.

XX Sequence 3120 BP; 760 A; 786 C; 830 G; 744 T; 0 other;

Query Match 5.6%; Score 17; DB 19; Length 3120;
Best Local Similarity 100.0%; Pred. No. 84;

Matches 17: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 100 gtggccgtgaaatgct 116
|||||
Db 2297 gtggccgtgaaatgct 2313

RESULT 32
AAV65317
ID AAV65317 standard; DNA: 3120 BP.

XX AC AAV65317;
XX DT 22-JAN-1999 (first entry)

XX DE Receptor protein tyrosine kinase (PTK) subtype tyro-10 encoding DNA.

XX KW PTK; receptor; protein tyrosine kinase; recombinant; grafting;
KW diagnosis; tumour; skin transplant; connective tissue; tyro-10; ss.
XX Rattus sp.

XX FH Key Location/Qualifiers
FT CDS 485..3049
ET /*tag= a
ET /product= "PTK subtype tyro-10"

XX US5837448-A.

XX PN 17-NOV-1998.

XX PD 02-MAY-1994; 94US-0237401.

XX PF 15-MAY-1992; 92US-0884486.

XX PR 02-MAY-1994; 94US-0237401.

XX (SALK) SALK INST BIOLOGICAL STUDIES.

XX PA Lai CHC, Lemke GE;

XX PI WPI: 1999-023436/02.

XX DR P-PSDB; AAW81409.

XX Nucleic acids encoding protein tyrosine kinase subtypes - for
PT identification of new sub:types and treatment of diseases associated
PT with the kinase

XX Claim 1: Columns 53-58; 47pp; English.

XX This DNA encodes a receptor protein tyrosine kinase (PTK) subtype
CC tyro-10. The invention provides sequences AAV65308 to AAV65313, AAV65315,
CC and AAV65317 to AAV65319 that encode proteins having a tyrosine kinase
CC domain and a tissue expression pattern of a receptor PTK subtype selected
CC from tyro-1, tyro-2, tyro-3, tyro-4, tyro-5, tyro-6, tyro-8, tyro-10,
CC tyro-11, and tyro-12, respectively. The polynucleotides are useful for
CC the detection of tyrosine kinase domain sequences and detection of
CC tissue expression patterns of PTK subtypes. The cDNAs can also be
CC injected into oocytes, the protein expressed, and expression products
CC screened for using antibodies against tyrosine kinase epitopes. These
CC subtypes sequences can be used for the design of oligonucleotides, for
CC use in amplification reactions to isolate other subtype sequences. These
CC detection protocols are used in the diagnosis of diseases associated
CC with (receptor) PTKs. Recombinant vectors expressing the subtypes can be
CC used to treat related diseases e.g. tumours, by introduction of the
CC vectors into skin transplants, then grafting these into the connective
CC tissue of the dermis, thus specifically targeting tumours as the
CC proteins are released from the matrix.

XX Sequence 3120 BP; 760 A; 786 C; 830 G; 744 T; 0 other;

Query Match 5.6%; Score 17; DB 20; Length 3120;
Best Local Similarity 100.0%; Pred. No. 84;

Matches 17: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 100 gtggccgtgaaatgct 116
|||||
Db 2297 gtggccgtgaaatgct 2313

RESULT 33
AAS22909
ID AAS22909 standard; DNA: 4008 BP.

XX AC AAS22909;

XX DT 24-OCT-2001 (first entry)

XX DE DNA encoding novel bone marrow polypeptide #3.

XX KW Bone marrow; diagnostic; therapeutic; gene therapy; antigenic;
KW haematopoiesis; myeloid; lymph cell disorder; tissue regeneration;
KW wound healing; nutritional supplement; immune disorder;
KW severe combined immunodeficiency; SCID; ds.

XX OS Homo sapiens.

XX PN WO200157187-A2.

XX PD 09-AUG-2001.

XX PF 05-FEB-2001; 2001WO-US03782.

XX PR 03-FEB-2000; 2000US-0496914.

XX PR 20-JUN-2000; 2000US-0598075.

XX PR 19-JUL-2000; 2000US-0620325.

XX PR 30-NOV-2000; 2000US-0250683.

XX PA (HYSE-) HYSEQ INC.

XX PI Ford JE, Boyle BJ, Tang YT, Liu C, Asundi V, Zhou P, Xue AJ;

XX PI Ren F, Drmanac RT;

XX DR WPI: 2001-488875/53.

XX DR P-PSDB; AAU14604.

XX Nucleic acids encoding bone marrow polypeptides, useful in diagnostic
PT and gene therapy -
PT Claim 1; Page 151-152; 392pp; English.

XX AAS22907-AAS23099 represent nucleic acids encoding novel bone marrow
CC polypeptides. The nucleic acids and corresponding proteins may be used
CC in the prevention, diagnosis and treatment of diseases associated with
CC inappropriate bone marrow polypeptide expression. For example, to treat
CC disorders associated with decreased expression by rectifying mutations
CC or deletions in a patient's genome that affect the activity of the
CC polypeptides by expressing inactive proteins or to supplement the
CC patient's own production of the polypeptide. Additionally, the nucleic
CC acids may be used to produce the polypeptides, by inserting the nucleic
CC acids into a host cell and culturing the cell to express the protein.
CC The nucleic acid and its complementary sequences may also be used as DNA
CC probes in diagnostic assays to detect and quantitate the presence of
CC similar nucleic acid sequences in samples, and therefore which patients
CC may be in need of restorative therapy. The proteins may also be used as
CC antigens in the production of antibodies against bone marrow proteins
CC and in assays to identify modulators of their expression and activity.
CC The anti-bone marrow protein antibodies and antagonists may also be used
CC to down regulate expression and activity. The antibodies may also be used
CC as diagnostic agents for detecting the presence of the protein in samples
CC (e.g. by enzyme linked immunosorbant assay (ELISA)). The proteins
CC may be used to regulate haematopoiesis activity, and consequently in the
CC treatment of myeloid or lymph cell disorders; in tissue regeneration,
CC such as wound healing; as a nutritional supplement; and in treatment of
CC immune disorders such as severe combined immunodeficiency (SCID).

SQ Sequence 4008 BP; 860 A; 1183 C; 1140 G; 824 T; 1 other;

Query Match 5.6%; Score 17; DB 22; Length 4008;

Best Local Similarity 100.0%; Pred. No. 83;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 276 cctctccaactctctgc 292

|||||

Db 2796 cctctccaactctctgc 2812

RESULT 34

ID AAQ28272 standard; cDNA; 4071 BP.

XX

AC AAQ28272;

XX

DT 15-FEB-1993 (first entry)

XX

DE A novel type III RTK gene - the KDR gene.

XX

KW Receptor tyrosine kinase; vascular endothelial cell growth factors;

KW cancer; tumour; diagnosing; monitoring; ss.

XX

OS Homo sapiens.

XX

FT Key Location/Qualifiers

FT CDS 1..4068

FT /*tag= a

XX

PN W09214748-A.

XX

PD 03-SEP-1992.

XX

PF 20-FEB-1992; 92WO-US01300.

XX

PR 22-FEB-1991; 91US-0657236.

XX

PA (AMCY) AMERICAN CYANAMID CO.

XX

PI Carrion ME, Terman BI;

XX

DR WPI; 1992-316117/38.

XX

DR P-PSDB; AAR26999.

XX

PT DNA encoding type III receptor tyrosine kinase - useful for

PT diagnosing the onset of cancer

XX

PS Claim 3; Fig 7; 101pp; English.

XX

CC This sequence represents a novel type III receptor tyrosine kinase

CC gene. A labelled EcoRI-BamHI DNA segment derived from Clone BTII1081.8

CC was used as a probe to rescreen a human endothelial cDNA library

CC (HL10246) for 5' full length DNA segments of the gene from which the

CC insert portion of BTII1081.8 is derived. A synthetic probe designed

CC from nucleotides 3297-3325 of BTII1081.8 is then used to isolate

CC more 3' full length clones. One of the clones, designated BTII1200.2

CC is cloned into pBluescript KS and the synthetic oligonucleotide

CC TCGACGCGC ATC GAG cloned, which contains the initial sequence Met-

CC Glu, the first two amino acids encoded by the KDR gene, forming

CC BTIV140, which is then purified on a CsCl density gradient. This

CC was sequenced, together with BTII1081.8, and BTII129.5 to comprise

CC the entire ORF of 4,068 nucleotides of the KDR gene.

XX

SQ Sequence 4071 BP; 1172 A; 894 C; 1024 G; 981 T; 0 other;

Query Match

Best Local Similarity 100.0%; Score 17; DB 13; Length 4071;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 163 ctcaagatcctcattca 179

Db 2656 ctcaagatcctcattca 2672

|||||

RESULT 35

AAV99829

ID AAV99829 standard; cDNA; 4071 BP.

XX

AC AAV99829;

XX

DT 12-APR-1999 (first entry)

XX

DE Human receptor tyrosine kinase KDR cDNA.

XX

KW KDR; receptor tyrosine kinase; human; signal transduction;

KW mitogen; neoangiogenesis; angiogenesis; diabetic retinopathy;

KW breast cancer; brain cancer; inflammation; rheumatoid arthritis;

KW psoriasis; contact dermatitis; hypersensitivity; antagonist;

KW gene therapy; ds.

XX

OS Homo sapiens.

XX

PN W09858053-A1.

XX

PD 23-DEC-1998.

XX

PF 17-JUN-1998; 98WO-US12569.

XX

PR 18-JUN-1997; 97US-0050962.

XX

PA (MERI) MERCK & CO INC.

XX

PI Kendall RL, Mao X, Tebben A, Thomas KA;

XX

DR WPI; 1999-095333/08.

XX

DR P-PSDB; AAW80997.

XX

PT Human receptor tyrosine kinase protein, KDR - useful e.g. to screen

PT for antagonists useful to treat diseases involving neoangiogenesis

PT e.g. diabetic retinal vascularization, cancers

XX

PS Claim 1; Fig 1a; 69pp; English.

XX

CC This nucleotide sequence encodes a novel receptor tyrosine kinase,

CC termed KDR (see AAW80997), that is expressed on human endothelial

CC cells. KDR is activated by vascular endothelial growth factor and

CC mediates a mitogenic signal. It is implicated in clinical

CC neoangiogenesis. KDR cDNA was isolated from a human umbilical vein

CC endothelial cell lambda phage cDNA library using a 576-bp DNA probe

CC that had been generated by PCR (see also AAV99850-53). The predicted

CC protein product has amino acid differences from the previously

CC published KDR sequence at positions 498 (Ala to Glu), 772 (Thr to

CC Ala), 787 (Gly to Arg), 835 (Asn to Lys), 848 (Glu to Val) and 1347

CC (Thr to Ser), producing a protein predicted by computer modeling to

CC have higher activity and functionality. The invention also relates

CC to recombinant vectors and recombinant hosts which contain a DNA

CC fragment encoding human KDR, a DNA fragment encoding the

CC intracellular portion of KDR with or without a membrane anchor

CC sequence, purified forms of associated human KDR, and human mutant

CC forms of KDR. KDR, fusion proteins or fragments can be used in

CC assays to identify antagonists and agonists of human KDR (claimed).

CC Antagonists of KDR useful for treating diseases involving

CC neoangiogenesis e.g. diabetic retinal vascularization, cancers

CC (e.g. brain, breast, etc.) and forms of inflammation e.g. rheumatoid

CC arthritis, psoriasis, contact dermatitis and hypersensitivity

CC reactions. The polynucleotides are useful to screen for KDR

CC antagonists/agonists and for gene therapy (e.g. by introducing a

CC gene portion encoding a KDR protein containing functional ligand

CC binding and membrane anchoring moieties but not tyrosine kinase

CC activity). They are also useful to measure levels of human KDR.

XX

SQ Sequence 4071 BP; 1169 A; 894 C; 1027 G; 981 T; 0 other;

```
Query Match          5.6%; Score 17; DB 20; Length 4071;
Best Local Similarity 100.0%; Pred. No. 83;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 163 ctcaagatcctcatcca 179
Db 2656 ctcaagatcctcatcca 2672

RESULT 36
AAF83308
ID AAF83308 standard; DNA: 4225 BP.
XX
AC AAF83308;
XX
DT 09-JUL-2001 (first entry)
XX
DE Human VEGFR-2 encoding DNA.
XX
KW Receptor protein; vascular endothelial growth factor receptor-2;
KW VEGFR-2; neuropilin-1; NP-1; co-receptor; human; angiogenic; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 70..4140
FT /*tag= a
FT /product= "VEGFR-2"
FT misc_feature 71..2350
FT /*tag= b
FT /*note= "extracellular domain coding fragment (AAF83310)"
XX
PN WO200131346-A2.
XX
PD 03-MAY-2001.
XX
PF 26-OCT-2000; 2000WO-US29579.
XX
PR 28-OCT-1999; 98US-0162367.
XX
PA (PROC ) PROCTER & GAMBLE CO.
XX
PI Rosenbaum JS, Whitaker GB, Limberg BJ;
XX
P-PSDB; AAB62475.
XX
WPI: 2001-308686/32.
XX
P-PSDB; AAB62475.
XX
Determining compounds which bind to a complex comprising vascular
endothelial growth factor receptor-2 and Neuropilin-1 to provide
superior pro- and anti-angiogenic agents -
XX
Example 1; Page 32-39; 82pp; English.
XX
The invention relates to determining whether a compound is capable of
binding to a receptor protein complex comprising a vascular endothelial
growth factor receptor-2 (VEGFR-2) receptor protein and a neuropilin-1
(NP-1) receptor protein. One method comprises introducing a sample
comprising the compound to the receptor protein and allowing the
compound to bind to the complex. Signaling through VEGFR-2 is enhanced
in the presence of the NP-1 co-receptor. The methods of the invention
can be used for identifying novel pro- and anti-angiogenic compounds.
The present sequence represents the DNA encoding a human VEGFR-2.
XX
Sequence 4225 BP; 1204 A; 940 C; 1067 G; 1014 T; 0 other;

Query Match          5.6%; Score 17; DB 22; Length 4225;
Best Local Similarity 100.0%; Pred. No. 83;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 163 ctcaagatcctcatcca 179
Db 2656 ctcaagatcctcatcca 2672

RESULT 37
AAF34763
ID AAV34763 standard; DNA: 4236 BP.
XX
AC AAV34763;
XX
DT 27-AUG-1998 (first entry)
XX
DE Human KDR genomic DNA.
XX
KW Kinase insert domain containing receptor; KDR; screening; inhibitor;
KW vascular endothelial growth factor; VEGF; angiogenesis; treatment;
KW cancer; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..4071
FT /*tag= a
FT /product= KDR
FT /*note= "kinase insert domain containing receptor"
XX
PN US5766860-A.
XX
PD 16-JUN-1998.
XX
PF 25-FEB-1997; 97US-0810116.
XX
PR 23-NOV-1992; 92US-0930548.
XX
PR 25-FEB-1997; 97US-0810116.
XX
PA (AMCY ) AMERICAN CYANAMID CO.
XX
PI Carrión ME, Terman BI;
XX
WPI: 1998-361682/31.
XX
P-PSDB; AAW59275.
XX
Screening assay for vascular endothelial cell growth factor
antagonists - using recombinant cells expressing receptor protein
XX
Claim 1; Fig 7A-W; 51pp; English.
XX
This sequence encodes a novel human growth factor receptor, kinase
insert domain containing receptor or KDR. This receptor is capable of
binding to the vascular endothelial cell growth factor, VEGF and is
used in a screening assay which identifies compounds that inhibit VEGF
action on KDR. Such compounds which inhibit binding of VEGF to the KDR
may inhibit angiogenesis and thus be useful for treating cancer.
XX
Sequence 4236 BP; 1216 A; 938 C; 1062 G; 1020 T; 0 other;

Query Match          5.6%; Score 17; DB 19; Length 4236;
Best Local Similarity 100.0%; Pred. No. 83;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 163 ctcaagatcctcatcca 179
Db 2656 ctcaagatcctcatcca 2672

RESULT 38
AAK78291
ID AAK78291 standard; DNA: 5414 BP.
XX
AC AAK78291;
XX
DT 07-NOV-2001 (first entry)
XX
```

DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:33103.
XX Human: immune; haematopoietic; immune/haematopoietic antigen; cancer;
KW cytostatic; gene therapy; vaccine; metastasis; ds.
XX Homo sapiens.
OS
PN WO200157182-A2.
XX
PD 09-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US01354.
XX
PR 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 07-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.
PR 11-JUL-2000; 2000US-0217496.
PR 14-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
PR 26-JUL-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226868.
PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 01-DEC-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 06-DEC-2000; 2000US-0256719.
PR 08-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.

PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Barash SC, Ruben SM;
XX
DR WPI; 2001-483426/52.
XX
XX Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
PT useful for preventing, diagnosing and/or treating cancers and
PT metastasis -
XX
PS Disclosure: SEQ ID NO 33103; 3071pp + Sequence Listing; English.
XX
CC AAK54951 to AAK64702 encode the human immune/hematopoietic antigen (I)
CC amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
CC activity, and can be used in gene therapy and vaccine production. (I)
CC proteins, and polynucleotides may be used in the prevention, diagnosis and
CC treatment of diseases associated with inappropriate (I) expression. For
CC example, they may be used to treat disorders associated with decreased
CC expression by rectifying mutations or deletions in a patient's genome
CC that affect the activity of (I) by expressing inactive proteins or to
CC supplement the patients own production of (I). Additionally, (I)
CC polynucleotides may be used to produce the secreted (I), by inserting
CC the nucleic acids into a host cell and culturing the cell to express the
CC protein. (I) proteins and polynucleotides may be used to prevent
CC diagnosis and treat immune/hematopoietic-related diseases, especially
CC cancers and cancer metastases of hematopoietic-derived cells. AAK64703
CC to AAK87694 represent human immune/hematopoietic antigen genomic
CC sequences from the present invention. AAK54942 to AAK54950 and AAM82169
CC represent sequences used in the exemplification of the present invention.
XX
SQ Sequence 5414 BP; 1287 A; 1382 C; 1330 G; 1415 T; 0 other;

Query Match 5.6%; Score 17; DB 22; Length 5414;
Best Local Similarity 100.0%; Pred. No. 83;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 7 ctgcacctggggagagt 23
|||||
Db 2804 ctgcacctggggagagt 2820

RESULT 39
ABL10071/c
ID ABL10071 standard; cDNA: 5656 BP.
XX
AC ABL10071;
XX
DT 26-MAR-2002 (first entry)

XX Drosophila melanogaster expressed polynucleotide SEQ ID NO 24695.
DE
XX
XX Drosophila: developmental biology; cell signalling; insecticide;
KW pharmaceutical; gene; ss.
XX
OS Drosophila melanogaster.

XX WO200171042-A2.
XX
XX
XX 27-SEP-2001.
XX
XX

XX 23-MAR-2001; 2001WO-US09231.
XX
XX 23-MAR-2000; 2000US-191637p.
XX 11-JUL-2000; 2000US-0614150.
XX
XX (PEKE) PE CORP NY.

XX Venter JC, Adams M, Li PWD, Myers EW;

XX WPI; 2001-656860/75.
DR P-PSDB; ABB65968.
XX
XX New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signalling and cell-cell
PT interactions -
XX
XX Claim 1; SEQ ID NO 24695; 21pp + Sequence Listing; English.
XX
CC The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC sequences (ABL01840-ABL16175) and the encoded proteins
CC (ABB57737-ABB72072).
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 5656 BP; 1364 A; 1607 C; 1375 G; 1310 T; 0 other;

Query Match 5.6%; Score 17; DB 23; Length 5656;
Best Local Similarity 100.0%; Pred. No. 83;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 248 tgatcgtggagttctgc 264
|||||
Db 1058 TGATCGTGGAGTTCTGC 1042

RESULT 40
ABI99504
ID ABI99504 standard; cDNA: 6730 BP.
XX
AC ABI99504;

XX 07-MAR-2002 (first entry)

XX Mouse ischaemic condition related cDNA sequence SEQ ID NO:479.

XX Mouse; ischaemia; compressive ischaemia; occlusive ischaemia;
KW vasospastic ischaemia; ischaemic condition; ischaemic disease; ss.

XX Mus musculus.

XX WO200188188-A2.

XX 22-NOV-2001.

XX 18-MAY-2001; 2001WO-JP04192.

XX 18-MAY-2000; 2000JP-0145977.

XX (UYNT-) UNIV NIHON SCHOOL JURIDICAL PERSON.

XX Ishikawa K, Asai S, Takahashi Y, Nagata T, Ishii Y;

XX WPI; 2002-034733/04.
DR P-PSDB; ABB57196.

XX Examining the ischemic condition (e.g. occlusive ischemia) by measuring
PT expression levels of particular genes defined in the specification or
PT by determining the expression profile of a gene group comprising these
PT genes -

XX Claim 2; Page 1319-1331; 2690pp; English.

XX The present invention describes a method for examining ischaemic
CC conditions, comprising measuring the expression levels of particular

CC genes (I) in a test sample or determining the expression profile of a
 CC gene group in the sample comprising genes selected from (I). The method
 CC is useful for examining the ischaemic condition (e.g. compressive
 CC ischaemia, occlusive ischaemia or vasospastic ischaemia) by measuring
 CC expression levels of particular genes (ABI99202 to ABI99912, encoding
 CC the protein sequences in AB857020 to AB857374) or by determining the
 CC expression profile of a gene group comprising these genes. The
 CC expression levels or expression profiles produced by these genes are
 CC used as an indicator when screening for ischaemic condition-improving
 CC drugs or therapeutics for ischaemic diseases. ABI99913 and ABI99914
 CC represent PCR primers for a mouse ischaemic condition related sequence,
 CC which are used in the exemplification of the present invention.
 XX
 SQ Sequence 6730 BP; 1656 A; 1850 C; 1740 G; 1482 T; 2 other;

Query Match 5.6%; Score 17; DB 24; Length 6730;
 Best Local Similarity 100.0%; Pred. No. 82;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 72 catccacaaggcgagca 88
 |||||
 Db 5829 catccacaaggcgagca 5845

RESULT 41
 AAT88206/c
 ID AAT88206 standard; cDNA: 8460 BP.

AC AAT88206;

XX 16-JAN-1998 (first entry)

XX cDNA for protein (OA-519) cross-reactive with hpr gene product.

XX OA-519; cross-reaction; haptoglobin related; hpr; antibody;
 KW epitope; haptoglobin 1; haptoglobin 2; cancer; breast cancer;
 KW prognosis assay; ss.

XX Homo sapiens.

XX Key Location/Qualifiers
 FT CDS 124..7653
 FT /*tag= a
 FT /product= OA-519

XX US5665874-A.

XX 09-SEP-1997.

XX 17-JAN-1989; 89US-0297722.

XX 24-JAN-1994; 94US-0188426.

XX 17-JAN-1989; 89US-0297722.

XX 04-DEC-1990; 90US-0622407.

XX 26-JUL-1991; 91US-0735522.

XX 24-JUL-1992; 92US-0917716.

XX 26-JUL-1993; 93US-0096908.

XX 05-JUN-1995; 95US-0469005.

XX (UYJO) UNIV JOHNS HOPKINS.

XX KuhaJda FP, Pasternack CR;

XX WPI; 1997-469516/43.

XX P-PSDB; AAW32881.

XX DNA encoding protein cross-reactive with hpr gene product - useful

XX to raise antibodies reactive with epitope(s) found on hpr gene

XX product, useful in cancer, especially breast cancer, prognosis

XX assays

XX Claim 2; Columns 43-60; 68pp; English.

XX The present sequence encodes a protein (OA-519) cross-reactive with
 CC the haptoglobin related (hpr) gene product. OA-519 can be used to
 CC raise antibodies reactive with epitopes found on the hpr gene
 CC product, but not on haptoglobin 1 or 2, useful in cancer,
 CC especially breast cancer, prognosis assays.

XX Sequence 8460 BP; 1453 A; 2864 C; 2655 G; 1487 T; 1 other;

Query Match 5.6%; Score 17; DB 18; Length 8460;
 Best Local Similarity 100.0%; Pred. No. 82;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 83 gcagcagctgtgacacc 99
 |||||
 Db 1738 GCAGCAGCTGTGACACC 1722

RESULT 42
 AAZ95007/c
 ID AAZ95007 standard; cDNA: 8470 BP.

XX AAZ95007;

XX 15-AUG-2000 (first entry)

XX Cancer specific gene Prol10 useful as prostate cancer marker.

XX Prostate cancer; cancer specific gene; CSG; diagnosis; monitoring;
 KW staging; imaging; therapy; metastasis; marker; human; Prol10; ds.

XX Homo sapiens.

XX WO200023111-A1.

XX 27-APR-2000.

XX 19-OCT-1999; 99WO-US24331.

XX 19-OCT-1998; 98US-0104737.

XX (DIAD-) DIADEXUS LLC.

XX Salceda S, Recipon H, Cafferkey R;

XX WPI; 2000-339531/29.

XX Diagnosing, staging and monitoring the presence and metastases of
 PT prostate cancer especially useful for treating prostate cancer
 PT comprises measuring changes in cancer specific gene levels -

Claim 7; Page 59-62; 74pp; English.

XX The present sequence is that of a full-length contig for cancer
 CC specific gene (CSG) Prol10 (clone 3277219H1); a corresponding
 CC expressed sequence tag is given in AAZ95006. The CSG was identified
 CC in a database search using the data mining Cancer Leads Automatic
 CC Search Package (CLASP), which allows the identification of highly
 CC expressed organ and cancer specific genes. Although not tissue
 CC specific, Prol10 expression is upregulated in prostate cancer
 CC tissues. It can be used as a diagnostic marker for prostate cancer
 CC cancer, and may also be a diagnostic marker for other types of
 CC cancer. The invention provides ESTs and full-length contigs for
 CC prostate CSGs (see AAZ94998-295017). The CSGs, polypeptides encoded
 CC by them, and antibodies that specifically bind CSG are used in new,
 CC claimed methods for detecting, diagnosing, monitoring, staging,
 CC imaging and treating prostate cancer. The new methods provide
 CC earlier diagnosis for the presence and metastasis of prostate
 CC cancer, and can be used to determine if a cancer has metastasized,
 CC or to monitor the progress or stage of the disease when it has not
 CC metastasized.

SQ Sequence 8470 BP; 1461 A; 2863 C; 2658 G; 1485 T; 3 other;

Query Match 5.6%; Score 17; DB 21; Length 8470;
Best Local Similarity 100.0%; Pred. No. 82;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

JY 83 gcagcagctgtgacacc 99
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Db 1740 GCAGCAGCTGTGACACC 1724

RESULT 43
AAA37760/C
ID AAA37760 standard; DNA; 8519 BP.

XX AC AAA37760;
XX DT 04-DEC-2000 (first entry)
XX DE Human fatty acid synthase (FAS) coding sequence.
XX KW Human; FAS; fatty acid synthase; infection; cancer; gene therapy; ds.
XX OS Homo sapiens.

FH Key Location/Qualifiers
FT 156..7691
FT CDS /*tag= a
FT /product= fatty_acid_synthase

XX WO2000051430-A1.
XX PD 08-SEP-2000.
XX PF 25-FEB-2000; 2000WO-US04825.
XX PR 03-MAR-1999; 99US-0261907.

XX PA (SMIK) SMITHKLINE BEECHAM CORP.
XX PI Bergsma DJ, Chapman C, Depiera ME, Ellis CE, Lonsdale J;
XX PL Mooney JL;
XX WPI; 2000-594133/56.
XX DR P-PSDB; AAY90349.

PT Novel fatty acid synthase polypeptides and polynucleotides encoding
PT them, for diagnosing and treating cancer and bacterial infections -
XX Claim 2; Page 28-30; 38pp; English.

XX This sequence encodes the human fatty acid synthase (FAS) of the
CC invention. The DNA, protein, antibodies against it, and antagonists and
CC agonists of FAS are useful for diagnosing and treating abnormal
CC expression of FAS. The FAS sequences are useful for treating cancers and
CC bacterial infections. The DNA sequence is also useful in gene therapy.

SQ Sequence 8519 BP; 1477 A; 2871 C; 2680 G; 1491 T; 0 other;

Query Match 5.6%; Score 17; DB 21; Length 8519;
Best Local Similarity 100.0%; Pred. No. 82;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 83 gcagcagctgtgacacc 99
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Db 1770 GCAGCAGCTGTGACACC 1754

RESULT 44
AAK79882/C
ID AAK79882 standard; DNA; 8864 BP.

XX AC AAK79882;
XX DT 07-NOV-2001 (first entry)
XX DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:34694.
XX KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
XX KW cytosolic; gene therapy; vaccine; metastasis; ds.
XX OS Homo sapiens.
XX PN WO200157182-A2.
XX PD 09-AUG-2001.
XX PF 17-JAN-2001; 2001WO-US01354.
XX PR 31-JAN-2000; 2000US-0179065.
XX PR 04-FEB-2000; 2000US-0180628.
XX PR 24-FEB-2000; 2000US-0184664.
XX PR 02-MAR-2000; 2000US-0186350.
XX PR 16-MAR-2000; 2000US-0189874.
XX PR 17-MAR-2000; 2000US-0190076.
XX PR 18-APR-2000; 2000US-0198123.
XX PR 19-MAY-2000; 2000US-0205515.
XX PR 07-JUN-2000; 2000US-0209467.
XX PR 28-JUN-2000; 2000US-0214886.
XX PR 30-JUN-2000; 2000US-0215135.
XX PR 07-JUL-2000; 2000US-0216647.
XX PR 07-JUL-2000; 2000US-0216880.
XX PR 11-JUL-2000; 2000US-0217487.
XX PR 14-JUL-2000; 2000US-0217496.
XX PR 26-JUL-2000; 2000US-0220963.
XX PR 26-JUL-2000; 2000US-0220964.
XX PR 14-AUG-2000; 2000US-0224518.
XX PR 14-AUG-2000; 2000US-0224519.
XX PR 14-AUG-2000; 2000US-0225213.
XX PR 14-AUG-2000; 2000US-0225214.
XX PR 14-AUG-2000; 2000US-0225267.
XX PR 14-AUG-2000; 2000US-0225267.
XX PR 14-AUG-2000; 2000US-0225268.
XX PR 14-AUG-2000; 2000US-0225447.
XX PR 14-AUG-2000; 2000US-0225757.
XX PR 14-AUG-2000; 2000US-0225758.
XX PR 14-AUG-2000; 2000US-0225759.
XX PR 18-AUG-2000; 2000US-0226279.
XX PR 22-AUG-2000; 2000US-0226681.
XX PR 22-AUG-2000; 2000US-0226868.
XX PR 22-AUG-2000; 2000US-0227182.
XX PR 23-AUG-2000; 2000US-0227009.
XX PR 30-AUG-2000; 2000US-0228924.
XX PR 01-SEP-2000; 2000US-0229287.
XX PR 01-SEP-2000; 2000US-0229343.
XX PR 01-SEP-2000; 2000US-0229344.
XX PR 01-SEP-2000; 2000US-0229345.
XX PR 05-SEP-2000; 2000US-0229509.
XX PR 05-SEP-2000; 2000US-0229513.
XX PR 06-SEP-2000; 2000US-0230437.
XX PR 06-SEP-2000; 2000US-0230438.
XX PR 08-SEP-2000; 2000US-0231242.
XX PR 08-SEP-2000; 2000US-0231243.
XX PR 08-SEP-2000; 2000US-0231244.
XX PR 08-SEP-2000; 2000US-0231413.
XX PR 08-SEP-2000; 2000US-0231414.
XX PR 08-SEP-2000; 2000US-0232080.
XX PR 12-SEP-2000; 2000US-0232081.
XX PR 14-SEP-2000; 2000US-0231968.
XX PR 14-SEP-2000; 2000US-0232397.
XX PR 14-SEP-2000; 2000US-0232398.
XX PR 14-SEP-2000; 2000US-0232399.

PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0234984.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249309.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.

PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
XX (HUMA-) HUMAN GENOME SCI INC.
XX PA
XX PI Rosen CA, Barash SC, Ruben SM;
XX DR WPI; 2001-483426/52.
XX Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
PT useful for preventing, diagnosing and/or treating cancers and
PT metastasis -
XX
PS Disclosure: SEQ ID NO 34694; 3071pp + Sequence Listing; English.
XX
CC AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)
CC amino acid sequences given in AAK82170 to AAK91921. (I) have cytostatic
CC activity, and can be used in gene therapy and vaccine production. (I)
CC proteins and polynucleotides may be used in the prevention, diagnosis and
CC treatment of diseases associated with inappropriate (I) expression. For
CC example, they may be used to treat disorders associated with decreased
CC expression by rectifying mutations or deletions in a patient's genome
CC that affect the activity of (I) by expressing inactive proteins or to
CC supplement the patients own production of (I). Additionally, (I)
CC polynucleotides may be used to produce the secreted (I), by inserting
CC the nucleic acids into a host cell and culturing the cell to express the
CC protein. (I) proteins and polynucleotides may be used to prevent,
CC diagnose and treat immune/haematopoietic-related diseases, especially
CC cancers and cancer metastases of haematopoietic-derived cells. AAK64703
CC to AAK87694 represent human immune/haematopoietic antigen genomic
CC sequences from the present invention. AAK54942 to AAK54950 and AAK82169
CC represent sequences used in the exemplification of the present invention.
XX
SQ Sequence 8864 BP; 1897 A; 2376 C; 2556 G; 2035 T; 0 other;

Query Match 5.6%; Score 17; DB 22; Length 8864;
Best Local Similarity 100.0%; Pred. No. 82;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 197 acgtggtaaacctctc 213
|||||
Db 8790 ACGTGGTCAACCTCCTC 8774

RESULT 45
ABLI0070/c
ID ABLI0070 standard; cDNA; 9889 BP.
XX ABLI0070;
XX
DT 26-MAR-2002 (first entry)
XX
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 24692.
DE Drosophila; developmental biology; cell signalling; insecticide;
KW pharmaceutical; gene; ss.
XX Drosophila melanogaster.
OS WO200171042-A2.
XX
PN
PD 27-SEP-2001.
XX
XX 23-MAR-2001; 2001WO-US09231.
XX 23-MAR-2000; 2000US-191637P.

PR 11-JUL-2000: 2000US-0614150.
XX (PEKE) PE CORP NY.
PA Venter JC, Adams M, Li PWD, Myers EW;
XX
PI WPI: 2001-656860/75.
XX P-PSDB: ABB65967.
DR
XX
XX New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signalling and cell-cell
PT interactions .
XX
XX Claim 1: SEQ ID NO 24692; 21pp + Sequence Listing; English.
XX
XX The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC sequences (ABL01840-ABL16175) and the encoded proteins
CC (ABB57737-ABB72072).
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 9889 BP; 2711 A; 2313 C; 2108 G; 2757 T; 0 other;

Query Match 5.6%; Score 17; DB 23; Length 9889;
Best Local Similarity 100.0%; Pred. NO. 82;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 248 tgatcgtggagttctgc 264
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Db 2520 TGATCGTGGAGTTCTGC 2504

Search completed: July 15, 2002, 23:09:50
Job time: 18408 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

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(without alignments)
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Title: US-09-375-248-1_COPY_2546_2848

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Gapop 60.0 , Gapext 60.0

Searched: 1797656 seqs, 10463268293 residues

Word size : 0

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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- 31: em_htg_inv.*
- 32: em_htg_other.*
- 33: em_htg_inv.*

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SUMMARIES

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4	303	100.0	4416	6	HSFLT4
5	303	100.0	4425	6	I44520
6	303	100.0	4425	9	HSU43143
7	303	100.0	4795	6	AR016569
8	303	100.0	4795	6	AR106406
9	252	83.2	4450	9	HSFLT4X
10	117	38.6	130129	2	AC108083
11	117	38.6	168347	2	AC025336
12	106	35.0	127488	2	AC022095
13	106	35.0	173341	2	AC106813
14	23	7.6	5284	10	MUSRTKA
15	23	7.6	260266	2	AL646088
16	21	6.9	4254	10	AF402786
17	21	6.9	4360	10	AF402785
18	21	6.9	161580	2	AC098957
19	20	6.6	4017	9	AF063657
20	20	6.6	4272	5	AB065372
21	20	6.6	7680	9	HSFLT
22	20	6.6	31360	1	SC9C7
23	20	6.6	208304	2	AC108477
24	19	6.3	78210	1	AB070949
25	19	6.3	80908	9	HS524E15
26	19	6.3	119916	2	AC105566
27	19	6.3	155825	2	AC106084
28	18	5.9	561	11	AF207872
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31	18	5.9	1307	1	RSU62291
32	18	5.9	1519	3	AB025557
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35	18	5.9	2405	9	AF049461
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37	18	5.9	4784	8	NEUATPPM
38	18	5.9	5359	8	NEUATPPM
39	18	5.9	6813	14	HA1CAPNS
40	18	5.9	10003	1	U67544
41	18	5.9	39314	1	SGR300302
42	18	5.9	71769	2	AC102135
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ALIGNMENTS

RESULT	1
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LOCUS	AR016568
DEFINITION	Sequence 1 from patent US 5776755.
ACCESSION	AR016568
VERSION	AR016568.1
KEYWORDS	GI:3972845
SOURCE	Unknown.
ORGANISM	Unknown.
REFERENCE	Unclassified.
AUTHORS	1 (bases 1 to 4195) Alitalo,K., Aprelikova,O., Pajusola,K., Armstrong,E., Korhonen,J. and Kaipainen,A.
TITLE	FLT4, a receptor tyrosine kinase
JOURNAL	Patent: US 5776755-A 1 07-JUL-1998;
FEATURES	Location/Qualifiers 1..4195 /organism="unknown"
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ORIGIN	
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Qy 61 tccgcttcggcatccacaaaggcagcagctgtgacaccgtggccgtgaaatgctgaaa 120
Db 2606 TCCGCTTTTCGGCATCCACAAAGGCGAGCAGCTGTGACACCGCTGGCCGTGAAATGCTGAAA 2665

Qy 121 gagggcgccacgacgacgacgacgacgacgacgacgacgacgacgacgacgacgac 180
Db 2666 GAGGGCGCCACGCGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 2725

Qy 181 atcggcaaccacctcaacgtgggtcaacctctcctcgggcggtgacacaaagcgcagggccc 240
Db 2726 ATCGGCAACCACCTCAACGTGGTCAACCTTCTCGGGCGCTGCACCAAGCGCGAGGCCCC 2785

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Qy 301 cgg 303
Db 2846 CGG 2848

RESULT 2
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LOCUS AR106405 4195 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 1 from patent US 6107046.
ACCESSION AR106405
VERSION AR106405.1 GI:12820935
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Alicalco, K., Aprelikova, O., Pajusola, K., Armstrong, E., Korhonen, J.,
TITLE Antibodies to FLT4, a receptor tyrosine kinase and uses thereof
JOURNAL
PATENT: US 6107046-A 1 22-AUG-2000;
FEATURES
LOCATION/Qualifiers
SOURCE 1. 4195
/organism="unknown"

BASE COUNT 889 a 1279 c 1305 g 722 t
ORIGIN

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Matches 303; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 61 tccgcttcggcatccacaaaggcagcagctgtgacaccgtggccgtgaaatgctgaaa 120
Db 2606 TCCGCTTTTCGGCATCCACAAAGGCGAGCAGCTGTGACACCGTGGCCGTGAAATGCTGAAA 2665

Qy 121 gagggcgccacgacgacgacgacgacgacgacgacgacgacgacgacgacgacgac 180
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Qy 181 atcggcaaccacctcaacgtgggtcaacctctcctcgggcggtgacacaaagcgcagggccc 240
Db 2726 ATCGGCAACCACCTCAACGTGGTCAACCTTCTCGGGCGCTGCACCAAGCGCGAGGCCCC 2785

Qy 241 ctcatggtgatcgtggagtgctgcaagtcgcaagtcgcaagtcgcaagtcgcaagtcgca 300
Db 2786 CTCATGGTGATCGTGGAGTCTTCCAAAGTACGGCAACCTCTCCAACTTCTCTCGCGCGCAAG 2845
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Qy 301 cgg 303
Db 2846 CGG 2848

RESULT 3
AR112506
LOCUS AR112506 4416 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 1 from patent US 6130071.
ACCESSION AR112506
VERSION AR112506.1 GI:14092406
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Alitalo, K. and Joukov, V.
TITLE Vascular endothelial growth factor C (VEGF-C) .DELTA.Cys.sub.156
protein and gene, and uses thereof
JOURNAL
PATENT: US 6130071-A 1 10-OCT-2000;
FEATURES
LOCATION/Qualifiers
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/organism="unknown"

BASE COUNT 941 a 1345 c 1355 g 774 t
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Db 2606 TCCGCTTTTCGGCATCCACAAAGGCGAGCAGCTGTGACACCGTGGCCGTGAAATGCTGAAA 2665

Qy 121 gagggcgccacgacgacgacgacgacgacgacgacgacgacgacgacgacgacgac 180
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Qy 241 ctcatggtgatcgtggagtgctgcaagtcgcaagtcgcaagtcgcaagtcgcaagtcgca 300
Db 2786 CTCATGGTGATCGTGGAGTCTTCCAAAGTACGGCAACCTCTCCAACTTCTCTCGCGCGCAAG 2845

Qy 301 cgg 303
Db 2846 CGG 2848

RESULT 4
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LOCUS HSFLT4 4416 bp mRNA linear PRI 30-NOV-1993
DEFINITION H. sapiens mRNA for FLT4, class III receptor tyrosine kinase.
ACCESSION X68203
VERSION X68203.1 GI:31433
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Aprelikova, O.
TITLE Direct Submission
JOURNAL
Submitted (01-SEP-1992) O. Aprelikova, University of Helsinki,
Cancer Biology Laboratory, Dept of Pathology, Haartmaninkatu 3,
```

00290 Helsinki, FINLAND
2 (bases 1 to 4416)
Aprelikova,O., Pajusola,K., Partanen,J., Armstrong,E., Alitalo,R.,
Bailey,S.K., McMahon,J., Wasmuth,J., Huebner,K. and Alitalo,K.
FLT4, a novel class III receptor tyrosine kinase in chromosome
5q33-qter
Cancer Res. 52 (3), 746-748 (1992)
92119639
COMMENT
FEATURES
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 Location/Qualifiers
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 /db_xref="taxon:9606"
 /chromosome="5q35"
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 /note="class III tyrosine kinase"
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 /protein_id="CAA48290.1"
 /db_xref="GI:388522"
 /db_xref="SWISS-PROT:P35916"
 /translation="HAORPEMORGAAALCLRLWLCLGLDLVSGYSMTPTLNITEES
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BASE COUNT 941 a 1345 c 1355 g 774 t 1 others
ORIGIN

Query Match 100.0%; Score 303; DB 9; Length 4416;
Best Local Similarity 100.0%; Pred. No. 4e-152;
Matches 303; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 tcgcgttcggcatcccaaggcgagcagctgtgacacccgtgcccgtgaaaatgctgaaa 120
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QY 121 gagggcgccagcgagcagcgcgctgagtgtcggaagctcaagatcctcattcac 180
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Db 2666 GAGGGCGCCACGCCGAGCAGCAGCGCGCTGATGTCGGAGCTCAAGATCCTCATTCAC 2725
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QY 181 atcggaaccactcaagtggtcaacctctcgggcggtgaccaaagccgagggccccc 240
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BASE COUNT 941 a 1345 c 1355 g 774 t 1 others
ORIGIN

Query Match 100.0%; Score 303; DB 9; Length 4416;
Best Local Similarity 100.0%; Pred. No. 4e-152;
Matches 303; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 tcgcgttcggcatcccaaggcgagcagctgtgacacccgtgcccgtgaaaatgctgaaa 120
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QY 121 gagggcgccagcgagcagcgcgctgagtgtcggaagctcaagatcctcattcac 180
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QY 181 atcggaaccactcaagtggtcaacctctcgggcggtgaccaaagccgagggccccc 240
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Db 2726 ATCGGCAACCACTCAACGTGGTCAACCTCTCTGGGGGTGCACCAAGCCGCGAGGCCCC 2785
QY 241 ctcatgggtgattgagttctgcaagtacggcaacctctcaactctctcgcgccaaag 300
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Db 2786 CTATGGTGATCGTGAGTTCGCAAGTACGGCAACCTCTCCAACCTCTCTCGCGCCCAAG 2845
QY 301 cgg 303
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Db 2846 CGG 2848
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RESULT 5
LOCUS I44520
DEFINITION Sequence 31 from patent US 5635177.
ACCESSION I44520
VERSION I44520.1 GI:2469233
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 4425)
AUTHORS Bennett,B.D., Goeddel,D. and Matthews,W.
TITLE Protein tyrosine kinase agonist antibodies
JOURNAL Patent: US 5635177-A 31 03-JUN-1997;
FEATURES Location/Qualifiers
 source
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 /organism="unknown"
BASE COUNT 939 a 1348 c 1361 g 777 t
ORIGIN

Query Match 100.0%; Score 303; DB 6; Length 4425;
Best Local Similarity 100.0%; Pred. No. 4e-152;
Matches 303; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 301 cgg 303
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Db 2857 CGG 2859
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RESULT 6
LOCUS HSU43143
DEFINITION Human receptor tyrosine kinase Flt4 (short form) mRNA, complete
 cds.
ACCESSION U43143
VERSION U43143.1 GI:1150990
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 4425)
AUTHORS Lee,J., Gray,A., Yuan,J., Luoh,S.-M., Avraham,H. and Wood,W.I.
TITLE Vascular Endothelial Growth Factor Related Protein (VRP): A Ligand and Specific Activator of the Tyrosine Kinase Receptor Flt4
JOURNAL Proc. Natl. Acad. Sci. U.S.A. (1996) In press
REFERENCE 2 (bases 1 to 4425)
AUTHORS Wood,W.I.
TITLE Direct Submission
JOURNAL Submitted (12-DEC-1995) William I. Wood, Molecular Biology, Genentech, Inc., 460 Pt. San Bruno Blvd., S. San Francisco, CA 94080, USA
FEATURES
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Location/Qualifiers
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31. .3927
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/note="also called SAL-SI or tk1"
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KVYTTQDSVFGVLLWEIFSLGASPYGVQIINEFCORLRDGTMRAPELATPAIR
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BASE COUNT 939 a 1348 c 1361 g 777 t
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Best Local Similarity 100.0%; Pred. No. 4e-152;
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Db 2677 GAGGCGCCACCGCGGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 2736
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Db 2737 ATCGGCAACCACTCAACGTGGTCAACCTCTCGGGGCGTGCACCAAGCCGAGGCC 2796
Qy 241 ctcatggtgtagctgtagtctctgcaaglacggaacacctctccaacttctctcgcgccaa 300
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Db 2797 CTCATGGTGATCGTGGAGTCTTGCAGGTACGGCAACCTCTCCAACCTTCTCGCGGCCAAG 2856
Qy 301 cgg 303
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Db 2857 CGG 2859
RESULT 7
AR016569
LOCUS AR016569 4795 bp DNA linear PAT 05-DEC-1998
DEFINITION Sequence 3 from patent US 5776755.
ACCESSION AR016569
VERSION AR016569.1 GI:3972846
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 4795)
AUTHORS Alitalo,K., Aprelikova,O., Pajusola,K., Armstrong,E., Korhonen,J. and Kaipainen,A.
TITLE FLT4, a receptor tyrosine kinase
JOURNAL Patent: US 5776755-A 3 07-JUL-1998;
FEATURES Location/Qualifiers
Source 1. 4795
/organism="unknown"
BASE COUNT 977 a 1490 c 1494 g 834 t
ORIGIN
Query Match 100.0%; Score 303; DB 6; Length 4795;
Best Local Similarity 100.0%; Pred. No. 4e-152;
Matches 303; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 301 cgg 303
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Db 2846 CGG 2848
RESULT 8
AR106406
LOCUS AR106406 4795 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 3 from patent US 6107046.
ACCESSION AR106406
VERSION AR106406.1 GI:12820936
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 4795)
AUTHORS Alitalo,K., Aprelikova,O., Pajusola,K., Armstrong,E., Korhonen,J., Kaipainen,A. and Matikainen,M.
TITLE Antibodies to Flt4, a receptor tyrosine kinase and uses thereof

JOURNAL FEATURES	Patent: US 6107046-A 3 22-AUG-2000;
SOURCE	Location/Qualifiers 1..4795
BASE COUNT	977 A 1490 C 1494 G 834 T
ORIGIN	/organism="unknown"
Query Match	100.0%; Score 303; DB 6; Length 4795;
Best local Similarity	100.0%; Pred. No. 4e-152;
Matches 303; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
OY 1	gaqcgctcacactgggagagdgctgcggtacgcgcctcggagggtggagacc 60
DB 2546	GAGCGCTCACCTGGGAGAGTGTCCGCACGGCCTTCGGGAAGTGTCGAAGCC 2605
OY 61	tccgcttcggcatccacaaggcagcagctgtgacacgtlggcgtgaaaatctgaaa 120
DB 2606	TCCGCTTTCCGCATCCACAAGCGCAGCAGCTGTGACACCCTGGCGGTGAAAATCCTCAAA 2665
OY 121	gagggcgccacggcagcagcgcgcgcgtgatgtcggagctcaagatactctattcac 180
DB 2666	GAGGGCGCCACGCCAGCAGCACCGCGCGCTGTGTGCGAGCTCAAGATCTCTATTTCAC 2725
OY 181	alcgccaacacctcaacgctgcacacctctcggggcgtagcaccagcgcagggcccc 240
DB 2726	ATCGGCAACCACTCAACGTGTCTAACCTCTCGGGGGCTGCACCAAGCCGAGGGCCCC 2785
OY 241	ctcatgtaatcgtagagtctgcaagtacgcagcaacctctccaactctcgtcgcccaag 300
DB 2786	CTCATGTAATCCTGAGTGTCTGCAAGTAGCGCAACCTCTCCAAC'TCTCTCGCGGCCAAG 2845
OY 301	cgg 303
DB 2846	CGG 2848
RESULT 9	
HSFLT4X	LOCUS
DEFINITION	H.sapiens Flt4 mRNA for transmembrane tyrosine kinase.
ACCESSION	X69878.S59182
VERSION	X69878.1 GI:297049
KEYWORDS	transmembrane tyrosine kinase; tyrosine kinase.
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 4450)
AUTHORS	Galland,F., Karanysheva,A., Pebusque,M.J., Borg,J.P., Rottapel,R., Dubreuil,P., Rosnet,O. and Birnbaum,D. The FLT4 gene encodes a transmembrane tyrosine kinase related to the vascular endothelial growth factor receptor
TITLE	Oncogene 8 (5), 1233-1240 (1993) 93241723
JOURNAL MEDLINE	2 (bases 776 to 1200)
REFERENCE	Galland,F., Karanysheva,A., Mattei,M.G., Rosnet,O., Marchetto,S. and Birnbaum,D. Chromosomal localization of FLT4, a novel receptor-type tyrosine kinase gene
AUTHORS	Genomics I3 (2), 475-478 (1992) 92307693
TITLE	Direct Submission
JOURNAL	Submitted (28-DEC-1992) F. Galland, INSERM, Unite 119, 27 Bd Lei Roure, Marseille 13009, FRANCE
FEATURES	Location/Qualifiers 1..4450
source	/organism="Homo sapiens" /db_xref="taxon:9606"
sig_peptide	22..87
CDS	22..3918

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BASE COUNT      960 a 1350 c 1354 g 786 t
ORIGIN
Query Match      83.2%; Score 252; DB 9; Length 4450;
Best Local Similarity 99.7%; Pred.No. 1.2e-124;
Matches 302; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 2608 TCGCGTTTTCGGCATCCACAAAGGCGACGAGCTGTGACACCGTGGCCGTGAAATGCTGAAA 2667
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QY 121 gagggcgccacggcgagcagccgcgcgtgatgtcggagctcaagatcctcattcac 180
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Db 2668 GAGGCGGCCACGCCAGCGAGCAGCGCGCTGATCGGAGCTCAAGATCCTCATTCAC 2727
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QY 181 atcgggaaccacatcaactgaactcctcctcgggcgctgacccaagcgagggccccc 240
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Db 2728 ATCGGAACACCATCAACGTGGTCAACCTCTCTCGGGCGCTGCACCAAGCGCGAGGCCCC 2787
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QY 241 ctcatgtgatcgtgagttctcaagtcagcgaacctctccaactctcctgcccgcgaag 300
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Db 2788 CTATGCTGATCGTGGAGTCTCTCAAGTACGGCAACCTCTCCAACATTCCTCGCGCGCAAG 2847
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QY 301 cgg 303
Db 2848 CGG 2850

RESULT 10
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LOCUS      Homo sapiens chromosome 5 clone CTD-2013L15, linear HTG 25-JAN-2002
DEFINITION AC108083
ACCESSION AC108083.1 GI:18369929
VERSION    HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
KEYWORDS   human.
SOURCE     Homo sapiens
ORGANISM   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
REFERENCE  1 (bases 1 to 130129)
AUTHORS    DOE Joint Genome Institute.
TITLE      Sequencing of Human Chromosome 5
JOURNAL    Unpublished
REFERENCE  2 (bases 1 to 130129)
AUTHORS    DOE Joint Genome Institute.
TITLE      Direct Submission
JOURNAL    Submitted (25-JAN-2002) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
COMMENT    -----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov
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Project Information
Center Project Name: 632820
Center clone name: CITB-H1_2013L15
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Summary Statistics
Consensus quality: 124488 bases at least Q40
Consensus quality: 128031 bases at least Q30
Consensus quality: 128842 bases at least Q20
Estimated insert size: 135000; agarose-fp estimation
Estimated insert size: 129829; sum-of-contigs estimation
Quality coverage: 7.66 in Q20 bases; agarose-fp estimation
Quality coverage: 7.97 in Q20 bases; sum-of-contigs estimation
* NOTE: This is a 'working draft' sequence. It currently
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* consists of 4 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 4320: contig of 4320 bp in length
* 4321 4420: gap of unknown length
* 4421 23712: contig of 19292 bp in length
* 23713 23812: gap of unknown length
* 23813 48602: contig of 24790 bp in length
* 48603 48702: gap of unknown length
* 48703 130129: contig of 81427 bp in length.
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Best Local Similarity 100.0%; Pred.No. 4.9e-52;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 19878 AGAGGCGCCACGGCCAGCAGCGCGCTGATGTCGGAGCTCAAGATCCTCATTTCA 19937
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QY 180 catcggaaccacctaactcctcctcctcctcctcctcctcctcctcctcctcctc 236
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Db 19938 CATCGGAACCACTCAACGTGTCACCTCTCTCGGGCGCTGCACCAAGCCCGCAGG 19994
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RESULT 11
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LOCUS      Homo sapiens chromosome 5 clone RP11-451H23 map 5, WORKING DRAFT
DEFINITION AC025336
ACCESSION AC025336.2 GI:7328761
VERSION    HTG; HTGS_PHASE1; HTGS_DRAFT.
KEYWORDS   human.
SOURCE     Homo sapiens
ORGANISM   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
REFERENCE  1 (bases 1 to 168347)
AUTHORS    Birren,B., Linton,L., Nusbaum,C. and Lander,E.
TITLE      Homo sapiens chromosome 5, clone RP11-451H23
JOURNAL    Unpublished
REFERENCE  2 (bases 1 to 168347)
AUTHORS    Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
Anderson,S., Baldwin,J., Barna,N., Bastien,V., Beda,F.,
Boguslavsky,L., Boukhgalter,B., Brown,A., Burkett,G.,
Campopiano,A., Castelle,A., Choapel,Y., Colangelo,M., Collins,S.,
Collymore,A., Cooke,P., Dearellano,K., Dewar,K., Diaz,J.S.,
Dodge,S., Domino,M., Doyle,M., Ferreira,P., FitzHugh,W., Gage,D.,
Galagan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L.,
Grand-Pierre,N., Grant,G., Hagos,B., Heaford,A., Horton,L.,
Howland,J.C., Iliev,I., Johnson,R., Jones,C., Kann,L., Karatas,A.,
Klein,J., LaRocque,K., Lamazares,R., Landers,T., Lehoczkv,J.,
Levine,R., Lieu,C., Liu,G., Locke,K., Macdonald,P., Marquis,N.,
McCarthy,M., McEwan,P., McGurk,A., McKernan,K., McPheeters,R.,
Meldrum,J., Meneus,L., Mihova,T., Miranda,C., Mienga,V., Morrow,J.,
Murphy,T., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,
O'Neill,D., Oliver,T.M., Oliver,J., Peterson,K., Pierre,N.,
Pisani,C., Pollara,V., Raymond,C., Riley,R., Rogov,P., Rothman,D.,
Roy,A., Santos,R., Schauer,S., Severy,P., Spencer,B.,
Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,
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Tesfaye,S., Theodore,J., Tirrell,A., Travers,M., Trigilio,J.,
Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W,J.,
Young,G., Zainoun,J., Zimmer,A. and Zody,M.

TITLE JOURNAL

COMMENT

Submitted (08-MAR-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Mar 25, 2000 this sequence version replaced gi:7210017.

All repeats were identified using RepeatMasker:

Smit, A.F.A. & Green, P. (1996-1997)

<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

----- Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WBIR

Web site: <http://www.seq.wi.mit.edu>

Contact: sequence_submissions@genome.wi.mit.edu

----- Project Information

Center project name: L6686

Center clone name: 451_H_23

----- Summary Statistics

Sequencing vector: M13; M77815; 100% of reads

Chemistry: Dye-terminator Big Dye; 100% of reads

Assembly program: Phrap; version 0.960731

Consensus quality: 150422 bases at least Q40

Consensus quality: 159524 bases at least Q30

Consensus quality: 163013 bases at least Q20

Insert size: 165247; sum-of-contigs

Quality coverage: 3.6 in Q20 bases; sum-of-contigs

FEATURES source

* NOTE: This is a 'working draft' sequence. It currently
* consists of 32 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

* 1 1389: contig of 1389 bp in length

* 1390 1489: gap of 100 bp

* 1490 3130: contig of 1641 bp in length

* 3131 3230: gap of 100 bp

* 3231 4942: contig of 1712 bp in length

* 4943 5042: gap of 100 bp

* 5043 6981: contig of 1939 bp in length

* 6982 7081: gap of 100 bp

* 7082 8708: contig of 1627 bp in length

* 8709 8808: gap of 100 bp

* 8809 10286: contig of 1478 bp in length

* 10287 10386: gap of 100 bp

* 10387 12212: contig of 1826 bp in length

* 12213 12312: gap of 100 bp

* 12313 14658: contig of 2346 bp in length

* 14659 14758: gap of 100 bp

* 14759 17941: contig of 3183 bp in length

* 17942 18041: gap of 100 bp

* 18042 21297: contig of 3256 bp in length

* 21298 21397: gap of 100 bp

* 21398 24992: contig of 3595 bp in length

* 24993 25092: gap of 100 bp

* 25093 27768: contig of 2676 bp in length

* 27769 27868: gap of 100 bp

* 27869 31188: contig of 3320 bp in length

* 31189 31288: gap of 100 bp

* 31289 33714: contig of 2426 bp in length

* 33715 33814: gap of 100 bp

* 33815 37277: contig of 3463 bp in length

* 37278 37377: gap of 100 bp

* 37378 42302: contig of 4925 bp in length

* 42303 42402: gap of 100 bp

* 42403 47816: contig of 5414 bp in length

* 47817 47916: gap of 100 bp

* 47917 52586: contig of 4670 bp in length

* 52587 52686: gap of 100 bp

* 52687 56567: contig of 3881 bp in length

* 56568 56667: contig of 100 bp

* 56668 61557: contig of 4890 bp in length

* 61558 61657: gap of 100 bp

* 61658 66724: contig of 5067 bp in length

* 66725 66824: gap of 100 bp

* 66825 71568: contig of 4744 bp in length

* 71569 71668: gap of 100 bp

* 71669 76578: contig of 4910 bp in length

* 76579 76678: gap of 100 bp

* 76679 83312: contig of 6634 bp in length

* 83313 83412: gap of 100 bp

* 83413 90053: contig of 6641 bp in length

* 90054 90153: gap of 100 bp

* 90154 99426: contig of 9273 bp in length

* 99427 99526: gap of 100 bp

* 99527 108015: contig of 8489 bp in length

* 108016 108115: gap of 100 bp

* 108116 118144: contig of 10029 bp in length

* 118145 118244: gap of 100 bp

* 118245 130468: contig of 12224 bp in length

* 130469 130568: gap of 100 bp

* 130569 142239: contig of 11671 bp in length

* 142240 142339: gap of 100 bp

* 142340 157135: contig of 14796 bp in length

* 157136 157235: gap of 100 bp

* 157236 168347: contig of 11112 bp in length.

* 56568 56667: gap of 100 bp

* 56668 61557: contig of 4890 bp in length

* 61558 61657: gap of 100 bp

* 61658 66724: contig of 5067 bp in length

* 66725 66824: gap of 100 bp

* 66825 71568: contig of 4744 bp in length

* 71569 71668: gap of 100 bp

* 71669 76578: contig of 4910 bp in length

* 76579 76678: gap of 100 bp

* 76679 83312: contig of 6634 bp in length

* 83313 83412: gap of 100 bp

* 83413 90053: contig of 6641 bp in length

* 90054 90153: gap of 100 bp

* 90154 99426: contig of 9273 bp in length

* 99427 99526: gap of 100 bp

* 99527 108015: contig of 8489 bp in length

* 108016 108115: gap of 100 bp

* 108116 118144: contig of 10029 bp in length

* 118145 118244: gap of 100 bp

* 118245 130468: contig of 12224 bp in length

* 130469 130568: gap of 100 bp

* 130569 142239: contig of 11671 bp in length

* 142240 142339: gap of 100 bp

* 142340 157135: contig of 14796 bp in length

* 157136 157235: gap of 100 bp

* 157236 168347: contig of 11112 bp in length.

FEATURES Location/Qualifiers

1. .168347

/organism="Homo sapiens"

/db_xref="taxon:9606"

/chromosome="5"

/map="5"

/clone="Rp11-451H23"

/clone_lib="RPC1-11 Human Male BAC"

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/note="assembly_fragment"

3231. .4942

/note="assembly_fragment"

5043. .6981

/note="assembly_fragment"

7082. .8708

/note="assembly_fragment"

8809. .10286

/note="assembly_fragment"

10387. .12212

/note="assembly_fragment"

12313. .14658

/note="assembly_fragment"

14759. .17941

/note="assembly_fragment"

18042. .21297

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21398. .24992

/note="assembly_fragment"

25093. .27768

/note="assembly_fragment"

27869. .31188

/note="assembly_fragment"

31289. .33714

/note="assembly_fragment"

33815. .37277

/note="assembly_fragment"

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/note="assembly_fragment"

42403. .47816

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47917. .52586

/note="assembly_fragment"

52687. .56567

/note="assembly_fragment"

56668. .61557

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/note="assembly_fragment"

56668. .61557

[illegible]

JOURNAL
REFERENCE 2 (bases 1 to 173341)
AUTHORS DOE Joint Genome Institute.
TITLE Direct Submission
JOURNAL Submitted (12-JAN-2002) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
COMMENT On Jan 25, 2002 this sequence version replaced gi:18139363.
-----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov

Project Information
Center Project Name: 1519801
Center clone name: RPCJ-11_586L9

Summary Statistics
Consensus quality: 164442 bases at least Q40
Consensus quality: 167261 bases at least Q30
Consensus quality: 167771 bases at least Q20
Estimated insert size: 186250; agarose-fp estimation
Estimated insert size: 172741; sum-of-contigs estimation
Quality coverage: 10.29 in Q20 bases; agarose-fp estimation
Quality coverage: 11.1 in Q20 bases; sum-of-contigs estimation
NOTE: This is a 'working draft' sequence. It currently consists of 7 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
1 1596: contig of 1596 bp in length
1597 1696: gap of unknown length
1697 3940: contig of 2244 bp in length
3941 4040: gap of unknown length
4041 5104: contig of 1064 bp in length
5105 5204: gap of unknown length
5205 6286: contig of 1082 bp in length
6287 6386: gap of unknown length
6387 20063: contig of 13677 bp in length
20064 20163: gap of unknown length
20164 82401: contig of 62238 bp in length
82402 82501: gap of unknown length
82502 173341: contig of 90840 bp in length.

FEATURES
source
Location/Qualifiers
1..173341
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="5"
/clone="RP11-586L9"
/clone_lib="RPCI human BAC library 11"
BASE COUNT 45837 a 42564 c 41389 g 42871 t 680 others
ORIGIN

Query Match 35.0%; Score 106; DB 2; Length 173341;
Best Local Similarity 100.0%; Pred. No. 4e-46;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 gggagagtcgcgctacgagcccttcgggaagtggtggaagccttcggttcggaatc 75
Db 97431 GGGAGAGTCGCGCTACGGCGCCCTTCGGGAAGGTGGTGGGAAGCTCCGCTTCGGCATC 97490
Qy 76 cacaagggcagcagctgtgacacccgtg9ccgtgaaatgctgaaag 121
Db 97491 CACAAGGCACAGCTGTGACACCGTGGCGGTGAANAATGCTGAAG 97536

RESULT 14
MUSRTKA
LOCUS 5284 bp mRNA linear ROD 09-AUG-1993
DEFINITION Mus musculus receptor tyrosine kinase (FLT4) mRNA, complete cds.

ACCESSION L07296
VERSION L07296.1 GI:293780
KEYWORDS receptor protein tyrosine kinase.
SOURCE Mus musculus (strain C57BL/6J, sub_species domesticus) cDNA to mRNA.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 5284)
AUTHORS Finnerty,H., Kelleher,K., Morris,G.E., Bean,K., Merberg,D.M., Kriz,R., Morris,J.C., Sookdeo,H., Turner,K.J. and Wood,C.R.
TITLE Molecular cloning of murine FLT and FLT4
JOURNAL Oncogene 8, 2293-2298 (1993)
MEDLINE 93330572
FEATURES Location/Qualifiers
1..5284
/organism="Mus musculus"
/strain="C57BL/6J"
/sub_species="domesticus"
/db_xref="taxon:10090"
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/gene="FLT4"
45..4136
/gene="FLT4"
/note="putative"
/codon_start=1
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/protein_id="AAA40077.1"
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ANNQSYHCYKYIKARIEGTAASTVFYDFKHPFINKPDTLLVNRKDSMWPCVL
SIPCLNTILBSQSSALHPDGOEVLWDDRGHRVPTOLLRDALYLCCETTFGQAEARA
LFVYHITGNELYDIQLYPKSMELLGKLYLNCVTWAEFDSGVTFDMDTPGQAEARA
KWPERRSQOHTLESILTINHNVSQNDLGPYVCEANNQIQRFEFTEVIVHEKPFIS
VEWLKGEVLEATGDELVLKPLVLAAYPPPEFYQYDKKAVTGRHNHPALVLEKTEA
SAGYITLWNSAAGLRQNLSELVNVPPHIIHEKASSPSIYSRHSROTLLCTAYGV
PQPLSVQWHRPWTCKTFAQRLRRQQRQDQPCQKDMKSVIYTDQVNPITSLDSWT
EFYEGNKTVSKLVADANYSAMYKCVVNVKVGDERLIVYVTTIPDGFSIESESE
DPLEGOSVRLSCRADNVTYELRWYRLNLTSLHDAQGNPLLLDCKNVHLPATLEAHL
EEAEPGARHATLSLNTPRVAPEDGQYVCEVQRRSODKHCKKYSVQALEAPRLTQ
NLTDLLVNSDSLEMRCPVAGAHVSVYVTKDGRKMEIVLIGTGVIAVFWVLLLLIFC
EDAGRYLCSVCNCAVNSAVAGESSDKSGMEIVLIGTGVIAVFWVLLLLIFC
NMKRAHADIKTGYLSIIMDPGEVLEEQCEYLSYDASQWEPFRELHGRVLCGAF
GKVVESAFIGNKSGSDTVAVKMLKEGATASBRHMLSELKILIHGNHLNVNLLG
ACTKPNGLMVIIEFCYKGNLNFRLVKRDTFNPAEKSPEORRRFRAMVEGAKARR
RPGSSORALFTRELKCGSARRAPLVQEAEDLWLSPLTHEDLYCYFQVARGHEFLAS
KCIHRDLAARNILLSSEDLVKICDFGLARDIYKDPDYVRKGSARLPLKMWAPESIFD
KYVTTOSDVMSFGVLLWEIFSLGASYPGVQIINEFCORLKDGTMRAPELATPAIRH
IMQSCWSDPKARPAFSDLVLEILGDLQGGWQEEEREMALHSSOSSSEDDGFMQAST
TALHITADADDSPSMHCHSLAARYNCVSPFGLARGTKTPGSSRMKTFEELPMTTP
TTYKASMDNOTDSGMVLAEEFEELSRHRPEGSFCKGPGQOHMDIPRGHPDPQGRRR
RPTQGAQGGKVFYNNEYGVSQCTEGDCPCPSAGSTFFADSS!"

BASE COUNT 1221 a 1533 c 1466 g 1064 t
ORIGIN

Query Match 7.6%; Score 23; DB 10; Length 5284;
Best Local Similarity 100.0%; Pred. No. 0.29;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 82 ggcagcagctgtgacacccgtggc 104
Db 2652 GGCAGCAGCTGTGACACCCGTGGC 2674

RESULT 15
AL646088
LOCUS 260266 bp DNA linear HTG 30-JAN-2002
DEFINITION Mus musculus chromosome 11 clone RP23-58E13, *** SEQUENCING IN
PROGRESS ***, in unordered pieces.
ACCESSION AL646088
VERSION AL646088.11 GI:18476932

KEYWORDS HTG: HTGS_PHASE1; HTGS_ACTIVEFIN; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE house mouse.
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLE 1 (sites)
JOURNAL Direct Submission
COMMENT Submitted (28-JAN-2002) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Feb 1, 2002 this sequence version replaced gi:18151535.
----- Genome Center
Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
----- Project Information
Center project name: BM58E13
----- Summary Statistics
Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid; L08752; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality: 258539 bases at least Q40
Consensus quality: 258926 bases at least Q30
Consensus quality: 259227 bases at least Q20
Insert size: 259766; sum-of-contigs
Insert size: 225486; 6.3% error; agarose-fp
Quality coverage: 9.68x in Q20 bases; sum-of-contigs Quality
coverage: 11.43x in Q20 bases; agarose-fp

* NOTE: This is a 'working draft' sequence.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

FEATURES

Source Location/Qualifiers
1..260266
/organism="Mus musculus"
/db_xref="taxon:10090"
/chromosome="11"
/clone="RP23-58E13"
/clone_lib="RPC1-23"
1..8902
misc_feature
/note="assembly_fragment:05530
fragment_chain:1"
9003..87162
misc_feature
/note="assembly_fragment:05707
fragment_chain:1"
87263..123670
misc_feature
/note="assembly_fragment:05852
fragment_chain:1"
123771..188404
misc_feature
/note="assembly_fragment:00429"
188505..214152
misc_feature
/note="assembly_fragment:05868"
214253..260266
/note="assembly_fragment:05872"
BASE COUNT 80139 a 55470 c 56089 g 68066 t 502 others
ORIGIN

Query Match 7.6%; Score 23; DB 2; Length 260266;
Best Local Similarity 100.0%; Pred. No. 0.2;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 82 ggcagcagctgtgacacgtggc 104
|||||
Db 162194 gccagcagctgtgacacgtggc 162216

RESULT 16
AF402786 4254 bp mRNA linear ROD 11-OCT-2001
LOCUS AF402786

DEFINITION

Rattus norvegicus receptor tyrosine kinase VEGFR-3kt (Vegfr3) mRNA,
complete cds, alternatively spliced.

ACCESSION

AF402786

VERSION

AF402786.1 GI:16033529

KEYWORDS

Norway rat.

SOURCE

Rattus norvegicus

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

REFERENCE

1 (bases 1 to 4254)

AUTHORS

Krishnan,J. and Sleeman,J.P.

TITLE

Characterization of a novel alternatively spliced form of VEGFR-3

JOURNAL

Unpublished

REFERENCE

2 (bases 1 to 4254)

AUTHORS

Krishnan,J. and Sleeman,J.P.

TITLE

Direct Submission

JOURNAL

Submitted (25-JUL-2001) Institut fuer Toxikologie und Genetik,
Forschungszentrum Karlsruhe, Postfach 3640, Karlsruhe 76021,
Germany

FEATURES

Location/Qualifiers
1..4254
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/strain="Sprague-Dawley"
/db_xref="taxon:10116"
1..4254
/gene="Vegfr3"
1..3279
/gene="Vegfr3"
/note="kinase domain truncated form of VEGFR-3;
alternatively spliced"
/codon_start=1
/product="receptor tyrosine kinase VEGFR-3kt"
/protein_id="AAL13270.1"
/db_xref="GI:16033530"
/translation="MQPGAALNRRLMLCLGLQGLANGYSMTPTLNTSDSYVIDTG
DSLSISCRGQHPLEWTRGAQEVLTGGKDSQEDTVQVDCGCEGTAPYCKAVLSLAOTH
ANNTSGYCYKYKIKARIECTAASYVYFVRDEQEPINKPTDLLNRRKDSMWYPCLY
SIPGLNITLRSSQSVLHPDQGEVLDMDRRMRVPTLLRLDALYLCQETTMDGDDFLSN
PFLVHTGNELYDIQLYPKKSLLELVGKLVNCTVMAEFDSTVQDQVDFDMDYDGGQAE
KWPPERQOQHTLSILTIHNVSQHDLGPVYCEANNGTQOFRESTEIVHEKPTIS
SAGVYTLALNSAAGLRQNI SLELVNPPHIHEKASSPSIYSRISROPTLCTTGV
POPSQVQHWHPWTCKTFAORSLRRRQPCQDMKNEVTTQDAVPIESLDTWT
ESVEGKNKTVSLIODANSYKCVFNKQDRLIYFYVTIIPDGSISERSE
DPLEGQSVRLSCRADNYTEHLRYRLNLSLTHDAQGNPLLLDCKNVHLFATPLEANL
EEAEPGARHATLSLNPVPAPEDEGDTVCVQDRRQDCKHKKYLSVQALEAPRLTQ
NLTDLLVNVRTSLMRCPCVAGAHVPSIVMYKDERLLEKESGIDLADSNQRLSTQVRE
EDAGRYLCYCNAGKGVNSASVAVESGDKSMEIVILIGTGVIAVFFVWLLLLIFC
NMRRPAHADIKTGLSLIMDPGEVPLEQCEYLSYDVQVSEWEPFRLHGLRVLHGCAF
GKVEASAFGINKGSCDTVAVKMLKEGATASPHALMSKELKILIHIGHNLVNVNLLG
ACTKPNGLMWIVFECKYGNLSFLRVKRETFDPYAEKSPQORRRFRAMVEGAKDRLR
RLGSTDRALFTRELKMGKSARRAPFQVEAEDLWLSPLTHEDLYCYFSQVARGHEFLAS
RKCIHRDLAARNLLSESIDVICKDFGLANDIYKDPDVRKGSARLPLTLTGYRSMRN
SASG"

BASE COUNT

989 a 1236 c 1224 g 805 t

ORIGIN

Query Match 6.9%; Score 21; DB 10; Length 4254;
Best Local Similarity 100.0%; Pred. No. 3.5;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 268 tacggcaacctctccaacttc 288
|||||
Db 2794 TACGGCAACCTCTCCAACCTTC 2814

RESULT

17
AF402785 4360 bp mRNA linear ROD 11-OCT-2001
LOCUS AF402785
DEFINITION Rattus norvegicus receptor tyrosine kinase VEGFR-3 (Vegfr3) mRNA,
complete cds, alternatively spliced.

[illegible]

Estimated insert size: 111412; sum-of-contigs estimation
Quality coverage: 0x in Q20 bases; agarose-fp estimation
Quality coverage: 1.5x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 75 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1 5831: contig of 5831 bp in length
5832 5931: gap of unknown length
5932 11384: contig of 5453 bp in length
11385 11484: gap of unknown length
11485 16895: contig of 5411 bp in length
16896 16995: gap of unknown length
16997 21784: contig of 4789 bp in length
21785 21884: gap of unknown length
21885 25354: contig of 3470 bp in length
25355 25454: gap of unknown length
25455 29460: contig of 4006 bp in length
29461 29560: gap of unknown length
29561 32307: contig of 2747 bp in length
32308 32407: gap of unknown length
32409 35343: contig of 2936 bp in length
35344 35443: gap of unknown length
35444 38216: contig of 2773 bp in length
38217 38316: gap of unknown length
38317 41183: contig of 2867 bp in length
41184 41283: gap of unknown length
41284 43599: contig of 2676 bp in length
43600 44059: gap of unknown length
44060 47285: contig of 3226 bp in length
47286 47385: gap of unknown length
47386 50539: contig of 3154 bp in length
50540 50639: gap of unknown length
50640 54276: contig of 3637 bp in length
54277 54376: gap of unknown length
54377 57921: contig of 3544 bp in length
57922 60505: contig of 2485 bp in length
60506 60605: gap of unknown length
60606 62900: contig of 2295 bp in length
62901 63000: gap of unknown length
63001 64914: contig of 1914 bp in length
64915 65014: gap of unknown length
65015 67533: contig of 2519 bp in length
67534 67633: gap of unknown length
67634 70777: contig of 3144 bp in length
70778 70877: gap of unknown length
70878 73509: contig of 2632 bp in length
73510 73609: gap of unknown length
73610 76056: contig of 2447 bp in length
76057 76156: gap of unknown length
76157 78450: contig of 2294 bp in length
78451 78550: gap of unknown length
78551 80050: contig of 1500 bp in length
80051 80150: gap of unknown length
80151 82169: contig of 2019 bp in length
82170 82269: gap of unknown length
82270 83776: contig of 1507 bp in length
83777 83876: gap of unknown length
83878 85747: contig of 1871 bp in length
85748 85847: gap of unknown length
85848 87806: contig of 1959 bp in length
87807 87906: gap of unknown length
87907 89679: contig of 1773 bp in length
89680 89779: gap of unknown length
89780 91266: contig of 1487 bp in length

* 91267 91366: gap of unknown length
91367 93812: contig of 2446 bp in length
93813 93912: gap of unknown length
93913 95639: contig of 1727 bp in length
95640 95739: gap of unknown length
95740 97396: contig of 1657 bp in length
97397 97496: gap of unknown length
97497 99145: contig of 1649 bp in length
99146 99245: gap of unknown length
99246 100913: contig of 1668 bp in length
100914 101013: gap of unknown length
101014 102955: contig of 1942 bp in length
102956 103055: gap of unknown length
103056 104468: contig of 1413 bp in length
104469 104568: gap of unknown length
104569 106375: contig of 1807 bp in length
106376 106475: gap of unknown length
106476 108691: contig of 2216 bp in length
108692 108791: gap of unknown length
108792 110626: contig of 1835 bp in length
110627 110726: gap of unknown length
110727 111801: contig of 1075 bp in length
111802 111901: gap of unknown length
111902 113358: contig of 1457 bp in length
113359 113458: gap of unknown length
113459 114629: contig of 1171 bp in length
114630 114729: gap of unknown length
114730 116364: contig of 1635 bp in length
116365 116464: gap of unknown length
116465 118200: contig of 1736 bp in length
118201 118300: gap of unknown length
118301 119530: contig of 1230 bp in length
119531 119630: gap of unknown length
119631 121318: contig of 1688 bp in length
121319 121419: gap of unknown length
121419 122620: contig of 1202 bp in length
122621 122720: gap of unknown length
122721 124128: contig of 1408 bp in length
124129 124228: gap of unknown length
124229 126159: contig of 1931 bp in length
126160 126259: gap of unknown length
126260 128394: contig of 2135 bp in length
128395 128494: gap of unknown length
128495 130496: contig of 2002 bp in length
130497 130596: gap of unknown length
130597 132111: contig of 1515 bp in length
132112 132211: gap of unknown length
132212 133294: contig of 1083 bp in length
133295 133394: gap of unknown length
133395 134851: contig of 1457 bp in length
134852 134951: gap of unknown length
134952 136002: contig of 1051 bp in length
136003 136102: gap of unknown length

Query Match 6.9% Score 21: DB 2; Length 161580;
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 21: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 268 tacggcaacctctccaaactc 288
|||||
Db 26979 TACGGCACTCTCCAACTC 26959

RESULT 19

AF063657

LOCUS

DEFINITION

mRNA, complete cds.

ACCESSION

AF063657

VERSION

AF063657.1

KEYWORDS

human.

SOURCE

ORGANISM Homo sapiens

AF063657 AF063657 4017 bp mRNA linear PRI 11-MAY-2001
Homo sapiens vascular endothelial growth factor receptor (FLT1)

REFERENCE 1 (bases 1 to 4017)
 AUTHORS Herley, M. T., Yu, Y., Whitney, R. G. and Sato, J. D.
 TITLE Characterization of the VEGF binding site on the Flt-1 receptor
 JOURNAL Biochem. Biophys. Res. Commun. 262 (3), 731-738 (1999)
 MEDLINE 99400442
 PUBMED 10471394
 REFERENCE 2 (bases 1 to 4017)
 AUTHORS Yu, Y., Whitney, R. G. and Sato, J. D.
 TITLE Direct Submission
 JOURNAL Submitted (06-MAY-1998) Adirondack Biomedical Research Institute,
 10 Old Barn Rd., Lake Placid, NY 12946, USA

FEATURES
 source
 1..4017
 Location/Qualifiers
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /cell_type="endothelium"
 /tissue_type="umbilical vein"
 1..4017
 /gene="FLT1"
 1..4017
 /gene="FLT1"
 /note="VEGFR: tyrosine kinase"
 /codon_start=1
 /product="vascular endothelial growth factor receptor"
 /protein_id="AAC16449.1"
 /db_xref="GI:3132831"

translation="MVSVDGVLGALLCLLLTGSSGSKLKDPELSUKGTQHIMQ
 AGOTLHLCREAAHKSLPMSKESERLSITKACRNGKQFCSTLTLTAAOANH
 GFYCKYLAVPTSKKTESAIYIFISDTGRPFVEMYSEIPIHMTGRELVPGRV
 TSNPTITVKKFPLEDTIPDGKRIIDMSRKGFIISNATYKEIGLTCATVNGHLYKT
 NYLHRTQNTIIDVOISTPRPKLLRGHTLTIVNCTATPLNTRVQMTSVYDEKNKRA
 SVRRIDQSNHANIYFVSILTIDKMNKDKGLYTCRVRSQSPKSVNTSVHIYDKAFI
 TVKIRKQOLTEVACACRSYRLSMKAKAPSPSPVWLKDLGPATEKSAARYLTRGYSLLI
 IDTAEAGNVTIILSKQSVFNKLTATLIVNWKFOIYEKAVSSFPDPALYPLGSRQ
 KLVTEGPIQPTIKWPHCNHNSCARDFCSNNEESFILDADSNMGRITESITOR
 MAILEGNMASTLVADRSIGIYICIASNKVGTGVRNLSFYITDVPNGFHVLEKEM
 PTEGEDLKLSTVNVKFLYRDVITLLTRVNNRMHYSISKQMAITKHSITLNLTIM
 NVSLQDSGTACRARNYTGTEILQKKEITRDOEAPYLLRNLSHDHTVAISSLTLD
 HANGVPEPQITWTKNNHKIOEPGIIILGCSSTLFERTVEDEGVYHCKATNOKGSV
 ESSAYLTVOGTSKSNLELITLCTCAVATLFWLLTLFLRKMKRSSEIKTDYLSII
 MDPEVPLDQCEPRLPYDASKWEARERLKGLSGRGAFGVQVQASAFGIKSPKTCR
 TVAVMLKCATASEYKALMTLKLILHIGHLNVNLLGACTKOGGLMWIVYECYK
 GNLSYLUKSRDLFFLNKDAALHMEPKKEMPEGLQGGKPRLDSTVSSEFASGFO
 EDKSLSDVEEEDSDGYPKEPIITMEDILSYFQVARGMEFLSSRKCIRDLAARNILL
 SENNVVICDFGLARDIYKNPDYVRKGDTRLPKWMAPESIFDKIYSTKSDVMSYGLV
 LWEIFSLGGSPYQVQMEDFCRSLREGMRAPYSTPEIYQIMLDCHHRDPKPRPR
 FAELVEKLDLLQANVQDCKDYPINAILTGNSGTYSTPAFSEDFKHSISAPKFN
 SGSSDDVRYVNAFKENSLEKIKTFEELLNPATSMFDYQDSDSTLLASPMLKRFMTWD
 SKPKRASKIDLURVTSKSGSLSDVSRPSCFSSCSGHVSEGRKRRFTYDHAELERKIAC
 CSPPPDYNVVLVSTPPI"

BASE COUNT 1236 a 915 c 903 g 963 t
 ORIGIN

Query Match 6.68; Score 20; DB 9; Length 4017;
 Best Local Similarity 100.0%; Pred. No. 12;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 106 gtgaatctgaagagg 125
 Db 2578 GTGAATCTGGAAGAGG 2597

RESULT 20
 AB065372 4272 bp mRNA linear VRT 13-FEB-2002
 LOCUS
 DEFINITION Gallus gallus mRNA for vascular endothelial growth factor
 receptor-1, complete cds.
 AB065372
 ACCESSION
 VERSION AB065372.1 GI:18652860
 KEYWORDS

SOURCE
 ORGANISM

Gallus gallus tissue:whole embryo mRNA.

Gallus gallus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
 Phasianinae; Gallus.

REFERENCE 1 (sites)

Yamauchi, S., Iwata, K. and Shibuya, M.

Soluble Flt-1 (VEGFR-1), a potent natural antiangiogenic molecule
 in mammals, is phylogenetically conserved in avians

Unpublished

REFERENCE 2 (bases 1 to 4272)

Shibuya, M.

Direct Submission

Submitted (11-JUL-2001) Masabumi Shibuya, University of Tokyo,
 Institute of Medical Science; 4-6-1 Shirokane-dai, Minato-ku, Tokyo,
 108-8639, Japan (E-mail:shibuya@ims.u-tokyo.ac.jp,
 Tel:81-3-5449-5550, Fax:81-3-5449-5425)

FEATURES

Location/Qualifiers

1..4272

/organism="Gallus gallus"

/db_xref="taxon:9031"

/tissue_lib="whole embryo"

267..4250

/gene="vegfr-1"

267..4250

/gene="vegfr-1"

/note="flt-1"

fms-like tyrosine kinase-1"

/codon_start=1

/product="vascular endothelial growth factor receptor-1"

/protein_id="BAB84690.1"

/db_xref="GI:18652861"

/translation="MPROLLSGTVLLGAFLLAGSTSGSKLKVPLSVNGRQHVQAG
 QTLNLTCEGMLHMSLPEALSKDRLNVTKYACGRNGTQFCSTLTLSRTOANDTGR
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 IAVTLKIPRETLIPDGKTIIDNNRGPRIPEATYRIFGLLSCETIGGHKYSKYLT
 HRETNIIDKLSPLVKLLGDSLATNCTKAARVQMTVYTGCAKRGSVTQ
 RIDOKNRANFYSLVIDKVRDIDKQYACHVKSFNKLYNTTVIVDKRFINLAR
 RRKTMLEAVAGKSRTRLPKMKVAFSPVETWLDGLPAAEKARYMKNLSLIKDVA
 EEDAGNPITLILKRWNLKSLNLTVLKNVKNPQIYENAVSFPDPLNLLSSKOVLTG
 TVYGPPKTIPTMMPYPCRNHKSRTGFCSTGPNLKTGNSIGNRQISIIERTAILI
 EGKNTASTLVAAEAKSGIYSCVSNKVGKAERNVFLVTPVSPGHISLEKVPLEG
 ENLVSCSANKFMYKDISWILPRTVNTQARKALNKEYSITLTLTRNVSLAHSCTY
 TCARNIFTEGVLQKDVSTRQAEAPALLRQMDPNTSNMACEQVHGIPQPI
 TWKNHEIQEESIILGPGSRMLFERVAEEDGLQCIATNLKGSVESTATVTVOG
 TVESNLELITLCTCAVATLFWLLTLFLRKLRPFVSETKTNHYSLSIIDPEVPL
 DEQCELPYDASKWEARERLKGLSGRGAFGVQVQASAFGIKSPKTCRIVAKMLK
 EGATASEYKALMTLKLILHIGHLNVNLLGACTKNGGPLVIVYECYGNLSYGLV
 SKRNFFSPTKDPISLQGLMKDKGIEPVEGKKORLASVTSSESFASSGQEDKSLDA
 EDEDEAAELYKLPLTWEDLISYFQVARGMEFLSSRKCIRDLAARNILLSENMYK
 ICDFGLARDIYKNPDYVRKGDARLPKWMAPESIFDKIYNKSDVMSYGLLMEIFSL
 CASPYGVQIDEDFCRSLREGMRAPQEATEIYQIMLDCHRSNPNRPFSELYKR
 LGDLJQASVQOEGKDIPLDITFAESGFPASPDLCKNEKFPVSPNCRSTERYIN
 TFKIPPORIKTFEELPKELVNDYQADSGMVLASEELKRFMTWTSKQKWTFCMK
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 HYSQPSI"

BASE COUNT 1266 a 1001 c 1083 g 922 t
 ORIGIN

Query Match 6.68; Score 20; DB 5; Length 4272;
 Best Local Similarity 100.0%; Pred. No. 12;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 34 ggcgccttcgggaaggtgg 53
 Db 2748 GGCGCCTTCGGGAAGGTGGT 2767

RESULT 21

HSFLT

LOCUS

DEFINITION Human flt mRNA for receptor-related tyrosine kinase.
 HSFLT 7680 bp mRNA linear PRI 15-NOV-1993

ACCESSION	X51602	QY	106	gtgaaaaatgctgaagagg	125
VERSION	X51602.1	Db	2827	gtgaaaaatgctgaagagg	2846
KEYWORDS	flt gene: fms-related tyrosine kinase gene; tyrosine kinase.				
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
AUTHORS	1 (bases 1 to 7680)				
TITLE	Shibuya, M.				
JOURNAL	Submitted (02-JAN-1989) Shibuya M., Institute of Medical Science, University of Tokyo, 4-6-1 Shirokane-dai, Minato-ku, Tokyo 108, Japan				
REFERENCE	2 (bases 1 to 7680)				
AUTHORS	Shibuya, M., Yamaguchi, S., Yamane, A., Ikeda, T., Tojo, A., Matsushima, H. and Sato, M.				
TITLE	Nucleotide sequence and expression of a novel human receptor-type tyrosine kinase gene (flt) closely related to the fms family				
JOURNAL	Oncogene 5 (4), 519-524 (1990)				
MEDLINE	90221591				
REFERENCE	3 (bases 1 to 7680)				
AUTHORS	Han, H.J., Fujiwara, T., Shin, S. and Nakamura, Y.				
TITLE	Dinucleotide repeat polymorphism in the 3' non-coding region of the FLT1 gene				
JOURNAL	Hum. Mol. Genet. 2 (12), 2204 (1993)				
MEDLINE	94154724				
COMMENT	Data kindly reviewed (20-JUL-1990) by Shibuya M.				
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	/clone="3-7, 3-5"				
	/tissue_type="placenta"				
	250..4266				
	/note="flt gene product (AA 1-1338)"				
	/codon_start=1				
	/protein_id="CAA35946.1"				
	/db_xref="GI:31432"				
	/db_xref="SWISS-PROT:P17948"				
	/translation="MVSYMDTGVLICALLSCLLLTGTSSGSKLKDPELSLKGTOHIMQ AGOTLHLCRGAAHKWSLPEWVSKESERLSITKSACRNGKQFCSTLTLTNAQNHIT GPYSCKYLAIVPTSKKTESAIYIPISDTGRPFVEMVSEIPEIIMHTGRELVI PCRV TSPNTVTLKFPDLTIPDGKRIIWDGSKGFIISNATYKEIGLLTCEATVNGHLYKT NVLRHRONTIIDVOISTPRPVKLHGLTILNCTATTPLNTRVQMTSPYDEKNKRA SVRRIDGNSHANIFYSVLTIDKMNKDKGLYTCRVSRGSPFSKSVNTSVHIDKAFI TVKHKQOVLETAVAGKSYRLSMKVAFPSPEVWMLKDLGPATEKSARYLTRYSLII KDVTEDAGNTVILLIKQSNVFNLTATLIVNVKPOLYKAVSFPPDAPLYLGSRO ILTCTAYGIPDPTIKFWHPCHNHSEARCFCSNNEESFILDADSNMGNIESTTOR MAIIEGKNKMASTLVVADSRISGIYICIASNKVGTGVNISFYITDPNGPHVNLKRM PTEGEDKLCTSVNKFYRDVTWILLRTVNNRTHYISIKQMAITKEHSITLNTIM NVSLQDSGTACRARNVYTGEEILQKKEITIRQEAAPYLLRNLSOHTVAISSTLTDG HANGVPEQITWFKNNHKIQOEPGIIILGSGSTLFIERVTEDEGVYHCKATNGKGS ESSAYLTVOGTSKSNLELITLTCTCVATLFWLLLLIIRKMRSSSEIKTDLSII MDQPEVLDEOCERLPYDASKEWFAFERKLKGLSGRGAFCVVOASAFGLIKK3PCR TVAVKMLGEGATSEYKALMTLKLTHIGHLVNVLNLLGACTKQGLGFLVIVYCYK GNLSYLSKSRDLFLNKAALHMEPKERKEPGLQCKPKRDSVTSSSFASGQ EDLSLSEEDDESDGFYKEPITMEDLISYSFOVARGMEFLSSRKCIRHLDARNILL SENNVVKICDFGLARDIYKNPDYVRKGDTRLPLKMAPESIFDKLYTSKSDWNSYGLV LWEIFLGSQSPYQVONDEDFCSRLRGRMRAREYSTPEIYQIMLDCWHDRKPRR FAELVEKLCDLLQANVQODGKDIPIINALITGNSGFTSYTFAFSEDFKESISAPKRN SGSSDDVRYVNAFKPMSLERIKTFEELLPNATSMFDDYQGDSTLLASPMKRFETWD SKPKASLKIDLRVTSKSKESGLSDVSRPSFCHSCSGHVEGSKRFRFTYDHAELERKIIAC CSPPPDVSNNVLYSTPPI"				
BASE COUNT	2279 a 1661 c 1739 g 2001 t				
ORIGIN					
Query Match	6.6%; Score 20; DB 9; Length 7680;				
Best Local Similarity	100.0%; Pred. No. 12;				
Matches	20: Conservative 0; Mismatches 0; Indels 0; Gaps 0;				

LOCUS	SC9C7	31360 bp	DNA	linear	BCT 12-JAN-1999
DEFINITION	Streptomyces coelicolor cosmid 9C7.				
ACCESSION	AL035161				
VERSION	AL035161.1	GI:4154059			
KEYWORDS	acetyltransferase; acyl-CoA dehydrogenase; acyl-peptide hydrolase; aminocyclase; ccr; coenzyme B12-dependent mutase; crotonyl CoA reductase; efflux protein; lyase; meaa; oxidoreductase; peptidase; tetR family; transcriptional regulator.				
SOURCE	Streptomyces coelicolor A3(2).				
ORGANISM	Streptomyces coelicolor A3(2).				
REFERENCE	1 (bases 1 to 31360)				
AUTHORS	Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.				
JOURNAL	Seeger, K.J. and Harris, D.				
REFERENCE	2 (bases 1 to 31360)				
AUTHORS	Unpublished				
JOURNAL	Bentley, S.D., Parkhill, J., Barrell, B.G. and Rajandream, M.A.				
REFERENCE	Submitted (08-JAN-1999) Streptomyces coelicolor sequencing project, Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA E-mail: barrell@sanger.ac.uk Cosmids supplied by Prof. David A. Hopwood, [3] John Innes Centre, Norwich Research Park, Colney, Norwich, Norfolk NR4 7UH, UK				
AUTHORS	3 (bases 1 to 31360)				
TITLE	Redenbach, M., Kieser, H.M., Denapaita, D., Eichner, A., Cullum, J., Kinashi, H. and Hopwood, D.A.				
JOURNAL	A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome				
MEDLINE	Mol. Microbiol. 21 (1), 77-96 (1996)				
COMMENT	97000351				
	Notes:				
	Streptomyces coelicolor sequencing at The Sanger Centre is funded by the BBSRC.				
	Details of S. coelicolor sequencing at the Sanger Centre are available on the World Wide Web.				
	(URL: http://www.sanger.ac.uk/Projects/S_coelicolor/) CDS are numbered using the following system eg SC7B7.01c. SC (S. coelicolor), 7B7 (cosmid name), .01 (first CDS), c (complementary strand).				
	The more significant matches with motifs in the PROSITE database are also included but some of these may be fortuitous. The length in codons is given for each CDS.				
	Usually the highest scoring match found by fasta -o is given for CDS which show significant similarity to other CDS in the database. The position of possible ribosome binding site sequences are given where these have been used to deduce the initiation codon. Gene prediction is based on positional base preference in codons using a specially developed Hidden Markov Model (Krogh et al., Nucleic Acids Research, 22(22):4768-4778(1994)) and the Frameplot program of Bibb et al., Gene 30:157-66(1984) as implemented at http://www.nih.go.jp/jun/cgi-bin/frameplot.pl .				
	CAUTION: We may not have predicted the correct initiation codon. Where possible we choose an initiation codon (atg, gtg, ttg or att) which is preceded by an upstream ribosome binding site sequence (optimally 5-13bp before the initiation codon). If this cannot be identified we choose the most upstream initiation codon.				
	IMPORTANT: This sequence MAY NOT be the entire insert of the sequenced clone. It may be shorter because we only sequence overlapping sections once, or longer, because we arrange for a small overlap between neighbouring submissions. Cosmid 9C7 lies between 1A1 and 1E6 on the AseI-A genomic restriction d fragment.				
FEATURES	Location/Qualifiers				
source	1..31360				
	/organism="Streptomyces coelicolor A3(2)"				
	/strain="A3(2)"				


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/clone="cosmid 9C7"
complement(1..147)
/genes="SC9C7.01c"
complement(<1..147)
/genes="SC9C7.01c"
/notes="SC9C7.01c, partial CDS, unknown, len: 49aa;
overlapping extreme N-terminal region of partial CDS,
SC1A11.2c from Streptomyces coelicolor cosmid 1A11."
/codon_start=1
/transl_table=1
/product="hypothetical protein SC9C7.01c"
/protein_id="CAA22713.1"
/db_xref="GI:4154060"
/translation="MTADYATYIAGLPRVLGAAAVPRDAAGRVLVVEPNVREGMAL
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1..112
/notes="Overlap with SC1A11 Streptomyces coelicolor cosmid
1A11."
332..1474
/genes="SC9C7.02"
332..1474
/genes="SC9C7.02"
/notes="SC9C7.02, conserved hypothetical protein, len:
380aa; similar to many eg. SW:YXAA_BACSU hypothetical
protein from Bacillus subtilis (382 aa) fasta scores; opt:
1045, z-score: 998.9, E(): 0, (46.3% identity in 374 aa
overlap)."
/codon_start=1
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/product="conserved hypothetical protein"
/protein_id="CAA22714.1"
/db_xref="GI:4154061"
/translation="MDGTRVLVAADKFKGSLTAVEAERVVTAGLRVRVVDVLVEALP
VADGGCTVAAAVAGFERREARVAGPLCEEVTAAYALRGOTAVVMEAASGLQLRPE
GVLPALPTSTYSGELLRAALDAGARTIVFGVGGATDLDGGAGMLAALGARFLDNGE
VPVAGGGGLAGLVSDLSGLDSRLSDVELVSLASDVNDPLTGPKGAPVYGPKGASPD
DTYDALAHAFKVLRTGEGVRAAEYVAAAPGAGGIGFGAGMLLGRFRPGIEV
MLDVLGFALERADLVITGEGSLDEQTLHGKAPAGVAAAARAAAGKGVAVVAGGRALP
AEVLGRAGIRRAYPLTVDPEPOVAKCIADAGPLIVERVAESIARDELA"
complement(1744..2526)
/genes="SC9C7.03c"
complement(1744..2526)
/genes="SC9C7.03c"
/notes="SC9C7.03c, probable integral membrane protein,
possible phosphatidylserine synthase, len: 260aa; similar
to many from prokaryotes (all putative) and eukaryotes eg.
SW:PSS_YEAST phosphatidylserine synthase from
Saccharomyces cerevisiae (275 aa) fasta scores; opt: 187,
z-score: 258.6, E(): 6.8e-07, (35.9% identity in 170 aa
overlap). Contains possible membrane spanning regions."
/codon_start=1
/transl_table=1
/product="putative phosphatidylserine synthase"
/protein_id="CAA22715.1"
/db_xref="GI:4154062"
/translation="MPLSLRLSIADTLTLGNATCGFMAVYFTTTGILPHLMGDSDESG
MARHSAATAVILMLCAAIFDLFDGLVARKLRSSPMGAELDNLSISFLGAPAYFLV
YGMVADDAVQVAAVAVVLLAVLRARFSCVTVKDGTFQGMSPSPFGALTVVSIVL
LELPVATLLAILGTAWLMVSRVEYKPKRGLAVAMLSKIVLSMGLLAGWAFDAPSGQ
LLLOTGCALOLVAGVIPLEATARRVNRFRNRARAQLP"
complement(2585..3241)
/genes="SC9C7.04c"
complement(2585..3241)
/genes="SC9C7.04c"
/notes="SC9C7.04c, conserved hypothetical protein, len:
218aa; similar to several hypothetical proteins eg.
TR:O271105 (EMBL:AE000875) Methanobacterium
thermoautotrophicum (223 aa) fasta scores; opt: 405,
z-score: 712.9, E(): 2e-32, (39.2% identity in 212 aa
overlap)."
/codon_start=1
/transl_table=1

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/protein_id="CAA22716.1"
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TAKAVAPATALAAGMLWFRDPEREITQGRVVPADGVQVQSIIMPKDGRTRVAIFMS
PLNVHVNRPAGLTVTSEVHPVGGVPAFNRKESNNERNVYHMFOTELGDIEMIQIAGA
VARRIVPVPGTKVQEGERVGLIRFGSRVDLYLPVEGVDEVVEGQTKVAGVTRIDRD"
complement(3412..4617)
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complement(3412..4617)
/genes="SC9C7.05c"
/notes="SC9C7.05c, possible acyl-CoA dehydrogenase, len:
401aa; similar to many from prokaryotes and eukaryotes
egs. SW:ACDB_BACSU acyl-CoA dehydrogenase from Bacillus
subtilis (379 aa) fasta scores; opt: 520, z-score: 1209.6,
E(): 0, (38.9% identity in 386 aa overlap) and
SW:ACDM_MOUSE acyl-CoA dehydrogenase from Mus musculus
(mouse) (421 aa) fasta scores; opt: 484, z-score: 1178.1,
E(): 0, (40.3% identity in 390 aa overlap). Contains Pfam
match to entry PF00441 Acyl-CoA_dh, Acyl-CoA
dehydrogenase."
/codon_start=1
/transl_table=1
/product="putative acyl-CoA dehydrogenase"
/protein_id="CAA22717.1"
/db_xref="GI:4154064"
/translation="MSRLAQTHGLTVDVOREILSTVRFVDKELIIPVATELEHREDEYPO
DIVGLKELGLFLGMLPIPEEYGGGLGESLLTYALCVETIARGMWSGIINTHFIYAYML
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LTNGQTSLLVALVLYKSDGHPGEGTAPHKSMITFLVEKEPGEVRPGTLTIPGKIDKMG
YKGVDTTELINDGLRIPANRVLGVTGREGYQMDGVGVGRVNVAAKRCGVAORAFEL
GVRYAQDRHTGKQIAHQAOIAQFKAENATYVEAAHAMVYNAARKKDSGERNDLEACH
AKYLASEYCKEVEDAFRIHGYGFGFSKEYETIERLYREAPMLLIGGTAEIOMNLIIGRR
LLEERFQG"
complement(3445..4590)
/genes="SC9C7.05c"
/notes="Pfam match to entry PF00441 Acyl-CoA_dh, Acyl-CoA
dehydrogenase."
complement(4620..5132)
/genes="SC9C7.06c"
complement(4620..5132)
/genes="SC9C7.06c"
/notes="SC9C7.06c, unknown, len: 170aa; similar to
TR:006163 (EMBL:Z95556) from Mycobacterium tuberculosis
(185 aa) fasta scores; opt: 342, z-score: 497.2, E():
2.1e-20, (38.8% identity in 152 aa overlap)."
/codon_start=1
/transl_table=1
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/protein_id="CAA22718.1"
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DANYAERTDFGKNVYVGNIIYLLGLMSVPDVGSKAJANLEISLKHVAPTFPHGDTV
YGQTVLDKNKPSKKNDRGINVHTGKYKQDGLVCFVRKVMVPTETTYTKERGGEQ
GRPELKEQG"
complement(5138..6157)
/genes="SC9C7.07c"
complement(5138..6157)
/genes="SC9C7.07c"
/notes="SC9C7.07c, probable lyase, len: 339aa; similar to

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Query Match      6.6%; Score 20; DB 1; Length 31360;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  24  gctcggtacggcgcttcg 43
      |||||
Db  30332  GCTCGGCTACGGCGCTTCG 30351

RESULT 23
AC108477

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LOCUS AC108477 208304 bp DNA linear HTG 31-JAN-2002
DEFINITION Homo sapiens chromosome 4 clone RP11-499F19, WORKING DRAFT
SEQUENCE, 11 unordered pieces.
ACCESSION AC108477
VERSION AC108477.3 GI:18450208
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 208304)
Waterston,R.H.
The sequence of Homo sapiens clone
Unpublished
REFERENCE 2 (bases 1 to 208304)
Waterston,R.H.
Direct Submission
Submitted (28-JAN-2002) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
COMMENT On Jan 31, 2002 this sequence version replaced gi:18425327.

----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: <http://genome.wustl.edu/gsc/index.shtml>
Contact: submissions@watson.wustl.edu
----- Project Information -----
Center project name: H_NH0499F19
----- Summary Statistics -----
Sequencing vector: M13; 0%
Sequencing method: plasmid; 100%
Chemistry: Dye-primer ET: 0% of reads
Assembly: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 202880 bases at least Q40
Consensus quality: 204376 bases at least Q30
Consensus quality: 205294 bases at least Q20
Insert size: 214000; agarose-fp
Insert size: 207304; sum-of-contigs
Quality coverage: 6.00 in Q20 bases; agarose-fp
Quality coverage: 6.25 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently
* consists of 11 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 2413: contig of 2413 bp in length
* 2414 2513: gap of unknown length
* 2514 4904: contig of 2391 bp in length
* 4905 5004: gap of unknown length
* 5005 9186: contig of 4182 bp in length
* 9187 9286: gap of unknown length
* 9287 17047: contig of 7761 bp in length
* 17048 17148: gap of unknown length
* 17148 32645: contig of 15498 bp in length
* 32646 32745: gap of unknown length
* 32746 48233: contig of 15488 bp in length
* 48234 48334: gap of unknown length
* 48334 82527: contig of 34194 bp in length
* 82528 82628: gap of unknown length
* 82628 100081: contig of 17454 bp in length
* 100082 100182: gap of unknown length
* 100182 123584: contig of 23403 bp in length
* 123585 123685: gap of unknown length
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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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LOCUS Streptomyces avermitilis polyene macrolide biosynthetic gene
DEFINITION cluster.
ACCESSION AB070949
VERSION AB070949.1 GI:15824136
KEYWORDS Streptomyces avermitilis DNA.
SOURCE Streptomyces avermitilis
ORGANISM Streptomyces avermitilis
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
REFERENCE 1 (bases 1 to 78210)
AUTHORS Omura,S., Ikeda,H., Ishikawa,J., Hanamoto,A., Takahashi,C.,
Shinose,M., Takahashi,Y., Horikawa,H., Nakazawa,H., Osonoe,T.,
Kikuchi,H., Shiba,T., Sakaki,Y. and Hattori,M.
TITLE Genome sequence of an industrial microorganism Streptomyces
avermitilis: Deducing the ability of producing secondary
metabolites
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 98 (21), 12215-12220 (2001)
PUBMED 11572948
REFERENCE 2 (bases 1 to 78210)
AUTHORS Ikeda,H.
TITLE Direct Submission
JOURNAL Submitted (01-SEP-2001) Haruo Ikeda, Kitasato University, Dept. of
Microbial Chemistry, School of Pharmaceutical Sciences, 5-9-1
Shirokane, Minato-ku, Tokyo 108-8641, Japan
(E-mail:ikedamc.pharm.kitasato-u.ac.jp, Tel:+81-3-5791-6242,
Fax:+81-3-3444-6197)
FEATURES Location/Qualifiers

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CDS	

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Db 18064 TCCACAGGGCAGCAGCTG 18082
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AC105566
LOCUS
DEFINITION Rattus norvegicus clone CH230-250A15, *** SEQUENCING IN PROGRESS
***, 61 unordered pieces.
AC105566 119916 bp DNA linear HTG 09-JAN-2002
AC105566.1 GI:18092788
VERSION HTG; HTGS_PHASE1.
KEYWORDS Norway rat.
SOURCE Rattus norvegicus
ORGANISM
Eukaryota; Metazoa
Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE
1 (bases 1 to 119916)
AUTHORS
Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-Osman,F.R., Allen,C.,
Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Banks,T., Barbara,J.,
Benton,J., Bimage,K., Blankenburg,K., Bonnin,D., Bouck,J.,
Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P., Buhay,C.,
Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C., Carron,T.F.,
Carter,M., Cavazos,S.R., Chacko,J., Chavez,D., Chen,G., Chen,R.,
Chen,Z., Chowdhry,I., Christopoulos,C., Cleveland,C.D., Cox,C.,
Coyle,M.D., Dathorne,S.R., David,R., Davila,M.L., Davis,C.,
Davy-Carroll,L., Dederich,D.A., Delaney,K.R., Delgado,O.,
Denn,A.L., Ding,Y., Dinh,H.H., Douthwaite,K.J., Draper,H.,
Dugan-Rocha,S., Durbin,K.J., Earnhart,C., Edgar,D., Edwards,C.C.,
Elhaj,C., Escotto,M., Falls,T., Ferraguto,D., Flagg,N., Ford,J.,
Foster,P., Frantz,P., Gabisi,A., Gao,J., Garcia,A., Garner,T.,
Garza,N., Gill,R., Gorrell,J.H., Guevara,W., Gunaratne,P., Hale,S.,
Hamilton,K., Harris,C., Harris,K., Hart,M., Havlik,P., Hawes,A.,
Hernandez,J., Hernandez,O., Hodgson,A., Hogues,M., Hollaway,C.,
Hollins,B., Homsli,F., Howard,S., Huber,J., Hulyk,S., Hume,J.,
Jackson,L.E., Jacobson,B., Jia,Y., Johnson,R., Jolivet,S.,
Joudah,S., Karlsson,E., Kelly,S., Khan,U., King,L., Korvah,J.,
Kovar,C., Kratovic,J., Kureshi,A., Landry,N., Leal,B., Lewis,L.C.,
Lewis,L., Li,J., Li,Z., Lichtarge,O., Lieu,C., Liu,J., Liu,W.,
Louisegh,H., Lozado,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R.,
Ma,J., Maheshwari,M., Mapua,P., Martin,R., Martindale,A.,
Martinez,E., Massey,E., Mawhiney,E., McLeod,M.P., Meador,M.,
Mel,G., Metzker,M., Miner,G., Miner,Z., Mitchell,T., Mohabbat,K.,
Morgan,M., Morris,S., Moser,M., Neal,D., Newton,J., Newton,N.,
Nguyen,A., Nguyen,N., Nguyen,N., Nickerson,E., Nwokenkwo,S.,
Ogun,M., Okwuonu,G., Oragunye,N., Oviedo,R., Pace,A., Payton,B.,
Peery,J., Perez,L., Peters,L., Pickens,R., Primus,E., Pu,L.L.,
Quiles,M., Ren,Y., Rives,M., Rojas,A., Rojubokan,I., Rolfe,M.,

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Ruiz,S., Savery,G., Scherer,S., Scott,G., Shen,H., Shooshtari,N.,
Sisson,I., Sodergren,E., Sonaike,T., Sparks,A., Stanley,H.,
Stone,H., Sutton,A., Svalek,A., Tabor,P., Tamerisa,A., Tamerisa,K.,
Tang,H., Tansey,J., Taylor,C., Taylor,T., Telford,B., Thomas,N.,
Thomas,S., Usmani,K., Vasquez,L., Vera,V., Villalon,D., Vinson,R.,
Wall,R., Wang,S., Ward-Moore,S., Warren,R., Washington,C.,
Watlington,S., Williams,G., Williamson,A., Wleczek,R., Wooden,S.,
Worley,K., Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D.,
Weinstock,C. and Gibbs,R.
Direct Submission
Unpublished
2 (bases 1 to 119916)
Worley,K.C.
Direct Submission
Submitted (09-JAN-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Bay Plaza, Houston, TX 77030, USA
----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: GNFC
Center clone name: CH230-250A15
----- Summary Statistics
Assembly program: Phrap; version 0.990329First call to
findPhrapList
Consensus quality: 85751 bases at least Q40
Consensus quality: 93994 bases at least Q30
Consensus quality: 102334 bases at least Q20
Estimated insert size: 82500; sum-of-contigs estimation
Quality coverage: 0x in Q20 bases; agarose-fp estimation
Quality coverage: 0.9x in Q20 bases; sum-of-contigs estimation
-----
* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 61 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
* 1 5417: contig of 5417 bp in length
* 5418 5517: gap of unknown length
* 5518 9404: contig of 3887 bp in length
* 9405 9504: gap of unknown length
* 9505 12699: contig of 3195 bp in length
* 12700 12799: gap of unknown length
* 12800 16317: contig of 3518 bp in length
* 16318 16417: gap of unknown length
* 16418 19344: contig of 2927 bp in length
* 19345 19444: gap of unknown length
* 19445 22566: contig of 3121 bp in length
* 22566 22665: gap of unknown length
* 22666 24996: contig of 2331 bp in length
* 24997 25096: gap of unknown length
* 25097 27065: contig of 1969 bp in length
* 27066 27165: gap of unknown length
* 27166 29582: contig of 2417 bp in length
* 29583 32613: contig of 2931 bp in length
* 32614 35399: contig of 2686 bp in length
* 35400 37557: gap of unknown length
* 37558 37657: gap of unknown length
* 37658 39153: contig of 1496 bp in length
* 39154 39253: gap of unknown length
* 39254 41229: contig of 1976 bp in length
* 41230 41329: gap of unknown length
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* 41330 43186: contig of 1857 bp in length
* 43187 43286: gap of unknown length
* 43287 45418: contig of 2132 bp in length
* 45419 45518: gap of unknown length
* 45519 47831: contig of 2313 bp in length
* 47832 47931: gap of unknown length
* 47932 49971: contig of 2040 bp in length
* 49972 50071: gap of unknown length
* 50072 51780: contig of 1709 bp in length
* 51781 51880: gap of unknown length
* 51881 53936: contig of 2056 bp in length
* 53937 54036: gap of unknown length
* 54037 56155: contig of 2119 bp in length
* 56156 56255: gap of unknown length
* 56256 58719: contig of 2464 bp in length
* 58720 58819: gap of unknown length
* 58820 60750: contig of 1931 bp in length
* 60751 60850: gap of unknown length
* 60851 61864: contig of 1014 bp in length
* 61865 61964: gap of unknown length
* 61965 63634: contig of 1670 bp in length
* 63635 63734: gap of unknown length
* 63735 65377: contig of 1643 bp in length
* 65378 65477: gap of unknown length
* 65478 66638: contig of 1161 bp in length
* 66639 66738: gap of unknown length
* 66739 67981: contig of 1242 bp in length
* 67982 68080: gap of unknown length
* 68081 69888: contig of 1808 bp in length
* 69889 71664: gap of unknown length
* 71665 71765: gap of unknown length
* 71766 73378: contig of 1614 bp in length
* 73379 73478: gap of unknown length
* 73479 74629: contig of 1151 bp in length
* 74630 74729: gap of unknown length
* 74730 75903: contig of 1174 bp in length
* 75904 76003: gap of unknown length
* 76004 77278: contig of 1275 bp in length
* 77279 77378: gap of unknown length
* 77379 79018: contig of 1640 bp in length
* 79019 79118: gap of unknown length
* 79119 80815: gap of unknown length
* 80816 83063: contig of 2248 bp in length
* 83064 83163: gap of unknown length
* 83164 85404: contig of 2241 bp in length
* 85405 85504: gap of unknown length
* 85505 87875: contig of 2371 bp in length
* 87876 87975: gap of unknown length
* 87976 89148: contig of 1173 bp in length
* 89149 89248: gap of unknown length
* 89249 91394: contig of 2146 bp in length
* 91395 92791: contig of 1297 bp in length
* 92792 92891: gap of unknown length
* 92892 94174: contig of 1283 bp in length
* 94175 94275: gap of unknown length
* 94276 95295: contig of 1021 bp in length
* 95296 95395: gap of unknown length
* 95396 96788: contig of 1393 bp in length
* 96789 96888: gap of unknown length
* 96889 98468: contig of 1580 bp in length
* 98469 98568: gap of unknown length
* 98569 99706: contig of 1138 bp in length
* 99707 99806: gap of unknown length
* 99807 101157: contig of 1351 bp in length
* 101158 101257: gap of unknown length
* 101258 103154: contig of 1897 bp in length
* 103155 104442: gap of unknown length
* 104443 104543: gap of unknown length
* 104544 105711: contig of 1169 bp in length

```

TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL

COMMENT

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* 105712 105811: gap of unknown length
* 105812 106936: contig of 1125 bp in length
* 106937 107036: gap of unknown length
* 107037 108459: contig of 1423 bp in length
* 108460 108559: gap of unknown length
* 108560 109929: contig of 1370 bp in length
* 109930 110029: gap of unknown length
* 110030 111272: contig of 1243 bp in length
* 111273 111373: gap of unknown length
* 111374 112564: contig of 1192 bp in length
* 112565 112664: gap of unknown length
* 112665 114426: contig of 1762 bp in length

Query Match      6.3%; Score 19; DB 2; Length 119916;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 106 gtgaataatctgaagagg 124
      |||||
DB 44969 GTGAAATCTGAAGAGG 44987

RESULT 27
AC106084
LOCUS      AC106084
DEFINITION Rattus norvegicus clone CH230-121C20, *** SEQUENCING IN PROGRESS HTG 12-JAN-2002
ACCESSION AC106084
VERSION    AC106084.1 GI:18138599
KEYWORDS   HTG; HTGS-PHASE1.
SOURCE     Norway rat.
ORGANISM   Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
            1 (bases 1 to 155825)
            Muzny D.M., Adams C., Adio-Oduola B., Ali-Osman, F.R., Allen, C.,
            Alsbrooks, S.L., Amarantunga, H.C., Are, J.R., Banks, T., Barbarella, J.,
            Benton, J., Bimaga, K., Blankenburg, K., Bonnin, D., Bouck, J.,
            Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Buhay, C.,
            Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T.F.,
            Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, R.,
            Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C.,
            Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C.,
            Davy-Carroll, L., Dederich, D.A., Delaney, K.R., Delgado, O.,
            Denn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, H.,
            Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C.C.,
            Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J.,
            Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T.,
            Garza, N., Gill, R., Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S.,
            Hernandez, J., Hernandez, O., Hodgson, A., Hogues, M., Holloway, C.,
            Hollins, B., Homs, F., Howard, S., Huber, J., Hulyk, S., Hume, J.,
            Jackson, L.E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S.,
            Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J.,
            Kovar, C., Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C.,
            Lewis, L., Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W.,
            Lousegh, H., Lozado, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R.,
            Ma, J., Maheshwari, M., Mapa, P., Martin, R., Martindale, A.,
            Martinez, E., Massey, E., Mawhiney, E., McLeod, M.P., Meador, M.,
            Mei, G., Metzger, M., Miner, G., Miner, Z., Mitchell, T., Mohabbat, K.,
            Morgan, M., Morris, S., Moser, M., Neale, D., Newton, J., Newton, N.,
            Nguyen, A., Nguyen, N., Nguyen, N., Nickerson, E., Nwokwen, S.,
            Oguh, M., Okwunonu, G., Oragunye, N., Oviedo, R., Pace, A., Payton, B.,
            Peery, J., Perez, L., Peters, L., Pickens, R., Primus, E., Pu, L.L.,
            Quiles, M., Ren, Y., Rivers, M., Rojas, A., Rojubokan, I., Rolfe, M.,
            Ruiz, S., Savory, G., Scherer, S., Scott, G., Shen, H., Shoohtari, N.,
            Sisson, I., Sodergren, E., Sonaike, T., Sparks, A., Stanley, H.,
            Stone, H., Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K.,
            Tang, H., Tansey, J., Taylor, C., Taylor, T., Telford, B., Thomas, N.,
            Thomas, S., Usmani, K., Vasquez, L., Vera, V., Villalob, D., Vinson, R.,
            Wall, R., Wang, S., Ward-Moore, S., Warren, R., Washington, C.,
            Watlington, S., Williams, G., Williamson, A., Wleczyk, R., Wooden, S.,

```

TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL

Worley, K., Wu, C., Wu, Y., Wu, Y.F., Zhou, J., Zorrilla, S., Nelson, D.,
Weinstock, G., and Gibbs, R.
Direct Submission
Unpublished
2 (bases 1 to 155825)
Worley, K.C.
Direct Submission
Submitted (12-JAN-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA

Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu

Project Information
Center project name: GHHP
Center clone name: CH230-121C20

Summary Statistics
Assembly program: Phrap; version 0.990329First call to
findPhrapList

COMMENT

Consensus quality: 123657 bases at least Q40
Consensus quality: 132258 bases at least Q30
Consensus quality: 137884 bases at least Q20
Estimated insert size: 107272; sum-of-contigs estimation
Quality coverage: 0x in Q20 bases; agarose-fp estimation
Quality coverage: 1.4x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 76 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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* 1 7184: contig of 7184 bp in length
* 7185 7284: gap of unknown length
* 7285 15297: contig of 8013 bp in length
* 15298 18433: contig of unknown length
* 18434 18533: contig of 3036 bp in length
* 18534 22113: contig of unknown length
* 22114 22213: gap of 3580 bp in length
* 22214 26552: contig of 4439 bp in length
* 26553 30160: contig of 3408 bp in length
* 30161 32493: contig of 2233 bp in length
* 32494 32593: gap of unknown length
* 32594 36039: contig of 3446 bp in length
* 36040 36139: gap of unknown length
* 36140 39230: contig of 3091 bp in length
* 39231 39331: gap of unknown length
* 39332 42441: contig of 3111 bp in length
* 42442 42541: gap of unknown length
* 42542 44851: contig of 2310 bp in length
* 44852 44952: gap of unknown length
* 44953 47222: contig of 2271 bp in length
* 47223 47322: gap of unknown length
* 47323 49738: contig of 2416 bp in length
* 49739 49838: gap of unknown length
* 49839 53036: contig of 3198 bp in length
* 53037 53136: gap of unknown length
* 53137 55214: contig of 2078 bp in length
* 55215 55314: gap of unknown length
* 55315 57167: contig of 1853 bp in length
* 57168 57267: gap of unknown length
* 57268 60624: contig of 3357 bp in length
* 60625 60724: gap of unknown length
* 60725 63477: contig of 2753 bp in length

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* 63478 63577: gap of unknown length
* 63578 65621: contig of 2044 bp in length
* 65622 65721: gap of unknown length
* 65722 67927: contig of 2206 bp in length
* 67928 68027: gap of unknown length
* 68028 69802: contig of 1775 bp in length
* 69803 69902: gap of unknown length
* 69903 71859: contig of 1957 bp in length
* 71860 71959: gap of unknown length
* 71960 74227: contig of 2268 bp in length
* 74228 74327: gap of unknown length
* 74328 76807: contig of 2480 bp in length
* 76808 76907: gap of unknown length
* 76908 79097: contig of 2190 bp in length
* 79098 79197: gap of unknown length
* 79198 81356: contig of 2159 bp in length
* 81357 81456: gap of unknown length
* 81457 82500: contig of 1044 bp in length
* 82501 82600: gap of unknown length
* 82601 83787: contig of 1187 bp in length
* 83788 83887: gap of unknown length
* 83888 85585: contig of 1698 bp in length
* 85586 85685: gap of unknown length
* 85686 87209: contig of 1524 bp in length
* 87210 87309: gap of unknown length
* 87310 89391: contig of 2082 bp in length
* 89392 89491: gap of unknown length
* 89492 90863: contig of 1372 bp in length
* 90864 90963: gap of unknown length
* 90964 92581: contig of 1618 bp in length
* 92582 92681: gap of unknown length
* 92682 94497: contig of 1816 bp in length
* 94498 94597: gap of unknown length
* 94598 95959: contig of 1362 bp in length
* 95960 96059: gap of unknown length
* 96060 97493: contig of 1434 bp in length
* 97494 97594: gap of unknown length
* 97594 98773: contig of 1280 bp in length
* 98774 98977: gap of unknown length
* 98978 100260: contig of 1287 bp in length
* 100261 100360: gap of unknown length
* 100361 101503: contig of 1143 bp in length
* 101504 101603: gap of unknown length
* 101604 102847: contig of 1244 bp in length
* 102848 102947: gap of unknown length
* 102948 104772: contig of 1825 bp in length
* 104773 104872: gap of unknown length
* 104873 106735: contig of 1863 bp in length
* 106736 106835: gap of unknown length
* 106836 108191: contig of 1356 bp in length
* 108192 108291: gap of unknown length
* 108292 109620: contig of 1329 bp in length
* 109621 109720: gap of unknown length
* 109721 110965: contig of 1245 bp in length
* 110966 111065: gap of unknown length
* 111066 112325: contig of 1260 bp in length
* 112326 112425: gap of unknown length
* 112426 114287: contig of 1862 bp in length
* 114288 114387: gap of unknown length
* 114388 115433: contig of 1046 bp in length
* 115434 115533: gap of unknown length
* 115534 116779: contig of 1246 bp in length
* 116780 116879: gap of unknown length
* 116880 118275: contig of 1396 bp in length
* 118276 118375: gap of unknown length
* 118376 120259: contig of 1884 bp in length
* 120260 120359: gap of unknown length
* 120360 122229: contig of 1870 bp in length
* 122230 122329: gap of unknown length
* 122330 124076: contig of 1747 bp in length
* 124077 124176: gap of unknown length
* 124177 125298: contig of 1122 bp in length
* 125299 125398: gap of unknown length
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* 125399 127106: contig of 1708 bp in length
* 127107 127206: gap of unknown length
* 127207 128266: contig of 1060 bp in length
* 128267 128366: gap of unknown length
* 128367 130055: contig of 1689 bp in length

Query Match
Best Local Similarity 6.3%; Score 19; DB 2; Length 155825;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 268 tacggcaacctctccaact 286
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Db 104433 TACGGCAACCTCTCCAAC 104451

RESULT 28
AF207872/c
LOCUS AF207872 561 bp DNA linear STS 24-OCT-2000
DEFINITION Ovis aries chromosome 18 clone ODBS565, sequence tagged site.
ACCESSION AF207872
VERSION AF207872.1 GI:7677203
KEYWORDS STS.
SOURCE sheep.
ORGANISM Ovis aries
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Caprinae; Ovis.
REFERENCE 1 (bases 1 to 561)
AUTHORS Fahrenkrug,S.C., Freking,B.A., Rexroad,C.E. III, Leymaster,K.A.,
Kappes,S.M. and Smith,T.P.L.
TITLE Comparative mapping of the ovine c1pg locus
JOURNAL Mamm. Genome 11 (10), 871-876 (2000)
MEDLINE 20458865
PUBMED 11003702
REFERENCE 2 (bases 1 to 561)
AUTHORS Fahrenkrug,S.C.
TITLE Direct Submission
JOURNAL Submitted (23-NOV-1999) Production Systems, USDA Meat Animal
Research Center, PO Box 166, Spur 18D, Clay Center, NE 68933, USA
FEATURES
source
Location/Qualifiers
1..561
/organism="Ovis aries"
/db_xref="taxon:9940"
/chromosome="18"
/clone="ODBS565"
/note="derived from BAC 56R3C11"
BASE COUNT 121 a 150 c 159 g 131 t
ORIGIN
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Query Match
Best Local Similarity 5.9%; Score 18; DB 11; Length 561;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 43 ggggaaggtggtggaagcc 60
|||||
Db 218 GGGGAAGGTGGTGAAGCC 201
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RESULT 29
HSA330119/c
LOCUS HSA330119 621 bp DNA linear PRI 01-OCT-2001
DEFINITION Homo sapiens genomic sequence surrounding NotI site, clone
NR1-XE6C.
ACCESSION AJ330119
VERSION AJ330119.1 GI:15874537
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 621)
AUTHORS Kutsenko,A.S., Gizatullin,R.Z., Al-Amin,A.N., Wang,F.,
```


Podowski,R.M., Matushkin,Y.G., Kvasha,S.M., Gyanchandani,A., Muravenko,O.V., Protopopov,A.I., Kashuba,V.I., Kisselev,L.L., Wasserman,W., Wahlestedt,C. and Zabarovsky,E.R.
Analysis of NotI flanking sequences: a new tool for gene discovery and verification of the human genome

JOURNAL Unpublished
REFERENCE 2 (bases 1 to 621)
AUTHORS Zabarovsky,E.R.
TITLE Direct Submission
JOURNAL Submitted (16-MAY-2001) Microbiology and Tumorbiology Centre, Karolinska Institute, Theorells vag, 3, Box 280, Stockholm 171 77, Sweden

FEATURES
source
1..621
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="NRI-XE6C"

BASE COUNT 137 a 198 c 207 g 78 t 1 others
ORIGIN

Query Match 5.9%; Score 18; DB 9; Length 621;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 32 acggcgcttcgggaagg 49
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DB 98 ACGGCGCTTCGGAAGG 81

RESULT 30
LOCUS HAUNKTRP/c 827 bp mRNA linear VRL 09-FEB-1999
DEFINITION Human astrovirus type 1 mRNA for non-structural protein.
ACCESSION Z16420
VERSION Z16420.1 GI:59401
KEYWORDS non-structural protein.
SOURCE Human astrovirus type 1.
ORGANISM Human astrovirus type 1
Viruses; ssRNA positive-strand viruses, no DNA stage; Astroviridae; Astrovirus.

REFERENCE 1 (bases 1 to 827)
AUTHORS Willcocks,M.M., Carter,M.J., Silcock,J.G. and Madeley,C.R.
TITLE A dot-blot hybridization procedure for the detection of astrovirus in stool samples
JOURNAL Epidemiol. Infect. 107 (2), 405-410 (1991)
MEDLINE 92037892
REMARK (sites)

REFERENCE 2 (bases 1 to 827)
AUTHORS Willcocks,M.M. and Carter,M.J.
TITLE Sequence analysis of a human Astrovirus
JOURNAL Unpublished
REFERENCE 3 (bases 1 to 827)
AUTHORS Willcocks,M.
TITLE Direct Submission

JOURNAL Submitted (06-OCT-1992) Willcocks M., University of Surrey, School of Biological Sciences, Guildford, Surrey, G42 5XH
FEATURES
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1..827
/organism="Human astrovirus type 1"
/db_xref="taxon:12456"

transit_peptide 718..726
/function="unknown"
BASE COUNT 267 a 163 c 204 g 193 t
ORIGIN

Query Match 5.9%; Score 18; DB 14; Length 827;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 165 caagatcctcattcacat 182

|||||
DB 79 CAAGATCCTCATTCACAT 62

RESULT 31
LOCUS RSU62291 1307 bp DNA linear BCT 08-AUG-1996
DEFINITION Rhodobacter sphaeroides copper containing nitrite reductase (nirK) gene, complete cds.

ACCESSION U62291
VERSION U62291.1 GI:1480719
KEYWORDS
SOURCE Rhodobacter sphaeroides.
ORGANISM Rhodobacter sphaeroides
Bacteria; Proteobacteria; alpha subdivision; Rhodobacter group; Rhodobacter.

REFERENCE 1 (bases 1 to 1307)
AUTHORS Tosques,I.E., Kwiatkowski,A.V., Shi,J. and Shapleigh,J.P.
TITLE Characterization and regulation of the gene encoding nitrite reductase in Rhodobacter sphaeroides

JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1307)
AUTHORS Direct Submission
TITLE Submitted (26-JUN-1996) Microbiology, Cornell University, Wing Hall, Ithaca, NY 14853-8101, USA
JOURNAL

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/db_xref="taxon:1063"

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/bound_moiety="Fnr"
evidence=not_experimental
136..1260
/gene="nirK"

CDS 136..1260
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/transl_table=11
/product="copper containing nitrite reductase"
/protein_id="AA05767.1"
/db_xref="GI:1480720"

/translation="MTRRAALVGAALASAPLVIRTAGAQAQAPQAQASAPVDLSNL
PRVHTLVPPFAHAEHQVAASGVINEFEMRIIEKEVOLDDEAYLQAMTFDGSIPGP
LMIVHEGDYVELTLINPPENTMPTNIDFHAATGALGGGLTLINPGEKVVYLFKATRA
GAFVYHCAPGPMIPHWVSGMAGCIWVLPDGLKDHEGKPVRYDTVYVIGESDHIIP
KDEDTYMRFPSTSEGYEDMVAVMDTLIPSHIVFNAGVAGLTGEGALKAKVGDNVLFV
HSQPKRDSRPHLIGHGDLVWETGKFHNAPERDLTFWIRGCTAGAAALKFLOPGVYA
YVNHNLIEAVHKGATASVLVEGENDDLMEQWPPVGLIG"

BASE COUNT 237 a 472 c 405 g 193 t
ORIGIN

Query Match 5.9%; Score 18; DB 1; Length 1307;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 122 agggcgccacgcgcgcg 139
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DB 1172 AGGGCGCCACGCCAGCG 1189

RESULT 32
LOCUS AB025557 1519 bp mRNA linear INV 18-NOV-1999
DEFINITION Branchiostoma belcheri mRNA for VEGFR-like, partial cds.
ACCESSION AB025557
VERSION AB025557.1 GI:6002454
KEYWORDS VEGFR-like.
SOURCE Branchiostoma belcheri cDNA to mRNA.
ORGANISM Branchiostoma belcheri

Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae; Branchiostoma.
1 (sites)
Suga,H., Hoshiyama,D., Kuraku,S., Katoh,K., Kubokawa,K. and Miyata,H.
TITLE
Protein tyrosine kinase cDNAs from amphioxus, hagfish, and lamprey: isoform duplications around the divergence of cyclostomes and gnathostomes
J. Mol. Evol. 49 (5), 601-608 (1999)
20020330
2 (bases 1 to 1519)
Suga,H.
Direct Submission
Submitted (31-MAR-1999) Hiroshi Suga, Faculty of Science, Kyoto University, Department of Biophysics, Kitashirakawa-Oiwakecho, Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
(E-mail:suga@biophys.kyoto-u.ac.jp, Tel: +81-75-753-4224, Fax: +81-75-753-4223)
FEATURES
source Location/Qualifiers
1..1519
/organism="Branchiostoma belcheri"
/db_xref="taxon:7741"
<1..1339
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/product="VEGFR-like"
/protein_id="BAA84747.1"
/db_xref="GI:6002455"
/translation="OVIEATAGIEKQCVAVVAVKMLKDDASSNEVKALMDELKILI HIGQHLNIVNLGACTKDGPIVIVCECKYGLNSYLGRKRKFVSEKQDRSRSSG YCNRVDSPNKCLRTVSKGLMNYDYTDGDEPLTLEDLVSYQVARGMDYLASK KCIHRDLARNYLLAKHNVYKICDFGLADVVRNPEYTKMGNAIPVQKMAPESEFDR SYTIQSDVMSYGLLWEIFELGSPYPGVQINEDFDKLRGCFRMRQPKHASDDLYOM MLCNRWSEPTPTTDLAESSSOLEATAQOXYLDLSPEIHDDSDGIPNPTPTDS FLPTPADCARQASPPASGNDNSRPERHSGDVIDEEAVKILMDHPGQRAYHSDA KALVPNSLGVKRGKGNSSNSVSSSHNSSGFHSYDEAPPDYNTVVTVDV"
BASE COUNT 395 a 415 c 401 g 308 t
ORIGIN
Query Match 5.9%; Score 18; DB 3; Length 1519;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 261 ctgcaagtagcgcaacct 278
|||||
DB 214 CTGCAAGTAGCGCAACCT 231
RESULT 33
AF049459
LOCUS AF049459 2065 bp mRNA linear PRI 28-NOV-1998
DEFINITION Homo sapiens nuclear DEAF-1 related transcriptional regulator protein mRNA, complete cds.
ACCESSION AF049459
VERSION AF049459.1 GI:3309562
KEYWORDS human.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 2065)
Huggenwik,J.I., Michelson,R.J., Collard,M.W., Ziemba,A.J., Gurley,P. and Mowen,K.A.
TITLE Characterization of a nuclear deformed epidermal autoregulatory factor-1 (DEAF-1)-related (NUDR) transcriptional regulator protein Mol. Endocrinol. 12 (10), 1619-1639 (1998)
JOURNAL 98444968
MEDLINE
AUTHORS 2 (bases 1 to 2065)
Huggenwik,J.I., Michelson,R.J., Collard,M.W., Ziemba,A.J., Gurley,P. and Mowen,K.A.
TITLE Direct Submission
Submitted (20-FEB-1998) Physiology, Southern Illinois University School of Medicine, 2053 Life Sciences III, Carbondale, IL 62901-6523, USA
FEATURES
source Location/Qualifiers
1..2329
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="11"
/cell_line="JEG-3 choriocarcinoma"
357..2012

62901-6523, USA
Location/Qualifiers
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/db_xref="taxon:9606"
/chromosome="11"
/cell_line="JEG-3 choriocarcinoma"
51..1748
/note="NUDR; similar to Homo sapiens suppressin, GenBank Accession Number AF007165; NUDR8 isoform, GenBank Accession Number AF049460, contains altered coding region near amino terminal alanine rich region"
/codon_start=1
/product="nuclear DEAF-1 related transcriptional regulator protein"
/protein_id="AAC79676.1"
/db_xref="GI:3309563"
/translation="MEDSDSAKQLGLAEAAVAAAAVAAAAAGGAEPEPVLRS DEDSEEDADSEARETPRTAVVAAEPGHMDGAEALPGDEAAAAFAEVTVT VANVGAAADNVTTTSVANAASISGHLVSGTALQIGDSLNTKATLIVVHTDGSIVT TGLKGPAAPLTPGQSPPTPLAPGQEGGTGYNDPSYDSELPVRCNIGSTLYKNR LCGSGRGRCIKGQENWSPTEFEAMAGRASSKDKRSIRYAGRPLOCLIQDILNPHA ASCTCAACDDMTLGGPVLFPVYKRRKKENELPTTPVKDKSPKNTILLPATAATFTT VTPSQIITSGALTEDRASTVEATVISESPAQGDVFAGATVQESVQPPCRASHPPEP HYPGTQDSCQIAPFPFAALPTSHPRVILTSIPALAVPPPTPKAAPALVPALVLELSEP RSWLYLEEMVNSLLNTAQLKTLFEQAKHASTYREANATNOAKIHADAERKQSCVNCG RSMLEGTGCHKVNYCTFCQKDKMDKHOHICGQSAAVTVQADEVHVAESVMEKVTV"
BASE COUNT 441 a 640 c 656 g 328 t
ORIGIN
Query Match 5.9%; Score 18; DB 9; Length 2065;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 32 acggcgcccttcgggaagg 49
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DB 18 ACGGCGCCTTCGGGAAGG 35
RESULT 34
AF049460
LOCUS AF049460 2329 bp mRNA linear PRI 28-NOV-1998
DEFINITION Homo sapiens nuclear DEAF-1 related transcriptional regulator protein 8 mRNA, complete cds.
ACCESSION AF049460
VERSION AF049460.1 GI:3309564
KEYWORDS human.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 2329)
Huggenwik,J.I., Michelson,R.J., Collard,M.W., Ziemba,A.J., Gurley,P. and Mowen,K.A.
TITLE Characterization of a nuclear deformed epidermal autoregulatory factor-1 (DEAF-1)-related (NUDR) transcriptional regulator protein Mol. Endocrinol. 12 (10), 1619-1639 (1998)
JOURNAL 98444968
MEDLINE
AUTHORS 2 (bases 1 to 2329)
Huggenwik,J.I., Michelson,R.J., Collard,M.W., Ziemba,A.J., Gurley,P. and Mowen,K.A.
TITLE Direct Submission
Submitted (20-FEB-1998) Physiology, Southern Illinois University School of Medicine, 2053 Life Sciences III, Carbondale, IL 62901-6523, USA
FEATURES
source Location/Qualifiers
1..2329
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="11"
/cell_line="JEG-3 choriocarcinoma"
357..2012

/note="NUDR8; similar to Homo sapiens suppressin, GenBank
Accession Number AF007165; NUDR isoform, GenBank Accession
Number AF049459, contains altered coding region near amino
terminal alanine rich region"
/codon_start=1
/product="nuclear DEAF-1 related transcriptional regulator
protein 8"
/protein_id="AAC79677.1"
/db_xref="GI:3309565"
/translation="MEDSDSAKOLGLADAAAAGGAEPEPVLSDSEEDADSEAE
ETPRVTAVVAAEPGHMDMGAEALPGDEAAAAFAEVTVTAVVGAADNVFTT
SVANAASISGRLTALQIGDSLNRKATLIQIGDSLNRKATLIQIGDSLNR
QSPPTPLAPGQEGKTYNWDPSYDELSPVCRNISGTYLKNRSGGGRGKIQGE
NWSPTPEAMAGRASSKDWKRSIRYAGRPLOCLIQIGILNPHAACTCAACDDMTL
SGPVLFPVYKRRKENELPTTPVKKDSKNITLLPATATFTVTPSGQITTSGLT
FDRASTVEATAVISEPAQGVFAGATVOEASVOPPCRAHPHEPHYPCYODSCQIAPF
PEALPSSHPIVLTSLPALAVPPPTTKAAPALVNGLELSEPSRWLYLEEVNLSL
NTAQLTKLFEQAKHASTYREAAATNQAKIHADAERKEQSCVNCGRAMECTGCHKVN
YCSTFCORKWKDHQICGQSAATVQADEVHVAESVMEKVTV"
BASE COUNT 464 a 739 c 734 g 392 t
ORIGIN

Query Match 5.9%; Score 18; DB 9; Length 2329;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 32 acggcgcccttcgggaag 49
|||||
Db 324 ACGGCGCTTCGGGAAG 341

RESULT 35
AF049461 2405 bp mRNA linear PRI 28-NOV-1998
LOCUS Pan troglodytes nuclear DEAF-1 related transcriptional regulator
DEFINITION protein mRNA, complete cds.
ACCESSION AF049461
VERSION AF049461.1 GI:3309566
KEYWORDS chimpanzee.
SOURCE Pan troglodytes
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.
REFERENCE 1 (bases 1 to 2405)
Huggenvik,J.I., Michelson,R.J., Collard,M.W., Ziemba,A.J.,
Gurley,P. and Mowen,K.A.
TITLE Characterization of a nuclear deformed epidermal autoregulatory
factor-1 (DEAF-1)-related (NUDR) transcriptional regulator protein
Mol. Endocrinol. 12 (10), 1619-1639 (1998)
JOURNAL 98444968
MEDLINE 2 (bases 1 to 2405)
AUTHORS Huggenvik,J.I., Michelson,R.J., Collard,M.W., Ziemba,A.J.,
Gurley,P. and Mowen,K.A.
TITLE Direct Submission
JOURNAL Submitted (20-FEB-1998) Physiology, Southern Illinois University
School of Medicine, 2053 Life Sciences III, Carbondale, IL
62901-6523, USA

FEATURES
Location/Qualifiers
1. .2405
/organism="Pan troglodytes"
/db_xref="taxon:9598"
/cell_line="CV-1"
/tissue_type="kidney"
396. .2093
/note="NUDR; similar to Homo sapiens suppressin, GenBank
Accession Number AF007165"
/codon_start=1
/product="nuclear DEAF-1 related transcriptional regulator
protein"
/protein_id="AAC79678.1"
/db_xref="GI:3309567"
/translation="MEDSDSAKOLGLAEAAVAAAAAAGGAEPEPVLRS

DEDESEADSEARETPTVAVMAAEPCHMDMGAEALPGDPDETAATAAAFAEVTTVT
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TGKGPAPLTPGQSPPTPLAPGQEGKTYNWDPSYDELSPVCRNISGTYLKNR
LGSGRGRGKIQGEGKTYNWDPSYDELSPVCRNISGTYLKNRSGGGRGKIQGE
ASCTCAACDDMTLSGPVLFPVYKRRKENELPTTPVKKDSKNITLLPATATFTT
VTPSGQITTSGLTFDRASTVEATAVISEPAQGVFAGATVOEASVOPPCRAHPHEP
HYPCYODSCQIAPFPEALPSSHPIVLTSLPALAVPPPTTKAAPALVNGLELSEP
RSWLYLEEVNLSLNTAQLTKLFEQAKHASTYREAAANOAKIHADAERKEQSCVNC
REAMNETGCHKVNYCSTFCORKWKDHQICGQSAATVQADEVHVAESVMEKVTV"
BASE COUNT 463 a 755 c 774 g 413 t
ORIGIN

Query Match 5.9%; Score 18; DB 9; Length 2405;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 32 acggcgcccttcgggaag 49
|||||
Db 363 ACGGCGCTTCGGGAAG 380

RESULT 36
AF188842 3614 bp mRNA linear VRT 17-MAY-2000
LOCUS Gallus gallus platelet-derived growth factor receptor alpha
DEFINITION (PDGFR-a) mRNA, complete cds.
ACCESSION AF188842
VERSION AF188842.1 GI:6014686
KEYWORDS chicken.
SOURCE Gallus gallus
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
REFERENCE 1 (bases 1 to 3614)
AUTHORS Alalotlis,P.
TITLE Platelet-derived growth factor A modulates limb chondrogenesis both
in vivo and in vitro
Mech. Dev. 94 (1-2), 13-24 (2000)
JOURNAL 20302546
MEDLINE 2 (bases 1 to 3614)
AUTHORS Alalotlis,P. and Mercola,M.K.
TITLE Direct Submission
JOURNAL Submitted (22-SEP-1999) MRC-LMCB, University College London, Gower
Street, London WC1E 6BT, UK

FEATURES
Location/Qualifiers
1. .3614
/organism="Gallus gallus"
/db_xref="taxon:9031"
1. .3614
/gene="PDGFR-a"
16. .3279
/gene="PDGFR-a"
/note="receptor tyrosine kinase"
/codon_start=1
/product="platelet-derived growth factor receptor alpha"
/protein_id="AA01460.1"
/db_xref="GI:6014687"
/translation="MGTPTPTFLILGCLFTGLTLLTQLPLPTIPVNRNEMVVLNSN
FTLCKSGDSEVSHQYVPTGSHRIDIRHEENNSGLFVTVLEVCNAAHTGMVVCYN
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VNSLDKPVAFYDSKSGFVGNFLAGPYCTKTVKVGFEKSLIKLDDIKVPSOKLVMLT
EALTKVYKGTETIVTVCVFDVFNWLNQWYKVGKGLIKLDDIKVPSOKLVMLT
IPDVLVKDGYDECTARHATKEVKNKVVITVHDGFIHLEPQFSPLEAVNLHVEYN
LWLLKNEDEIKRYTFSLLIQVPALIIDLMDHOGSAGROTFRCLAECTPLPDVEWLV
KDIKCSNDSWTLLTNISDTHMEALDERNWEVSQVTFQVEETLAVRCVARNDLG
AVTREKLVAPTLRSELTVAAVAVLLVLIISLIVLIIVKOKPYEIRWRVIESIS
PDGHEYIYDDPMOLPYDSRPFPRDGLVILGSGAFGVVGGTAGYLSRSPQVWKY
AVKMLKPTARSEKALMSELKIMTHLGPLNINLLGACTKSGPTIITEYCFYGD
VNYLHKRNDFLSRHPKPKDIDFGMPADESTRSYVLSFENTGYMDMKQADTT
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TYQVARGMEFLASKNCVHRDLAARNVLLAQQKIYKICDFGLARDIMHDSNYSVSGKSTF
LPYKMAPEISFDNLYTTLSDVWSIGILLWEIFSLGGILYPCMMVDSTFYKIKISGYR
MAKPDHATNEVTEIMVKWNNPEKRPSPFYLSEIVESLLPCEYKKSYEKIHLDPLKS
DPAPVTRMGDCDNAYIGVTVYKNEDKIKDRESGFDEQLSADSGVITPLPDIPVSED
ELGKRNHSSOTSSESAIETSGSSSTFIKREDETIEDIMDDIGIDSDSLVEDSFL"
BASE COUNT      1070 a   735 c   882 g   927 t
ORIGIN

Query Match      5.9%;   Score 18;   DB 5;   Length 3614;
Best Local Similarity 100.0%;   Pred. No. 1.5e+02;
Matches 18;   Conservative 0;   Mismatches 0;   Indels 0;   Gaps 0;

QY  103 gccgtgaaaaatgctgaaa 120
      |||||
Db  1888 GCCGTGAAAATGCTGAAA 1905

RESULT 37
NEUATPPM/c
LOCUS      NEUATPPM      4784 bp      DNA      linear      PLN 27-APR-1993
DEFINITION Neurospora crassa plasma membrane H+ ATPase gene, complete cds.
ACCESSION J02602
VERSION J02602.1 GI:168764
KEYWORDS H+ ATPase.
SOURCE Neurospora crassa (strain 75-OR23-1A) DNA, clone gNA2.
ORGANISM Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariales; Sordariaceae; Neurospora.
REFERENCE 1 (bases 1 to 4784)
AUTHORS Addison,R.
TITLE Primary structure of the Neurospora plasma membrane H+-ATPase
deduced from the gene sequence: Homology to Na+/K+-, Ca2+-, and
K+-ATPases
JOURNAL J. Biol. Chem. 261, 14896-14901 (1986)
MEDLINE 87033715
FEATURES             Location/Qualifiers
     source          1..4784
                     /organism="Neurospora crassa"
                     /db_xref="taxon:5141"
     exon            <1118..1297
                     /note="plasma membrane H+ ATPase"
     CDS              join(1118..1297,1356..1562,1687..1820,1885..4079,
                     4147..4193)
                     /note="plasma membrane H+ ATPase"
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                     /db_xref="GI:168765"
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                     NMKEKENHFLKFLGFVGP IQFMEGAAVLAAGLEDWDFGVICGLLLLNAAVGV
                     QEFQAGSIVDELKKTALAKAVLRDGT LKETEAPVVPDGLQVVEGTIIPADGRIVT
                     DDAPLDVQSAITGESLAVDKHGQDVFASSAVKRGFAFVITATGNTFTVGRAALY
                     NAASGSGHTEVLNGTITLLIVLFTLLIVVSSFRSNPVIQILEFTAITIGV
                     PVGLPAVYTTMAGVAAYLAKKKAIVOKLSAIEAGVEILCSDKTGLTKNKLSLHD
                     PYTVAGVDPEDMLTACLAASRRKKGIDAIDKAPLSKLYIPRAKSYKSVLYKVLQFHP
                     FDPKSVAVAVVESPOGERITCVKGAFLFVLTVEEDHP IPEEVDQAYKNKVAEFATR
                     GFSLGVARRRGESWEILGIMPCMDPPRHDTYKTCVCAKTLGLS IKMLTGDVAGIAR
                     ETSRLGLGTNIYNAERLLGLGGDMPGSEVDVFEAADGFAEVFPQHKYNVVEILQO
                     RGYLVAMTQGVNDAPSLKKADTCIAVEGSDAARSADIVFLAPLGAALIDALKTSR
                     QIFHRMAYVYVRIALSHLEIFLGLHIALILNSRLNTELVEVFFATFAIDVATLAIYDN
                     APQSOTPVKNLPLKMGMSVLLGVAVGTWITVTMYAOGENGIVQNFNGMDEVLV
                     LQMSLEWLIFFITRANGPEWSSPSQLSGAIFLVDILATCFTIWGWFHSDSTIVA
                     VRIWIFSGIFGIMGGVYVILQDSVGFNLHMGKSPKGNQKRSLEDFFVVSQIRYST
                     QHEKSQ"
     intron           1298..1355
                     /note="H+ ATPase cds intron A"
     exon            1356..1562
                     /number=2
     intron           1563..1686
                     /note="H+ ATPase cds intron B"
     exon            1687..1820

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/number=3
1821..1884
/note="H+ ATPase cds intron C"
1885..4079
/number=4
4080..4146
/note="H+ ATPase cds intron D"
4147..>4193
/note="plasma membrane H+ ATPase"
/number=5
BASE COUNT      943 a   1470 c   1143 g   1228 t
ORIGIN      51 bp upstream of faqi site.

Query Match      5.9%;   Score 18;   DB 8;   Length 4784;
Best Local Similarity 100.0%;   Pred. No. 1.4e+02;
Matches 18;   Conservative 0;   Mismatches 0;   Indels 0;   Gaps 0;

QY  200 tggtaaacactcctcgagg 217
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Db  2850 TGGTCAACCTCCTCGGG 2833

RESULT 38
NEUATPASE/c
LOCUS      NEUATPASE      5359 bp      DNA      linear      PLN 12-AUG-1994
DEFINITION N.crassa plasma membrane ATPase gene, complete cds.
ACCESSION M14085 M23211 M23212
VERSION M14085.1 GI:168760
KEYWORDS ATPase.
SOURCE N.crassa (strain 74-OR23-1A) DNA (library of R.Geever and N.Niles),
clones pKH[4,5,14]; cDNA to mRNA (library of M.Sachs and
U.Rajbhandary), clones S[7,10,18].
ORGANISM Neurospora crassa
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariales; Sordariaceae; Neurospora.
REFERENCE 1 (bases 1 to 5359)
AUTHORS Hager,K.M., Mandala,S.M., Davenport,J.W., Speicher,D.W.,
Benz,E.J.,Jr. and Slayman,C.W.
TITLE Amino acid sequence of the plasma membrane ATPase of Neurospora
crassa: Deduction from genomic and cDNA sequences
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 83, 7693-7697 (1986)
MEDLINE 87017015
REFERENCE 2 (sites)
AUTHORS Aaronson,L.R., Hager,K.M., Davenport,J.W., Mandala,S.M., Chang,A.,
Speicher,D.W. and Slayman,C.W.
TITLE Biosynthesis of the plasma membrane H+-ATPase of Neurospora crassa
JOURNAL J. Biol. Chem. 263, 14552-14558 (1988)
MEDLINE 89008310
COMMENT Draft entry and computer-readable sequence for [1] kindly provided
by K.M.Hager, 05-JAN-1987.
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:5141"
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     TATA_signal      963..969
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     CAAT_signal      991..997
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                     /citation=[2]
     CAAT_signal      1008..1012
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     TATA_signal      1102..1108
                     /note="homologue; putative"
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     CAAT_signal      1120..1124
                     /note="homologue; putative"
                     /citation=[2]
     CAAT_signal      1138..1142
                     /note="homologue; putative"
                     /citation=[2]

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CAAT_signal 1168..1173
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/citation=[2]
exon (1191.1199)..1199
/note="ATPase mRNAs"
/number=1
prim_transcript 1192..4562
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prim_transcript 1192..4564
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prim_transcript 1192..4561
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prim_transcript 1199..4561
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Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 200 tgggtcaacctctctcgagg 217
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Db 2979 TGGTCAACCTCTCTCGGGG 2962

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LOCUS Human astrovirus type 1 genes for capsid protein and nonstructural
DEFINITION protein.
ACCESSION 225771
VERSION 225771.1 GI:410445
KEYWORDS capsid protein; nonstructural protein.

SOURCE
ORGANISM Human astrovirus type 1.
Viruses: ssRNA positive-strand viruses, no DNA stage; Astroviridae;
Astrovirus
1 (bases 5779 to 6813)
Willcocks,M.M. and Carter,M.J.
The 3' terminal sequence of a human astrovirus
Archives of virology. 124 (3-4), 279-289 (1992)
MEDLINE 92296896
PUBMED 1605739
2 (bases 4000 to 6813)
Willcocks,M.M. and Carter,M.J.
Identification and sequence determination of the capsid protein
gene from human astrovirus
FEMS Microbiol. Lett. (1993) In press
3 (bases 1 to 6813)
Willcocks,M.M., Brown,T.D., Madeley,C.R. and Carter,M.J.
The complete sequence of a human astrovirus
The Journal of general virology. 75 (Pt 7), 1785-1788 (1994)
MEDLINE 94292930
PUBMED 8021608
REMARK (sites)
4 (bases 1 to 6813)
Willcocks,M.
Direct Submission
Submitted (24-AUG-1993) Willcocks M., University of Newcastle upon
Tyne, Framlington Place, Newcastle upon Tyne, Tyne and Wear, UK
5 (bases 1 to 6813)
Willcocks,M.M. and Carter,M.J.
Sequence analysis of a human Astrovirus
Unpublished
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BASE COUNT 2039 a 1496 c 1559 g 1719 t
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Best Local Similarity 100.0%; Pred. No. 1.4e+02; Indels 0; Gaps 0;
Matches 18; Conservative 0; Mismatches 0;
Qy 165 caaagatcctcatccatc 182
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Db 1664 CAAGATCCTCATTCACAT 1647
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U67544
LOCUS Methanococcus jannaschii section 86 of 150 of the complete genome. BCT 28-JAN-1998
DEFINITION Methanococcus jannaschii
ACCESSION U67544 L77117
VERSION U67544.1 GI:1591671
KEYWORDS
SOURCE Methanococcus jannaschii.
ORGANISM Methanococcus jannaschii
Archaea; Euryarchaeota; Methanococci; Methanococcales;
Methanococcaceae; Methanococcus.
REFERENCE 1 (bases 1 to 10003)
AUTHORS Sult,C.J., White,O., Olsen,G.J., Zhou,L., Fleischmann,R.D.,
Sutton,G.G., Blake,J.A., Fitzgerald,L.M., Clayton,R.A.,
Gocayne,J.D., Kerlavage,A.R., Dougherty,B.A., Tomb,J., Adams,M.D.,
Reich,C.I., Overbeek,R., Kirkness,E.F., Weinstock,K.G.,
Merrick,J.M., Glodek,A., Scott,J.D., Geoghagen,N.S., Weidman,J.F.,
Fuhrmann,J.L., Nguyen,D.T., Utterback,T., Kelley,J.M.,
Peterson,J.D., Sadow,P.W., Hanna,M.C., Cotton,M.D., Hurst,M.A.,
Roberts,K.M., Kaine,B.B., Borodovsky,M., Klenk,H.P., Fraser,C.M.,
Smith,H.O., Woese,C.R. and Venter,J.C.
Complete genome sequence of the methanogenic archaeon,
Methanococcus jannaschii
Science 273 (5278), 1058-1073 (1996)
JOURNAL Science 273 (5278), 1058-1073 (1996)
MEDLINE 96337999
REFERENCE 2 (bases 1 to 10003)
AUTHORS Sult,C.J., White,O., Olsen,G.J., Zhou,L., Fleischmann,R.D.,
Sutton,G.G., Blake,J.A., Fitzgerald,L.M., Clayton,R.A.,
Gocayne,J.D., Kerlavage,A.R., Dougherty,B.A., Tomb,J., Adams,
M.D., Reich,C.I., Overbeek,R., Kirkness,E.F., Weinstock,K.G.,
Merrick,J.M., Glodek,A., Scott,J.D., Geoghagen,N.S., Weidman,J.F.,
Fuhrmann,J.L., Nguyen,D.T., Utterback,T., Kelley,J.M.,

Peterson, J.D., Sadow, P.W., Hanna, M.C., Cotton, M.D., Hurst, M.A., Roberts, K.M., Kaine, B.B., Borodovsky, M., Klenk, H.P., Fraser, C.M., Smith, H.O., Woese, C.R. and Venter, J.C.
 Direct Submission
 Submitted (27-AUG-1996) The Institute for Genomic Research, 9712 Medical Center Dr, Rockville, MD 20850, USA
 On Oct 3, 1996 this sequence version replaced gi:1564047.
 Location/Qualifiers
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DB 7186 CAACCTCTCCAACTTCCT 7203

RESULT 41
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DEFINITION
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cant gene, canRA gene and canRB gene.
AJ300302
ACCESSION
AJ300302.1
GI:12231153
VERSION
AB030302.1
KEYWORDS
ABC-transporter; aminotransferase; can RB gene; canA gene; canC
gene; canF gene; canRA gene; cant gene; Cho-like protein;
cytochrome P-450; ferredoxine; PABA synthase; thioesterase.
SOURCE
Streptomyces griseus.
ORGANISM
Streptomyces griseus
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
REFERENCE
1 (bases 1 to 39314)
Campelo,A.B.
Thesis (2000) Department of Microbiologia, Universidad de Leon,
Leon, Spain
2 (bases 1 to 39314)
Campelo,A.B. and Gil,J.A.
Cloning and characterization of a gene cluster from Streptomyces
griseus IMRU 3570 involved in candididin production
Unpublished
3 (bases 1 to 39314)
Gil,J.A.
Direct Submission
Submitted (14-NOV-2000) Gil J.A., Microbiologia, Universidad de
Leon, Campus de Vegazana s/n, 24071, SPAIN
Location/Qualifiers
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ORIGIN

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Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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ACCESSION AC102135
VERSION AC102135.1 GI:17061221
KEYWORDS HTG; HTGS_PHASE0.
SOURCE house mouse.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
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REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS

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1 (bases 1 to 71769)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Mus musculus, clone RP23-253J5
Unpublished
2 (bases 1 to 71769)
Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,
Anderson,S., Barna,N., Bastien,V., Boguslavskiy,L., Boukhgalter,B.,
Brown,A., Camarata,J., Campopiano,A., Chang,J., Chazaro,B.,
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Seaman,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N.,
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Topham,K., Travers,M., Travis,N., Trigilio,J., Vassiliev,H.,
Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,
Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
Direct Submission
Submitted (23-NOV-2001) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
All repeats were identified using RepeatMasker:
Smit,A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L18082
Center clone name: 253_J_5
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* NOTE: This record contains 87 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.
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TITLE
JOURNAL
COMMENT

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Best Local Similarity 100.0%; Pred. No. 1.1e+02;

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Db 36239 TCACATCGGCAACCACT 36256

RESULT 43

AC060793/c

LOCUS

DEFINITION

AC060793

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

Homo sapiens chromosome 2 clone -2012A7 map 2, LOW-PASS SEQUENCE

74586 bp

DNA

linear

HTG 20-APR-2000

SAMPLING

AC060793.1

GI:7622457

HTG; HTGS_PHASE0.

human.

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 74586)

Birren,B., Linton,L., Nusbaum,C. and Lander,E.

Homo sapiens chromosome 2, clone -2012A7

Unpublished

2 (bases 1 to 74586)

Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,

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Anderson,S., Baldwin,J., Barna,N., Bastien,V., Beda,F.,
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Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J.,
Young,G., Zainoun,J., Zimmer,A. and Zody,M.
Direct Submission
Submitted (20-APR-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L9522
Center clone name: 2012_A_7
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* NOTE: This record contains 94 individual
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* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.
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* 30905 31004: gap of 100 bp
* 31005 31693: contig of 689 bp in length
* 31694 31793: gap of 100 bp
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* 32510 32609: gap of 100 bp
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* 33281 33380: gap of 100 bp
* 33381 34080: contig of 700 bp in length
* 34081 34180: gap of 100 bp
* 34181 34878: contig of 698 bp in length
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* 35766 36470: contig of 705 bp in length
* 36471 36570: gap of 100 bp
* 36571 37268: contig of 698 bp in length
* 37269 37368: gap of 100 bp
* 37369 38060: contig of 692 bp in length
* 38061 38160: gap of 100 bp
* 38161 38848: contig of 688 bp in length
* 38849 38948: gap of 100 bp
* 38949 39627: contig of 679 bp in length
* 39628 39727: gap of 100 bp

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TITLE
JOURNAL

COMMENT

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Query Match 5.9% Score 18; DB 2; Length 74586;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 255 ggagttctgcaagtcagc 272
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Db 3179 GGAGTTCTGCAAGTACGG 3162

RESULT 44

NCBI
LOCUS Neurospora crassa DNA linkage group II BAC clone B1D1 76072 bp DNA linear PLN 13-NOV-2001
DEFINITION Neurospora crassa DNA linkage group II BAC clone B1D1.
ACCESSION AL355927
VERSION AL355927.1 GI:7800790
KEYWORDS
SOURCE Neurospora crassa.

ORGANISM

Neurospora crassa
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariales; Sordariaceae; Neurospora.

REFERENCE

AUTHORS Schulte, U., Aign, V., Hoheisel, J., Brandt, P., Fartmann, B.,
Holland, R., Nyakatura, G., Mewes, H. W. and Mannhaupt, G.
JOURNAL Unpublished
AUTHORS 2 (bases 1 to 76072)
TITLE Direct Submission
JOURNAL German Neurospora genome project.

Submitted (09-NOV-2001) MIPS, Institut fuer Bioinformatik,
GSF-Forschungszentrum fuer Umwelt und Gesundheit, GmbH,
Ingolstaedter Landstrasse 1, D-85764 Neuherberg, FRG E-mail:
G.Mannhaupt@gsf.de Project Coordinator: Ulrich Schulte, Institute
of Biochemistry, Heinrich-Heine-University, D-40225 Duesseidorf,
E-mail: ulrich-schulte@uni-duesseidorf.de
BAC clone 1D1 (strain OR74A) is available at the Fungal Genetic

Stock Center, http://www.fgsc.net
Sequencing was performed by MWG Biotech AG, Ebersberg, Germany,
http://www.mwgna.com
Information on performance of analysis and a more detailed
annotation of this entry and other sequences of linkage groups II
and V can be viewed at: http://mips.gsf.de/proj/neurospora.
FEATURES
source
1. .76072
/organism="Neurospora crassa"
/db_xref="taxon:5141"
/chromosome="6"
360. .752
/gene="B1D1.010"
join(360. .513.631. .752)
/gene="B1D1.010"
/note="contains EST gb:AI329523"
/codon_start=1
/product="putative protein"
/protein_id="CAD11428.1"
/db_xref="GI:16944430"
NGYILAPWQASRSIGPLNSPQTVPLPSRSRLGTHVSRVATLYCT"
360. .513
/gene="B1D1.010"
/number=1
514. .630
/gene="B1D1.010"
/number=1
631. .752
/gene="B1D1.010"
/number=2
3428. .5684
/gene="B1D1.040"
complement(join(3428. .4703.4796. .4866.5068. .5137,
5235. .5258.5659. .5684))
/gene="B1D1.040"
complement(join(3428. .4703.4796. .4866.5068. .5137,
5235. .5258.5659. .5684))
/gene="B1D1.040"
TREMBL:AE003628.11"
/codon_start=1
/product="conserved hypothetical protein"
/protein_id="CAD11429.1"
/db_xref="GI:16944431"
/translation="MLHRLFSFRNSFKMIRRDVSLPACQSPKLKLGPHFKLPNNH
QRFPSEVKEPHSVLSKRLSRSLVPQPLHPVIPPSPILSTPIAGTSPALPQPHL
PPLPASLAYSPLGP IKKHGEDAHEAGTGERTRDGYNTPEPILSPVNLPPSGSA
YVGETFSTLCANHNAPPIGEGGTSVKKTIRDVK IEAEMQTSGOTTLYLGDGDD
NAGSGSTANADNDNVITGNSAGGDSNNATEKTETETVATLDLLPLTGLTKILN
FGLKEETHVLGVTVSYEATETSGTRAFKMYQFICKPSLIVRTKAGPLSPVPK
AGNKKRRRRVLEAQLENCSEDAILLLEKALAEVQGLKWRDCNWAGIGVGGQEST
MTGEGISQQSQSQSQGPPRRPPLQPGSEQLCFIIEKGGEGCDREDEGECEAEVE
EKNGRIDFGYMLAWRTENGRGSLTLKLGTKHKVPR"
360. .513
/gene="B1D1.040"
/number=1
complement(4704. .4795)
/gene="B1D1.040"
/number=1
complement(4796. .4866)
/gene="B1D1.040"
/number=2
complement(4867. .5067)
/gene="B1D1.040"
/number=2
complement(5068. .5137)
/gene="B1D1.040"
/number=3
complement(5138. .5234)
/gene="B1D1.040"
/number=3
complement(5235. .5258)

abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping Group. Further information can be found at <http://www.sanger.ac.uk/HGP/Chr1> RP5-870F10 is from the library RPC1-5 constructed by the group of pieter de Jong. For further details see <http://www.chori.org/bacpac/home.htm>

VECTOR: pCVPAC2
IMPORTANT: This sequence is not the entire insert of clone RP5-870F10. It may be shorter because we sequence overlapping sections only once, except for a short overlap.
The true right end of clone RP5-870F10 is at 84481 in this sequence. The true right end of clone RP4-566D2 is at 2000 in this sequence.

FEATURES
source Location/Qualifiers
1..84481
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="1"
/map="q42.11-42.3"
/clone="RP5-870F10"
/clone_lib="RPC1-5"
BASE COUNT 21334 a 20549 c 21075 g 21523 t
ORIGIN

Query Match 5.9%; Score 18; DB 9; Length 84481;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 ggctgacactggggagag 22
|||||
DB 51196 GCCTGCACCTGGGGAGAG 51179

Search completed: July 15, 2002, 23:25:30
Job time: 24383 sec


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QY 829 gaagcagcagagcggggtaagtgggtgccccagcagcgtccccagcagccccacacaga 888
Db 1 CAAGCAGGCAGAGCGGGTAAAGTGGGTGCCCGCAGCGAGCGCTCCAGCAGCACACAGA 60

QY 889 actctccagcactctgaccatccacaacgctcagccagcagcagcctggctgtatgtgtg 948
Db 61 ACTCTCAGACATCTTGACCATCCACACAGCTCAGCCAGCAGCACCTGGGCTCGTATGTGTG 120

QY 949 caagggccaaacggcactccagcgatcttcgggagagcagccagggtcattgtgcattgaaaa 1008
Db 121 CAAGGCCAACACGGCATCCAGCGATTTCCGGAGAGCACCAGAGGTCAATTGTGCATGAAAA 180

QY 1009 lcccttcatacagctcgaatggtctcaaaagagaccatcctggagagccacgagagacga 1068
Db 181 TCCCTTTCATCAGCGTCGAGTGGCTCAAAAGGACCCATCCTGGAGAGCCACGGCAGGAGACGA 240

QY 1069 gctggtgaagctgcccgtgaagctggcagcgtacccccccgcccagttccagtggtacaa 1128
Db 241 ACTGCTGAAGCTGCCGCTGAAGCTGGCAGCATACCCCGCCCGAGTTCACAGTGGTACAA 300

QY 1129 ggatggaagcactgtctccgggcccacagtcacatgcccctggtgtctcaaggaggtgac 1188
Db 301 GGATGGAAGGACATGTCTCGGGGCCACAGTCCACATGCCCTGGTGTCAAGAGAGGTGAC 360

QY 1189 agagggcagcagcagcactacacccctcgccctgtgaaactccgctgtaagcctgagggcg 1248
Db 361 AGGGCCACACAGCAGCCTACACCCCTCGCCCTGTGGAATCTCCGCTGTGGCCTGAGGCG 420

QY 1249 caacatcagcctgagctggtggtgaatgtgccccccacagatacatgagagggcct 1307
Db 421 CAACATCAGCCTGGAGCTGGTGGTGAATGTGCCCCCCCCCAGATACATACAGAGGAGGCT 479

RESULT 2
BE778623
LOCUS
DEFINITION BE778623 601466167F1 NIH_MGC_67 920 bp mRNA linear EST 20-OCT-2000
mRNA sequence.
ACCESSION BE778623
VERSION BE778623.1 GI:10199821
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE NIH-MGC http://mgi.nci.nih.gov/.
JOURNAL 1 (bases 1 to 920)
COMMENT National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LL9618 row: f column: 17
High quality sequence stop: 716.
Location/Qualifiers
1..920
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3869200"
/clone_lib="NIH_MGC_67"
/tissue_type="retinoblastoma"
/lab_host="DH10B (phage-resistant)"
/notes="Organ: eye; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.75 kb. Library constructed by Life
Technologies."
BASE COUNT 236 a 240 c 268 g 176 t

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ORIGIN

Query Match 8.5%; Score 350; DB 10; Length 920;
 Best Local Similarity 100.0%; Pred. No. 1.6e-145;
 Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 3461 atgctgaactgctgctcgcgagaccccaagcgagacgtcattctcggagctggtgag 3520
Db 1 ATGCTGAACCTGCTGCTCGGAGACCCCAAGCGGAGACCTGCATTTCTCGGAGCTGCTGAG 60

QY 3521 atcctgggggacctgctccagggcgagggctcgaagagaagaggagggtctgcattggcc 3560
Db 61 ATCTCTGGGGACCTGCTCCAGGGCAGGGCTGCAAGAGGAAGAGGAGGTCTGCATGCC 120

QY 3581 ccgcgagctctcagagctcagaagagggcagcttctcgcaggtgtccaccatggcccta 3640
Db 121 CCGCGCAGCTCTCAGAGCTCAGAAGAGGGCAGCTTTCTCGAGGTGTCACCATGGGCCCTA 180

QY 3641 cacatgcgccagcgtgacgctgagagcagccgcgaagcctgcagcgccacagcctgagcc 3700
Db 181 CACATGCCCAGCTGACGCTGAGGACAGCCGCCAAGCCTGCAGCGCCACACGCTGGCC 240

QY 3701 gccaggtattacaactgggtgctcttcccggtgctcggccagaggggtgagaccctg 3760
Db 241 GCCAGGTATTACAACCTGGGTGCTCTTTCCCGGGTGCCTGGCCAGAGGGGCTGAGACCGT 300

QY 3761 ggtctctccaggtgaagacatttgaggaattcccatgaccccaacgac 3810
Db 301 GGTCTCTCAGGATGAAGACATTTTGAGGAATTCCTCCATGACCCCAACGAC 350

```

RESULT 3

```

BE281514
LOCUS
DEFINITION BE281514 601155083F1 NIH_MGC_21 687 bp mRNA linear EST 13-JUL-2000
mRNA sequence.
ACCESSION BE281514
VERSION BE281514.1 GI:9156534
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE NIH-MGC http://mgi.nci.nih.gov/.
JOURNAL 1 (bases 1 to 687)
COMMENT National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCMI03 row: f column: 22
High quality sequence stop: 590.
Location/Qualifiers
1..687
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3138453"
/clone_lib="NIH_MGC_21"
/tissue_type="choriocarcinoma"
/lab_host="DH10B (phage-resistant)"
/notes="Organ: placenta; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCAGCAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit

```

FEATURES

source

TITLE Pediatric Leukemia cDNA Sequencing Project
JOURNAL Unpublished (2000)
COMMENT Contact: Dr. Judith F. Margolin
Texas Children's Cancer Center and Human Genome Sequencing Center
at Baylor College of Medicine
1102 Bates, MC3-3320 Houston, TX 77030, USA
Tel: 832-824-4536
Fax: 832-825-4038
Email: clones@txccc.org
Citation: Carninci, P. and Hayashizaki, Y. High efficiency
full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)
Seq primer: M13 primer

FEATURES
source
1. .348
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="TCBAP6345"
/clone_lib="Pediatric pre-B cell acute lymphoblastic
leukemia Baylor-HGSC project-TCBA"
/sex="male"
/tissue_type="leukopheresis"
/cell_type="pre-B cell"
/dev_stage="pediatric 2 years"
/lab_host="DH10B"
/note="Vector: lambda PSB; Site_1: BamHI; Site_2: EcoRI;
first strand cDNA was primed with an anchored
XhoI-oligo(dT) primer [5'GGAGACTCAGCGCCGAGGAGGAG(T)VN
3': V-A-C-G; N-A-C,G,T] and then dg tailed. Second strand
was primed with a BamHI-dc primer
15'AGAGAGCTCGATCCGCCGCCAATAATAAT(C) 3'].
Double-stranded cDNA was then digested with BamHI and XhoI
and directionally cloned into the BamHI and SalI sites of
lambda PSB vector. Library went through one round of
normalization. Library was constructed by Wei Yu at RIKEN
of Japan (Carninci P, Westover A, Nishiyama Y, Ohsumi T,
Itoh M, Nagaoaka S, Sasakini, Okazaki Y, Muramatsu M,
Schneider C, Hayashizaki Y, High efficiency selection of
full-length cDNA by improved biotinylated cap trapper.,
DNA Res 4: 1, 61-6, Feb 28, 1997)"
BASE COUNT 74 a 105 c 107 g 60 t 2 others
ORIGIN

Query Match 5.1%; Score 209; DB 10; Length 348;
Best Local Similarity 100.0%; Pred. No. 1.8e-82;
Matches 209; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 302 gtgttgctgtgcacgaggtacatgccaaacgacacagcagctactgtctactacaag 361
|||||
Db 109 GTGTTGCTGCTGCACGAGGTACATGCCAACGACACAGCGAGCTAGCTCTGCTACTACAAG 168
QY 362 tacataagcagcagctcagagggaccacgcccagcagctcctactgttctgtgagagac 421
|||||
Db 169 TACATCAAGGCACGATCAGGCGCACCGCGCGGAGCTCTTGTCTGAGAGAC 228
QY 422 tttagcagccattcatcaacagcctgacacgctcttggtaacaggagagcagccatg 481
|||||
Db 229 TTTGACGACCCATTTCATCAACAGCCTGACACGCTCTTGGTCAACAGGAGACGCCCATG 288
QY 482 tgggtgcccgtgtgtgtgtccatccccgg 510
|||||
Db 289 TGGGTGCCCTGTGTTGTGTCCTATCCCGG 317

RESULT 6
BM172350
LOCUS BM172350 598 bp mRNA linear EST 04-DEC-2001
DEFINITION imagec4_2001/smu279bdf41.x1 NIH_MGC_97 Homo sapiens cDNA clone
IMAGE:4830201 5', mRNA sequence.
ACCESSION BM172350
VERSION BM172350.1 GI:17311913
KEYWORDS EST.
SOURCE human.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 598)
AUTHORS Kale, P. I., Harsch, T. J., Folta, P. A., Nelson, D. O., Sanders, C. G. and
Prange, C. K.
TITLE The I.M.A.G.E. Consortium quality control effort: clone
resequencing for verification
JOURNAL Unpublished (2001)
COMMENT Other ESTs: BG717758
Contact: Prange CK
The I.M.A.G.E. Consortium
Lawrence Livermore National Laboratory
Livermore, CA, USA
Email: help@image.llnl.gov
This read has been verified (found to hit its original self in the
correct orientation), as part of the I.M.A.G.E. Consortium quality
control effort. High quality sequence is defined as having 100 or
more base pairs with a phred quality value of 20 or greater, where
a sliding window of 4 base pairs with a phred quality value of 15
or greater marks the beginning and end of the sequence. For
information on obtaining this clone, please contact
info@image.llnl.gov.
Plate: L1AM10750 row: p column: 10
Seq primer: -21ml3
High quality sequence stop: 598.

FEATURES
source
1. .598
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4830201"
/clone_lib="NIH_MGC_97"
/lab_host="DH10B"
/note="Organ: testis; Vector: pBluescriptR (modified
pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI (gtc9ag
); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTVN-3',
size-selected for average insert size 2.2 kb and
normalized to ROT 5. This is a primary library enriched
for full-length clones and constructed using the
Cap-trapper method (Carninci, in preparation). Library
constructed by M. Brownstein (NIMH/NHGRI, National
Institutes of Health). Note: this is a NIH_MGC Library."
BASE COUNT 114 a 196 c 197 g 90 t 1 others
ORIGIN

Query Match 5.0%; Score 206; DB 10; Length 598;
Best Local Similarity 99.6%; Pred. No. 4.2e-81;
Matches 256; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 ccacgcagcggccggagatgcagcggggcgccgctgtgcctgcgaactggcctcg 60
|||||
Db 66 CCACGCGCAGCGCGCGGAGATGCACGGGGCGCGCGCTGTGCTTGCACACTGTGGCTCTG 125
QY 61 cctgggactcctggagcggcctgggtgagtggtactccatgacccccccgacctgaaacat 120
|||||
Db 126 CCTGGACTTCTGGACGGCCTGGTGAGTGGCTACTTCCATGACCCCGCCGACCTTGAACAT 185
QY 121 cacggaggagtcacacgctcatcgacacccggtgacagcctgtccatctcctgcaggggaca 180
|||||
Db 186 CACGGAGGAGTCACACGCTCATCGACACCGGTGACAGCGCTGTCCATCTCTCTCAGGGGACA 245
QY 181 gcacccctcagtggtggttggccagagatcaggaggcgccaccagcagagacaagga 240
|||||
Db 246 GCACCCCTCGAGTGGGCTTGGCCAGGAGCTCAGAGGCGCCGACGCCACCGGAGACAAGGA 305
QY 241 cagcgaggacacggggg 257
|||||
Db 306 CAGCGAGGACACGGGGG 322

RESULT 7
AA367842

LOCUS	AA367842	284 bp	mRNA	linear	EST 21-APR-1999
DEFINITION	EST79262 Placenta I Homo sapiens cDNA similar to tyrosine kinase, receptor FL74, class III, mRNA sequence.				
ACCESSION	AA367842				
VERSION	AA367842.1 GI:2020386				
KEYWORDS	EST.				
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
AUTHORS	1 (bases 1 to 284)				
	Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A., Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstein,K.G., Gocayne,J.D., White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C., Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D., Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S., Glodak,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkley,P.S.Jr., Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M., Moreno-Palauques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M., Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R., Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y., Bednarek,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J., Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A., He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K., Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Meissner,P.S., Olsen,H., Raymond,L., Wei,Y.F., Ming,J., Xu,C., Yu,G.L., Ruben,S.M., Dillion,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C., Fraser,C.M. and Venter,J.C.				
TITLE	Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence				
JOURNAL	Nature 377 (6547 Suppl), 3-174 (1995)				
MEDLINE	96026280				
COMMENT	Other_ESTs: THC85507 Contact: Kerlavage, AR Bioinformatics The Institute for Genomic Research 9712 Medical Center Drive, Rockville, MD 20850 USA Tel: 3018699056 Fax: 3018699423 Email: arkerlavetigr.org For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (http://www.tigr.org/tdb/hgi/hgi.html) Seq primer: M13-21.				
FEATURES	Location/Qualifiers				
source	1..284 /organism="Homo sapiens" /db_xref="ATCC (Inhost):172752" /db_xref="taxon:9606" /clone_lib="Placenta I" /tissue_type="placenta" /dev_stage="fetus" /note="Organ: placenta; Vector: pBluescript SK-; Site_1: EcoRI; Site_2: EcoRI"				
BASE COUNT	56 a 91 c 91 g 46 t				
ORIGIN					
Query Match	4.6%; Score 189; DB 9; Length 284;				
Best Local Similarity	99.6%; Pred. No. 1.5e-73;				
Matches 239;	Conservative 0; Mismatches 1; Indels 0; Gaps 0;				
Qy 2541	cccgagagcggtgcacctgggagagtgctcgagctacgagcgcttcgggaagtgtg 2600 				
Db 1	CCCGAGAGCGGCTGCACCTGGGAGAGTGTCTGGCTACGGCGGCTTCGGGAAGGTGTGG 60 				
Qy 2601	aagcctccgttttcggcatcccaaggcgagctgtgacacccgtggccgtgaaatgc 2660 				
Db 61	AAGCCTCCGCTTTCGGCATCCAGAGGCGCAGCAGCTGTGACACCGTGGCCGTGAAATGC 120 				
Qy 2661	tgaagaggcgccacgagccagcagcagccagcgctgtatgtcggagctcaagatctca 2720 				
Db 121	TGAAGAGGCGCCACGGCAGCAGCAGCCCGCGTGTATGTCGGAGCTCAAGATCCTCA 180 				

Qy 3909 tcag 3912
||||
Db 181 TCAG 184

RESULT 9

AW872408
LOCUS
DEFINITION
hl91g10.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3009378 3'
similar to gb:X68203 TYROSINE-PROTEIN KINASE RECEPTOR FLT4
PRECURSOR (HUMAN); mRNA sequence.

ACCESSION
AW872408

VERSION
AW872408.1 GI:8006461

KEYWORDS
EST.

SOURCE
human.

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 591)

REFERENCE
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

AUTHORS
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

TITLE
Tumor Gene Index

JOURNAL
Unpublished (1997)

COMMENT
Contact: Robert Strausberg, Ph.D.

Email: cgaps-r@mail.nih.gov

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.

cDNA Library Preparation: M. Bento Soares, Ph.D.

DNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL, send email to:

info@image.llnl.gov

Seq primer: -40UP from Gibco

High quality sequence stop: 428.

Location/Qualifiers

1..591

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:3009378"

/clone_lib="NCI_CGAP_Lu24"

/tissue_type="carcinoid"

/lab_host="DH10B"

/note="Organ: lung; Vector: pT7T3D-Pac (Pharmacia) with a

modified polylinker; Plasmid DNA from the normalized

library NCI_CGAP_Lu5 was prepared, and ss circles were

made in vitro. Following HAP purification, this DNA was

used as tracer in a subtractive hybridization reaction.

The driver was PCR-amplified cDNAs from a pool of 5,000

clones made from the same library (cloneids

1414920-1417991 and 1520904-1522439). Subtraction by Bento

Soares and M. Fatima Bonaldo."

162 a 146 c 166 g 117 t

BASE COUNT

ORIGIN

Query Match

Best Local Similarity 4.5%; Score 184; DB 9; Length 591;

Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3729 ccgggtgcttgcagagggtgagaccgtgtgtccctccaggatgaagacatttgagg 3788

|||||

Db 1 CCGGGTGCCTGGCCAGAGGGGCTGAGACCCGCTGTTCTCCAGGATGAAGACATTGAGG 60

Qy 3789 aattccccatgaccccaagacctacaaggctctgtgagacacacagacagtgga 3848

|||||

Db 61 AATTCCCCATGACCCCAAGACCTACAAAGGCTCTGTGGACCAACCCAGACAGTGGGA 120

Qy 3849 tggctgtgctcgagggaggtttgagcagatagagagcaggcatagacagaagcgcct 3908

|||||

Db 121 TGGTGTGGCCTCGGAGGAGTTTGACCATAGAGAGCAGGCATAGACAAGAAAGCGGCT 180

Qy 3909 tcag 3912
||||
Db 181 TCAG 184

RESULT 10

BE245906
LOCUS
DEFINITION
TCBAP1D3468 Pediatric pre-B cell acute lymphoblastic leukemia
Baylor-HGSC Project-TCBA Homo sapiens cDNA clone TCBAP3468, mRNA
sequence.

ACCESSION
BE245906

VERSION
BE245906.1 GI:9097654

KEYWORDS
EST.

SOURCE
human.

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 365)

REFERENCE
Wei,Y., Tsang,Y.T.M., Mei,G., Ku,J.M., Ali-Osman Jr.,F.R., Muzny,D.

, Bouck,J., Gibbs,R.A. and Margolin,J.F.

Pediatric Leukemia cDNA Sequencing Project

Unpublished (2000)

TITLE
JOURNAL

COMMENT
Contact: Dr. Judith F. Margolin

Texas Children's Cancer Center and Human Genome Sequencing Center

at Baylor College of Medicine

1102 Bates, MC3-3320 Houston, TX 77030, USA

Tel: 832-824-4536

Fax: 832-825-4038

Email: clones@ccc.org

Citation: Carninci, P. and Hayashizaki, Y. High efficiency

full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)

Seq primer: M13 primer.

FEATURES

source

Location/Qualifiers

1..365

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="TCBAP3468"

/clone_lib="Pediatric pre-B cell acute lymphoblastic

leukemia Baylor-HGSC project-TCBA"

/sex="male"

/tissue_type="leukopheresis"

/cell_type="pre-B cell"

/dev_stage="pediatric 2 years"

/lab_host="DH10B"

/note="Vector: lambda pSB; Site_1: BamHI; Site_2: EcoRI;

First strand cDNA was primed with an anchored

XhoI-oligo(dT) primer (5'GGAGACTCGAGCGCCGAGGAGGAG(T)VN

3'; V=A,C,G; N=A,C,G,T) and then dG tailed. Second strand

was primed with a BamHI-dc primer

(5'AGAGCTCGGATCGCGCGCGCAATATAAT(C) 3').

Double-stranded cDNA was then digested with BamHI and XhoI

and directionally cloned into the BamHI and SalI sites of

lambda pSB vector. Library went through one round of

normalization. Library was constructed by Wei Yu at RIKEN

of Japan (Carninci P., Westover A., Nishiyama Y., Ohsumi T,

Itoh M, Nagaoka S, Sasakini, Okazaki Y, Muramatsu M,

Schneider C, Hayashizaki Y, High efficiency selection of

full-length cDNA by improved biotinylated cap trapper..

DNA Res 4: 1, 61-6, Feb 28, 1997)

78 a 107 c 112 g 68 t

BASE COUNT

ORIGIN

Query Match

Best Local Similarity 3.6%; Score 148; DB 10; Length 365;

Matches 198; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 343 ctacgtctgctactacaagtcacacagcagcatcgagccaccagcgccgcagctc 402

|||||

Db 149 CTACGTCCTGCTACTACAAGTACATCAGGCACGCATCGAGGGCCACCGCGCGCAGCTC 208

|||||

Qy 403 ctacgtgttcgtgagactttgagcagcattcatcaacaagcctgacagcgtctggt 462

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|||||
Db 209 ATACGTGTCGTGAGAGACTTTGAGCACCATTATCAACAAGCCTGACAGCGTCTTGCT 268
Qy 463 caacaggaagacgcacatgtgggtccctgtctgtgtgtccatccccgcctcaatgtcac 522
|||||
Db 269 CAACAGGAAGACGCATGTGGTGCCCTGTCTGTGTGCCATCCCGGCCCTCAATGTCCAC 328
Qy 523 gctgcgtcgcaaaactcg 541
|||||
Db 329 GCTGCGCTCGCAAGACTCG 347

RESULT 11
AA223868
LOCUS
DEFINITION
  AA223868 344 bp mRNA linear EST 11-MAR-1998
  cd10h2.r1 Stratagene NT2 neuronal precursor 937230 Homo sapiens
  cDNA clone IMAGE:651143 5' similar to gb:X68203 TYROSINE-PROTEIN
  KINASE RECEPTOR FLT4 PRECURSOR (HUMAN);, mRNA sequence.
ACCESSION
  AA223868
VERSION
  AA223868.1 GI:1844453
KEYWORDS
  EST.
SOURCE
  human.
ORGANISM
  Homo sapiens
REFERENCE
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS
  Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
  Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin
  J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B.,
  White,Y., Wyllie,T., Waterston,R. and Wilson,R.
  WashU-NCI human EST Project
  Unpublished (1997)
  Contact: Wilson RK
  Washington University School of Medicine
  444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
  Tel: 314 286 1800
  Fax: 314 286 1810
  Email: est@watson.wustl.edu
  This clone is available royalty-free through LLNL; contact the
  IMAGE Consortium (info@image.llnl.gov) for further information.
  Insert Length: 1275 Std Error: 0.00
  Seq primer: -28ml3 rev1 ET from Amersham
  High quality sequence stop: 238.
FEATURES
  source
  1..344
  /organism="Homo sapiens"
  /db_xref="GDB:5588193"
  /db_xref="taxon:9606"
  /clone="IMAGE:651143"
  /issue_type="neuroepithelial cells"
  /dev_stage="Ntera-2 neuroepithelial cells"
  /lab_host="SOLR (kanamycin resistant)"
  /note="Organ: brain; Vector: pBluescript SK-; Site:1:
  EcoRI; Site:2: XhoI; Cloned unidirectionally. Primer:
  Oligo dt. Uninduced, exponentially growing neuroepithelial
  cells (Ntera-2/cl.D1). Average insert size: 1.0 kb;
  Uni-ZAP XR Vector; -5' adaptor sequence: 5' GAATTCGGCAGCAG
  3' -3' adaptor sequence: 5' CTCGAGTGTGTTTTTTTTTTT 3'"
BASE COUNT
  65 a 92 c 115 g 56 t 6 others
ORIGIN
  3.5%; Score 143; DB 9; Length 344;
  Query Match
  Best Local Similarity 100.0%; Pred. No. 6.2e-53;
  Matches 143; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

|||||
Qy 3257 tggatggccctgaagcatcttcgacaaaggtgtacacacgagagtgacgtgtgtgcc 3316
|||||
Db 1 TCGATGGCCCTCGAAAGCATCTTCGACAAGGTGTACACCACGACGAGTGACGTGTGTCC 60
Qy 3317 ttgggggtctctctgggaagatctctctctgggggctccccgcctacccctggggtgcag 3376
|||||

```

```

Db 61 TTTGGGTGCTTCTCTGGGAGATCTTCTCTCTGGGGCCCTCCCGGTACCCCTGGGGTGCAG 120
Qy 3377 atcaatgaggagttctgccagcg 3399
|||||
Db 121 ATCAATGAGGAGTTCTGCCAGCG 143

RESULT 12
T28462
LOCUS
DEFINITION
  T28462 411 bp mRNA linear EST 06-SEP-1995
  Kinase receptor FLT4, class III (HT:1601), mRNA sequence.
ACCESSION
  T28462
VERSION
  T28462.1 GI:610560
KEYWORDS
  EST.
SOURCE
  human.
ORGANISM
  Homo sapiens
REFERENCE
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS
  Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A., Bult
  C.J., Lee,N., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D., White
  O., Sutton,G., Blake,J.A., Brandon,R.C., Chiu,M.-W., Clayton,R.A.,
  Cline,R.T., Cotton,M.D., Earle-Hughes,J., Fine,L.D., FitzGerald
  L.M., FitzHugh,W.M., Fritchman,J.L., Geoghagen,N.S.M., Glodek,A.,
  Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinklejr,P.S., Kelley,J.M.,
  Klinek,K.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M.,
  Moreno-Palancques,R.F., McDonald,L.A., Nguyen,D.T., Pellegriano,S.M.,
  Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R.A.,
  Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y.,
  Bednarek,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.-J.,
  Dimke,D., Feng,P., Ferrie,A., Fischer,C., Hastings,G.A., He,W.-W.,
  Hu,J.-S., Greene,J.M., Gruber,J., Hudson,P., Kim,A., Kozak,D.L.,
  Kunsch,C., Ji,H., Li,H., Meissner,P.S., Olsen,H., Raymond,L., Wei
  M.R., Wing,J., Xu,C., Yu,G.-L., Ruben,S.M., Dillon,P.J., Fannon
  M.R., Rosen,C.A., Haseltine,W.A., Fields,C., Fraser,C.M. and
  Venter,J.C.
  Initial Assessment of Human Gene Diversity and Expression Patterns
  Based Upon 83 Million Basepairs of cDNA Sequence
  Nature 377, 3-174 (1995)
  96026280
  Contact: Venter, JC
  The Institute for Genomic Research
  932 Clopper Rd, Gaithersburg, MD 20878
  Tel: 3018699056
  Fax: 3018699423
  Email: tdbinfo@tdb.tigr.org
  For clone availability, additional sequence and expression
  information related to this EST, please contact the TIGR database
  (tdbinfo@tdb.tigr.org)
  Seq primer: M13 Reverse.
FEATURES
  source
  Location/Qualifiers
  1..411
  /organism="Homo sapiens"
  /db_xref="ATCC (inhost):102639"
  /db_xref="taxon:9606"
  /clone.lib="Human kidney"
  /note="Organ: kidney"
BASE COUNT
  123 a 87 c 110 g 86 t 5 others
ORIGIN
  3.2%; Score 133; DB 10; Length 411;
  Query Match
  Best Local Similarity 100.0%; Pred. No. 1.9e-48;
  Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

|||||
Qy 3780 catttgaggaaattccccatgaccccaacgacctacaagcctctgtggacaacacagacag 3839
|||||
Db 1 CATTTGAGGAATTCCTCCATGACCCCAACGACCTACAAAGGCTCTGTGTGACAACACAGAC 60
Qy 3840 acagtgaggatggtgctgctggcctcgaggaggtttgagcagatagagagcagcagacaaag 3899
|||||
Db 61 ACATGGGATGGTGTCTGCGCTCGGAGGAGTTTGAGCAGATAGAGAGCAGGCATAGACAAG 120

```

QY 3900 aaagcggttcag 3912
|||||
Db 121 AAGCGGCTTCAG 133

RESULT 13
AW950116
LOCUS AW950116 546 bp mRNA linear EST 01-JUN-2000
DEFINITION EST362081 MAGE resequences, MAGA Homo sapiens cDNA, mRNA sequence.
ACCESSION AW950116
VERSION AW950116.1 GI:8139652
KEYWORDS EST.
SOURCE human.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 546)
Hegde, P., Qi, R., Abernathy, K., Dharap, S., Gaspard, R., Gay, C., Holt
I.E., Saeed, A.I., Sharov, V., Lee, N.H., Yeatman, T.J. and
Quackenbush, J.
Assessment of gene expression patterns in a model of colon tumor
metastasis using a 19,200 element cDNA microarray
Unpublished (2000)
Contact: John Quackenbush
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 3528
Fax: 301 838 0208
Email: johnq@tigr.org
Plate: 9
Seq primer: Reverse.

FEATURES
source
Location/Qualifiers
1..546
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="MAGE resequences, MAGA"
/note="Vector: pBluescriptSKm"

BASE COUNT 155 a 125 c 151 g 115 t
ORIGIN

Query Match 3.2%; Score 132; DB 9; Length 546;
Best Local Similarity 100.0%; Pred. No. 5.5e-48;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3781 atttgaggattccccatgaccccaacgacctacaaaggctctgtggacaaccagacaga 3840
|||||
Db 1 ATTTGAGGAATTCCCATGACCCCAACGACCTACAAAGGCTCTGTGGACAACGACAGACA 60

QY 3841 cagtggatggtgctggcctcgaggagtttgacgacagatagagcagcagcatagacaaga 3900
|||||
Db 61 CAGTGGATGCTGCTGGCCCTCGAGGAGTTTGAGCAGATAGACGAGCGCATAGACAAGA 120

QY 3901 aagcggttcag 3912
|||||
Db 121 AAGCGGCTTCAG 132

RESULT 14
AW950567
LOCUS AW950567 587 bp mRNA linear EST 01-JUN-2000
DEFINITION EST362637 MAGE resequences, MAGA Homo sapiens cDNA, mRNA sequence.
ACCESSION AW950567
VERSION AW950567.1 GI:8140223
KEYWORDS EST.
SOURCE human.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 587)
Hegde, P., Qi, R., Abernathy, K., Dharap, S., Gaspard, R., Gay, C., Holt
I.E., Saeed, A.I., Sharov, V., Lee, N.H., Yeatman, T.J. and

Quackenbush, J.
Assessment of gene expression patterns in a model of colon tumor
metastasis using a 19,200 element cDNA microarray
Unpublished (2000)
Contact: John Quackenbush
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 3528
Fax: 301 838 0208
Email: johnq@tigr.org
Plate: 16
Seq primer: Reverse.

FEATURES
source
Location/Qualifiers
1..587
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="MAGE resequences, MAGA"
/note="Vector: pBluescriptSKm"

BASE COUNT 162 a 150 c 155 g 120 t
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 5.6e-48;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3781 atttgaggattccccatgaccccaacgacctacaaaggctctgtggacaaccagacaga 3840
|||||
Db 1 ATTTGAGGAATTCCCATGACCCCAACGACCTACAAAGGCTCTGTGGACAACGACAGACA 60

QY 3841 cagtggatggtgctggcctcgaggagtttgacgacagatagagcagcagcatagacaaga 3900
|||||
Db 61 CAGTGGATGCTGCTGGCCCTCGAGGAGTTTGAGCAGATAGACGAGCGCATAGACAAGA 120

QY 3901 aagcggttcag 3912
|||||
Db 121 AAGCGGCTTCAG 132

RESULT 15
AQ801382/c
LOCUS AQ801382 497 bp DNA linear GSS 09-AUG-1999
DEFINITION HS_5394_AL_E12_T7A RPCI-11 Human Male BAC Library Homo sapiens
genomic clone Plate-970 Col-23 Row-I, DNA sequence.
ACCESSION AQ801382
VERSION AQ801382.1 GI:5718714
KEYWORDS GSS.
SOURCE human.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 497)
Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,
Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
Hood, L.
Sequence-tagged connectors: A sequence approach to mapping and
scanning the human genome
Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
99380589

REFERENCE
AUTHORS
Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.bufo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.bufo.edu/ordering_bac.htm)
or from Resear h Genetics (info@resgen.com). BAC end Web Server:
http://www.htsc.washington.edu
Plate: 970 row: 1 column: 23

Seq primer: T7
Class: BAC ends
High quality sequence stop: 497.

FEATURES

Location/Qualifiers
1..497
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="Plate-970 Col-23 Row-I"
/clone_lib="RPCI-11 Human Male BAC Library"
/sex="male"
/note="Vector: pBACE3.6; Site_1: EcoRI; Site_2: EcoRI;
Male blood DNA was isolated from one randomly chosen donor
and partially digested with a combination of EcoRI and
EcoRI methylase. Size selected DNA was cloned into the
pBACE3.6 vector at EcoRI sites"

BASE COUNT 90 a 147 c 146 g 110 t 4 others

ORIGIN

Query Match 3.1%; Score 127; DB 12; Length 497;
Best Local Similarity 100.0%; Pred. No. 9.4e-46;
Matches 127; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3985 ttgagcgggggcccgagagagccaggtgttttacacagcagtagtgaggagctgcgga 4044
|||||
DB 341 TCAGCGGGGGCCCGAGGAGCCAGGTGTTTACAAACAGCGAGTATGGGAGCTGTCGGA 282
|||||

QY 4045 gccagcgaggaggaccactgtcccgctctgcccggtgaccttcttcacagacaacag 4104
|||||
DB 281 GCCAAGCGAGGAGGACCACTGCTCCCGCTCTGCCCGCGTGACTTTTTCACAGACAACAG 222
|||||

QY 4105 ctactaa 4111
DB 221 CTTACTAA 215

RESULT 16

AG038807/c
LOCUS AG038807 702 bp DNA linear GSS 01-NOV-2001
DEFINITION Pan troglodytes DNA, clone: PTB-015L14.F, genomic survey sequence.
ACCESSION AG038807
VERSION AG038807.1 GI:16567532
KEYWORDS GSS: GSS (genome survey sequence).
SOURCE Pan troglodytes male lymphoblast DNA, clone_lib:PTB Chimpanzee Male
BAC Library clone:PTB-015L14.F.

ORGANISM

Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
1 (sites)
Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
Totoki, Y., Watanabe, H. and Sakaki, Y.

BAC end sequences of Library PTB

Unpublished

2 (bases 1 to 702)

Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
Totoki, Y., Watanabe, H. and Sakaki, Y.

Direct Submission

Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC); Japan
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail: chimpbes@sc.riken.go.jp, URL: http://hgp.gsc.riken.go.jp/,
Tel: 81-45-503-9111, Fax: 81-45-503-9170)

Clones are derived from the chimpanzee BAC library PTB This BAC end
was generated during the R&D process and may have higher chance of
clone tracking errors.

PRIMERS

Sequencing: -21M13

LIBRARY

Vector : pKS145

R.Site 1 : SacI

R.Site 2 : SacI

Location/Qualifiers

1..702

FEATURES

source

/organism="Pan troglodytes"
/db_xref="taxon:9598"
/clone="PTB-015L14.F"
/sex="male"
/cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"
BASE COUNT 146 a 223 c 199 g 131 t 3 others
ORIGIN

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Best Local Similarity 99.4%; Pred. No. 1.7e-43;
Matches 172; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 832 gcaggcagagcgggtaagtgggtgccgagcagctccacgacagccacacagaact 891
|||||
DB 351 GCAGGCAGAGCGGGGTAAAGTGGGTGCCCGAGCGAGCTCCCGACGACCCACAGAACT 292
|||||

QY 892 ctccagcatcctgaccatccacaacgtcagccagcagacctggctctgtgtgcaa 951
|||||

DB 291 CTCAGCATCTGACCATCCACAACGTGAGCCAGCAGCACTGGCTCGTATGTGCGA 232
|||||

QY 952 ggccaacaacggcagcagcagatttcgggagagcagcagaggtcattgtgcag 1004
|||||

DB 231 GGCCAACAACGGCATCCAGCGATTTCGGGAGAGCCGAGGTCAATGTGCGATG 179
|||||

RESULT 17

AA368924
LOCUS AA368924/c 344 bp mRNA linear EST 21-APR-1997
DEFINITION EST80250 Placenta I Homo sapiens cDNA similar to similar to
tyrosine kinase, receptor FLT4, class III, mRNA sequence.

ACCESSION AA368924

VERSION AA368924.1 GI:2021242

KEYWORDS EST.

SOURCE human.

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS

Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A., Bult
, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White
, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C., Clayton, R.A.,
Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D., Fitzgerald
, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S., Glodok, A.,
Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S., Jr., Kelley, J.M.,
Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M.,
Moreno-Palauques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M.,
Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R.,
Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.P., Li, Y.,
Bednarek, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J.,
Dimke, D., Feng, D.-F., Fertie, A., Fischer, C., Hastings, G.A., He, W.W.,
Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K., Kozak, D.L.,
Kunsch, C., Hungjun, J., Li, H., Weissner, P.S., Olsen, H., Raymond, L.,
Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M., Dillon, P.J., Fannon
, M.R., Rosen, C.A., Haseltine, W.A., Fields, C., Fraser, C.M. and
Venter, J.C.

TITLE

Initial assessment of human gene diversity and expression patterns
based upon 83 million nucleotides of cDNA sequence

JOURNAL

MEDLINE

COMMENT

Nature 377 (6547 Suppl), 3-174 (1995)

96026280

Other_ESTS: THCI92054

Contact: Kerlavage, AR

Bioinformatics

The Institute for Genomic Research

9712 Medical Center Drive, Rockville, MD 20850 USA

Tel: 3018699056

Fax: 3018699423

Email: arkerlav@tigr.org

For clone availability, additional sequence and expression

information related to this EST, please check the TIGR Human Gene

Index (<http://www.tigr.org/tdb/hgi/hgi.html>)

Seq primer: M13-21.

FEATURES	Location/Qualifiers	
	1..344	
source	/organism="Homo sapiens"	
	/db_xref="AFCC (inhost):173624"	
	/db_xref="taxon:9606"	
	/clone_lib="Placenta I"	
	/tissue_type="placenta"	
	/dev_stages="fetus"	
	/note="Organ: placenta; Vector: pBluescript SK-; Site_1: EcoRI; Site_2: EcoRI"	
	92 a 70 c 111 g 71 t	
BASE COUNT	71 t	
	71 t	
ORIGIN		
Query Match	2.6%; Score 105; DB 9; Length 344;	
	Best Local Similarity 99.4%; Pred. No. 6.3e-36;	
Matches	155; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
QY	1211 accctgcctgtggaactccgtgctggcctgagcgcaacatcagcctgagctggtg 1270	
Db	332 ACCCTGCCCTGTGGAACCTCCGCTGCTGCCCTGAGCGCGCAACATCAGCCTGAGCTGGTG 273	
QY	1271 gtgaatgtgccccccagatgacatgagaaggaggcctctctccccagcattctactcgct 1330	
Db	272 GTGAATGTGCCCGCCAGATGATGAGAAGGAGGCGCTCTCCCGCAGCATCTACTCGCGT 213	
QY	1331 cacagccgagcgcctcaccctgacggcctacggg 1366	
Db	212 CACAGCGCGCAGCGCCCTCACCTGCACGCGCTACGGG 177	
RESULT 18		
AW950105	277 bp mRNA linear EST 01-JUN-2000	
	LOCUS	
DEFINITION	EST362070 MAGE resequences, MAGA Homo sapiens cDNA, mRNA sequence.	
	AW950105	
ACCESSION	AW950105.1 GI:8139640	
	VERSION	
KEYWORDS	EST.	
	SOURCE	
ORGANISM	Homo sapiens	
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
REFERENCE	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	
	1 (bases 1 to 277)	
AUTHORS	Hegde, P., Qi, R., Abernathy, K., Dharap, S., Gaspard, R., Gay, C., Holt	
	, I. E., Saeed, A. I., Sharov, V., Lee, N. H., Yeatman, T. J. and	
Quackenbush, J.		
	Assessment of gene expression patterns in a model of colon tumor	
metastasis using a 19,200 element cDNA microarray		
	Unpublished (2000)	
Contact: John Quackenbush		
	The Institute for Genomic Research	
9712 Medical Center Dr., Rockville, MD 20850, USA		
	Tel: 301 838 3528	
Fax: 301 838 0208		
	Email: johnq@igf.org	
Plate: 9		
	Seq primer: Reverse.	
FEATURES	Location/Qualifiers	
	1..277	
source	/organism="Homo sapiens"	
	/db_xref="taxon:9606"	
	/clone_lib="MAGE resequences, MAGA"	
	/note="Vector: pBluescriptSKm"	
BASE COUNT	90 a 57 c 63 g 67 t	
	67 t	
ORIGIN		
Query Match	2.3%; Score 93; DB 9; Length 277;	
	Best Local Similarity 100.0%; Pred. No. 1.4e-30;	
Matches	93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	3781 atttgagaattccccatgacccccacgacctacaaaagctctctgtggacaaccagacaga 3840	

Db	1 ATTTGAGGAATTCCCATGATGACCCCAACGACCTACAAAGGCTCTGTGGACAACCAACACAGACA 60	
QY	3841 cagtgagtggtgctggcctcgaggagtttga 3873	
Db	61 CAGTGGAGTGTGCTGGCTCGGAGGAGTTTGA 93	
RESULT 19		
AW950105	498 bp DNA linear GSS 14-JUL-1999	
	LOCUS	
DEFINITION	HS_5438_B1_A05_T7A RPCI-11 Human Male BAC Library Homo sapiens	
	genomic clone Plate-1014 Col-9 Row-B, DNA sequence.	
ACCESSION	AW950105.1 GI:5487527	
	VERSION	
KEYWORDS	GSS.	
	SOURCE	
ORGANISM	Homo sapiens	
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
REFERENCE	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	
	1 (bases 1 to 498)	
AUTHORS	Mahairas, G. G., Wallace, J. C., Smith, K., Swartzell, S., Holzman, T.,	
	Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M. D. and	
Hood, L.		
	Sequence-tagged connectors: A sequence approach to mapping and	
scanning the human genome		
	Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)	
JOURNAL	99380589	
	MEDLINE	
COMMENT	Contact: Mahairas GG, Wallace JC, Hood L	
	High Throughput Sequencing Center	
University of Washington		
	401 Queen Anne Avenue North, Seattle, WA 98109, USA	
Tel: (206) 616-3618		
	Fax: (206) 616-3887	
Email: jwallace@u.washington.edu		
	Clones are derived from the human BAC library RPCI-11. For BAC	
library availability, please contact Pieter de Jong		
	(pieter@dejong.med.buffalo.edu). Clones may be purchased from	
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)		
	or from Resear h Genetics (info@resgen.com). BAC end Web Server:	
http://www.hsc.washington.edu		
	Plate: 1014 row: B column: 9	
Seq primer: T7		
	Class: BAC ends	
High quality sequence stop: 498.		
	Location/Qualifiers	
FEATURES	1..498	
	/organism="Homo sapiens"	
source	/db_xref="taxon:9606"	
	/clone_lib="Plate-1014 Col-9 Row-B"	
	/clone_lib="RPCI-11 Human Male BAC Library"	
	/sex="male"	
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;		
	Male blood DNA was isolated from one randomly chosen donor	
and partially digested with a combination of EcoRI and		
	EcoRI Methylase. Size selected DNA was cloned into the	
pBACe3.6 vector at EcoRI sites"		
	BASE COUNT 85 a 152 c 133 g 127 t 1 others	
ORIGIN		
Query Match	2.1%; Score 85; DB 12; Length 498;	
	Best Local Similarity 100.0%; Pred. No. 6e-27;	
Matches	85; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1592 aatgccaacgtgtctgcatgtacaaagtgtgtgtctctccaaagggtggccagatgag 1651	
Db	383 AATGCCAACGTGTCTGCCATGTACAAAGTGTGTGTCTCCAAACAGGTGGCCAGGATGAG 442	
QY	1652 cggctcatctactctctctgtgacca 1676	
Db	443 CGGCTCATCTACTTCTTATGTGACCA 467	

RESULT 20	AA368926	211 bp	mRNA	linear	EST 21-APR-1997
LOCUS	AA368926				
DEFINITION	receptor FLR4, class III, mRNA sequence.				
ACCESSION	AA368926				
VERSION	AA368926.1	GI:2021244			
KEYWORDS	EST.				
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo. 1 (bases 1 to 211)				
AUTHORS	Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fulton,R.A., Bult C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Cocayne,J.D., White ,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C., Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D., FitzGerald ,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S., Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S., Jr., Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M., Moreno-Palancoes,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M., Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R., Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y., Bednarek,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J., Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A., He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K., Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Weissner,P.S., Olsen,H., Raymond,L., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M., Dillion,P.J., Fannon ,M.R., Rosen,C.A., Haseitine,W.A., Fields,C., Fraser,C.M. and ,Venter,J.C.				
TITLE	Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence				
JOURNAL	Nature 377 (6547 Suppl), 3-174 (1995)				
MEDLINE	96026280				
COMMENT	Other_ESTs: THC85507 Contact: Kerlavage, AR Bioinformatics The Institute for Genomic Research 9712 Medical Center Drive, Rockville, MD 20850 USA Tel: 3018699056 Fax: 3018699423 Email: arkerlavetlgr.org For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (http://www.tigr.org/tdb/hgi/hgi.html) Seq primer: M13-21.				
FEATURES	Location/Qualifiers				
source	1..211 /organism="Homo sapiens" /db_xref="ATCC (inhost):173626" /db_xref="taxon:9606" /clone_lib="placenta 1" /tissue_type="placenta" /dev_stage="fetus" /note="Organ: Placenta; Vector: pBluescript SK-; site_1: EcoRI; Site_2: EcoRI"				
BASE COUNT	46 a 71 c 36 t 4 others				
ORIGIN					
Query Match	1.9%; Score 79; DB 9; Length 211;				
Best Local Similarity	100.0%; Pred. No. 2.6e-24;				
Matches	79; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
QY	1623 tgggtctcaacagggtggccagatgagcggctcatcttctatgtgaccacatcc 1682				
Db	1 TGGTCTCCACACAGGTGGCCAGATGAGCGGCTCATCTTCTATGTGACCACCATCC 60				
QY	ccgacgggttcacatcga 1701				
Db	61 CCGACGGCTTCACCATCGA 79				

RESULT 21	BG015039/c	327 bp	mRNA	linear	EST 24-JAN-2001
LOCUS	BG015039				
DEFINITION	QV2-GN0208-221200-579-g06 GN0208 Homo sapiens cDNA, mRNA sequence.				
ACCESSION	BG015039				
VERSION	BG015039.1	GI:12466844			
KEYWORDS	EST.				
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo. 1 (bases 1 to 327)				
AUTHORS	Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare ,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.				
TITLE	Shotgun sequencing of the human transcriptome with ORF expressed sequence tags				
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)				
MEDLINE	20202663				
COMMENT	Contact: Simpson A.J.G. Laboratory of Cancer Genetics Ludwig Institute for Cancer Research Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil Tel: +55-11-2704922 Fax: +55-11-2707001 Email: asimpson@ludwig.org.br This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl1-QV2&tl2-QV2-GN0208-221200-579-g06&tl3-2000-12-22&tl4-1) Seq primer: puc 18 forward High quality sequence stop: 218.				
FEATURES	Location/Qualifiers				
source	1..327 /organism="Homo sapiens" /db_xref="taxon:9606" /clone_lib="GN0208" /dev_stage="Adult" /note="Organ: placenta.normal; Vector: puc18; site_1: SmaI ; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."				
BASE COUNT	65 a 84 c 99 g 79 t				
ORIGIN					
Query Match	1.5%; Score 61; DB 10; Length 327;				
Best Local Similarity	100.0%; Pred. No. 3.1e-16;				
Matches	61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
QY	1537 ctggaccgagcttctgtggagggaagaataagactgtgacagctggtgatccagaatgc 1596				
Db	327 CTGGACCGAGCTTCTGTGAGGGAAGAATAAGACTGTGACAGCTGTCGATCCAGAATGC 268				
QY	1597 c 1597				
Db	267 C 267				

RESULT 22	BG717758	810 bp	mRNA	linear	EST 08-MAY-2001
LOCUS	BG717758				
DEFINITION	602698040F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:483201 5', mRNA sequence.				
ACCESSION	BG717758				
VERSION	BG717758.1	GI:13996945			

```

KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE 1 (bases 1 to 810)
JOURNAL NIH-MGC http://mgc.nci.nih.gov/.
COMMENT National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10750 row: p column: 10
High quality sequence start: 8
High quality sequence stop: 240.
FEATURES
Location/Qualifiers
1..810
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4830201"
/clone_lib="NIH_MGC_97"
/lab_host="DH10B"
/notes="Organ: testis; Vector: pBluescriptR (modified
pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI (gtcgag
); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTVN-3',
size-selected for average insert size 2.2 kb and
normalized to ROT 5. This is a primary library enriched
for full-length clones and constructed using the
Cap-trapper method (Carninci, in preparation). Library
constructed by M. Brownstein (NIH/NHGRI, National
Institutes of Health). Note: this is a NIH_MGC Library."
BASE COUNT 163 a 237 c 252 g 158 t
ORIGIN

Query Match 1.3%; Score 52; DB 10; Length 810;
Rest Local Similarity 100.0%; Pred. No. 3.8e-12;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 35 gcgctgtcctgcgactgtgctctgcctgagactcctgaacgacctgggtga 86
|||||
Db 118 GCGCTGTGCTCGCACTGGCTCTGCTGGACTCTCGGACCTCTGGACGCGCTGGTCA 169

RESULT 23
AA868172/c
LOCUS
DEFINITION AA868172 610 bp mRNA linear EST 04-JAN-1999
ak38f09.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1408265
3' similar to gb:X68203 TYROSINE-PROTEIN KINASE RECEPTOR FLT4
PRECURSOR (HUMAN); mRNA sequence.
ACCESSION AA868172
VERSION AA868172.1 GI:2963617
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE 1 (bases 1 to 610)
JOURNAL NCI-CCGAP http://www.ncbi.nlm.nih.gov/ncicgap.
COMMENT National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo
, Ph.D.

cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CCGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 1499 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 400

```

```

cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CCGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 1919 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 417.
FEATURES
Location/Qualifiers
1..610
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1408265"
/clone_lib="Soares_testis_NHT"
/sex="male"
/lab_host="DH10B"
/notes="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was prepared from mRNA obtained from Clontech Laboratories
, inc., and primed with a Not I - oligo(dT) primer [5'
TGTTACCAATCTGAAGTGGGAGCGGCCCAATTTTTTTTTTTT 3'].
Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT7T3 vector. Library
went through one round of normalization to Cot5, and was
constructed by Bento Soares and M. Fatima Bonaldo."
BASE COUNT 133 a 155 c 148 g 174 t
ORIGIN

Query Match 1.2%; Score 50; DB 9; Length 610;
Rest Local Similarity 100.0%; Pred. No. 2.9e-11;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3852 tgcctgcctcgaggagctttgagcagatagagcagcgagcagcagacaaga 3901
|||||
Db 586 TGCTGGCTCGGAGGAGTTTGACAGATAGAGCAGCAGCAGCAAGAA 537

RESULT 24
AI553743/c
LOCUS
DEFINITION AI553743 877 bp mRNA linear EST 12-MAY-1999
tn28c09.x1 NCI-CCGAP_Brn25 Homo sapiens cDNA clone IMAGE:2168944 3'
similar to gb:X68203 TYROSINE-PROTEIN KINASE RECEPTOR FLT4
PRECURSOR (HUMAN); contains element MER22 repetitive element ;, mRNA
sequence.
ACCESSION AI553743
VERSION AI553743.1 GI:4486106
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE 1 (bases 1 to 877)
JOURNAL NCI/NINDS-CCGAP http://www.ncbi.nlm.nih.gov/ncicgap.
COMMENT National Cancer Institute / National Institute of Neurological
Disorders and Stroke, Brain Tumor Genome Anatomy Project
(CGAP/BRGAP), Tumor Gene Index
Unpublished (1998)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CCGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 1499 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 400

```

```

FEATURES
  source
    POLYA-No.
      Location/Qualifiers
        1..877
          /organism="Homo sapiens"
          /db_xref="taxon:9606"
          /clone_image="IMAGE:2168944"
          /clone_lib="NCI CGAP Brn25"
          /tissue_type="anaplastic oligodendroglioma"
          /lab_host="DH10B"
          /note="Organ: Brain; Vector: pT7T3D-Pac (Pharmacia) with a
          modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
          strand cDNA was primed with a Not I - oligo(dT) primer [5',
          TGTTACCAATCTCAAGTCGACGCGGCATAGGTTTATTTTATTTTATTTT
          T 3']; double-stranded cDNA was ligated to Eco RI
          adaptors (Pharmacia), digested with Not I and cloned into
          the Not I and Eco RI sites of the modified pT7T3 vector.
          Library is normalized, and was constructed by Bento
          Soares and M.Fatima Bonaldo."
        BASE COUNT      152 a   257 c   260 g   202 t
        ORIGIN
          Query Match
          Best Local Similarity 1.2%; Score 49; DB 9; Length 877;
          Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3579 cccgcgcagctctcagagctcagaagaggcagctctcgcaggtgtc 3627
|||||
Db 741 CCCGCGCAGCTCTCAGAGCTCAGAGGCGCAGCTTCTCGCAGGTGTC 693

RESULT 25
CNS054KM/c
LOCUS
DEFINITION
  Tetraodon nigroviridis genome survey sequence T3 end of clone
  009L17 of library A from Tetraodon nigroviridis, genomic survey
  sequence.
ACCESSION
  AL320863.1 GI:9553747
VERSION
  GSS; genome survey sequence.
KEYWORDS
  Tetraodon nigroviridis.
SOURCE
  Tetraodon nigroviridis
  ORGANISM
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
    Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
    Tetraodontidae; Tetraodon.
    1 (bases 1 to 1091)
    Roest Crolius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
    Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
    Saurin,W. and Weissenbach,J.
    Estimate of human gene number provided by genome-wide analysis
    using Tetraodon nigroviridis DNA sequence
    Nat. Genet. 25 (2), 235-238 (2000)
    20296633
  TITLE
    2 (bases 1 to 1091)
    Crolius,H.R., Jaillon,O., Dasilva,C., Ozouf-Costaz,C., Fizames,C.,
    Fischer,C., Bouneau,L., Billault,A., Quetier,F., Saurin,W.,
    Bernot,A. and Weissenbach,J.
    Characterization and repeat analysis of the compact genome of the
    freshwater pufferfish tetraodon nigroviridis
    Genome Res. 10 (7), 939-949 (2000)
    20359837
  REFERENCE
    3 (bases 1 to 1091)
    Genoscope.
    Direct Submission
    Submitted (12-APR-2000) to the EMBL/GenBank/DBJ databases
    This sequence is a single read and was generated as part of a large
    scale clone-end sequencing project of the Tetraodon nigroviridis
    genome. For more information, please take a look at
    http://www.genoscope.cns.fr/Tetraodon.
    Location/Qualifiers
      1..1091
        /organism="Tetraodon nigroviridis"
FEATURES
  source
    Location/Qualifiers
      1..877
        /db_xref="taxon:9606"
        /clone_image="IMAGE:2168944"
        /clone_lib="NCI CGAP Brn25"
        /tissue_type="anaplastic oligodendroglioma"
        /lab_host="DH10B"
        /note="Organ: Brain; Vector: pT7T3D-Pac (Pharmacia) with a
        modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
        strand cDNA was primed with a Not I - oligo(dT) primer [5',
        TGTTACCAATCTCAAGTCGACGCGGCATAGGTTTATTTTATTTTATTTT
        T 3']; double-stranded cDNA was ligated to Eco RI
        adaptors (Pharmacia), digested with Not I and cloned into
        the Not I and Eco RI sites of the modified pT7T3 vector.
        Library is normalized, and was constructed by Bento
        Soares and M.Fatima Bonaldo."
      BASE COUNT      152 a   257 c   260 g   202 t
      ORIGIN
        Query Match
        Best Local Similarity 1.2%; Score 49; DB 9; Length 877;
        Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3579 cccgcgcagctctcagagctcagaagaggcagctctcgcaggtgtc 3627
|||||
Db 741 CCCGCGCAGCTCTCAGAGCTCAGAGGCGCAGCTTCTCGCAGGTGTC 693

RESULT 25
CNS054KM/c
LOCUS
DEFINITION
  Tetraodon nigroviridis genome survey sequence T3 end of clone
  009L17 of library A from Tetraodon nigroviridis, genomic survey
  sequence.
ACCESSION
  AL320863.1 GI:9553747
VERSION
  GSS; genome survey sequence.
KEYWORDS
  Tetraodon nigroviridis.
SOURCE
  Tetraodon nigroviridis
  ORGANISM
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
    Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
    Tetraodontidae; Tetraodon.
    1 (bases 1 to 1091)
    Roest Crolius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
    Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
    Saurin,W. and Weissenbach,J.
    Estimate of human gene number provided by genome-wide analysis
    using Tetraodon nigroviridis DNA sequence
    Nat. Genet. 25 (2), 235-238 (2000)
    20296633
  TITLE
    2 (bases 1 to 1091)
    Crolius,H.R., Jaillon,O., Dasilva,C., Ozouf-Costaz,C., Fizames,C.,
    Fischer,C., Bouneau,L., Billault,A., Quetier,F., Saurin,W.,
    Bernot,A. and Weissenbach,J.
    Characterization and repeat analysis of the compact genome of the
    freshwater pufferfish tetraodon nigroviridis
    Genome Res. 10 (7), 939-949 (2000)
    20359837
  REFERENCE
    3 (bases 1 to 1091)
    Genoscope.
    Direct Submission
    Submitted (12-APR-2000) to the EMBL/GenBank/DBJ databases
    This sequence is a single read and was generated as part of a large
    scale clone-end sequencing project of the Tetraodon nigroviridis
    genome. For more information, please take a look at
    http://www.genoscope.cns.fr/Tetraodon.
    Location/Qualifiers
      1..1091
        /organism="Tetraodon nigroviridis"
FEATURES
  source
    Location/Qualifiers
      1..877
        /db_xref="taxon:99883"
        /clone_image="IMAGE:2168944"
        /clone_lib="A"
        /note="Genoscope sequence ID : C0AA009CF09A1-end : T3"
      BASE COUNT      294 a   228 c   294 g   242 t   33 others
      ORIGIN
        Query Match
        Best Local Similarity 100.0%; Score 38; DB 12; Length 1091;
        Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2438 gacatcagacggctacgtctccatcatcatcatgaccc 2475
|||||
Db 362 GACATCAAGACGGCTACCTCTCCATCATCATGACCC 325

RESULT 26
BB647382
LOCUS
DEFINITION
  BB647382 RIKEN full-length enriched, 10 days neonate cerebellum Mus
  musculus cDNA clone B930088118 5', mRNA sequence.
ACCESSION
  BB647382
VERSION
  BB647382.1 GI:16481711
KEYWORDS
  EST.
SOURCE
  house mouse.
  ORGANISM
    Mus musculus
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
    1 (bases 1 to 570)
    Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanganaki,T., Hara,A.,
    Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda
    ,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M.,
    Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki
    ,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H.,
    Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T.,
    Muramatsu,M. and Hayashizaki,Y.
    RIKEN Mouse ESTs (Arakawa,T., et al. 2001)
    Unpublished (2001)
    TITLE
      RIKEN Mouse ESTs (Arakawa,T., et al. 2001)
    JOURNAL
    COMMENT
      Contact: Yoshihide Hayashizaki
      Laboratory for Genome Exploration Research Group, RIKEN Genomic
      Sciences Center(GSC), Yokohama Institute
      The Institute of Physical and Chemical Research (RIKEN)
      1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
      Tel: 81-45-503-9222
      Fax: 81-45-503-9216
      Email: genome-res@gsr.riken.go.jp,
      URL:http://genome.gsc.riken.go.jp/
      Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
      ,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
      Normalization and subtraction of cap-trapper-selected cDNAs to
      prepare full-length cDNA libraries for rapid discovery of new
      genes. Genome Res. 10 (10), 1617-1630 (2000)
      wagi,K., Fujiwara,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
      Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
      ,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
      Hayashizaki,Y.
      RIKEN integrated sequence analysis (RISA) system--384-format
      sequencing pipeline with 384 multicapillary sequencer. Genome Res.
      10 (11), 1757-1771 (2000)
      Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara
      ,Y. and Hayashizaki,Y.
      Computer-based methods for the mouse full-length cDNA
      encyclopedia: real-time sequence clustering for construction of a
      nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
      Kondo,S., Shingawa,A., Saito,T., Kiyosawa,H., Yamanaka,I., Aizawa
      ,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and
      Hayashizaki,Y.
      Computational Analysis of Full-Length Mouse cDNAs Compared with
      Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
      Please visit our web site (http://genome.gsc.riken.go.jp) for
      further details.
      e mouse tissues.

```

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/organism="Homo sapiens"  
/db_xref="taxon:9606"  
/clone_lib="GN0134"  
/dev_stage="Adult"
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/note="Organ: placenta_normal; Vector: puc18; Site_1: SmaI
 ; Site_2: SmaI; A mini-library was made by cloning
 products derived from ORESTES PCR (U.S. Letters Patent
 application No. 196,716 - Ludwig Institute for Cancer
 Research) profiles into the pUC 18 vector. Reverse
 transcription of tissue mRNA and cDNA amplification were
 performed under low stringency conditions."
 54 a 48 c 64 g 50 t

Query Match 0.7%; Score 29; DB 10; Length 216;
 Best Local Similarity 100.0%; Pred. No. 0.062;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 900 tcttaccatccacagacgagcagcagc 928
 Db 47 TCCTGACCATCCACACAGCTGCGCTGC 19

RESULT 29
 BG815223
 LOCUS
 DEFINITION
 dec02f10.y1 NICHD XGC Emb2 Xenopus laevis cDNA clone IMAGE:4405795
 5' similar to TR:Q91897 Q91897 FIBROBLAST GROWTH FACTOR RECEPTOR
 PRECURSOR. ; mRNA sequence.
 ACCESSION
 BG815223
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 African clawed frog.

REFERENCE
 AUTHORS
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
 Xenopodinae; Xenopus.
 1 (bases 1 to 189)
 Clifton, S., Johnson, S.L., Blumberg, B., Song, J., Hillier, L., Pape, D.,
 Martin, J., Wylie, T., Underwood, K., Theising, B., Bowers, Y., Person
 , B., Gibbons, M., Harvey, N., Ritter, E., Jackson, Y., McCann, R.,
 Waterston, R. and Wilson, R.
 Washu Xenopus EST project, 1999
 Unpublished (1999)
 Contact: Sandy Clifton, Ph.D.
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810

FEATURES
 source
 1. .189
 /organism="Xenopus laevis"
 /db_xref="taxon:8355"
 /clone="IMAGE:4405795"
 /clone_lib="NICHD XGC Emb2"
 /tissue_type="embryo, stage 17/19"
 /lab_host="DH10B (phage-resistant)"
 /note="Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI;
 Cloned unidirectionally. Primer: Oligo dT. Average insert
 size 2.1 kb. Constructed by Life Technologies."
 49 a 48 c 50 g 42 t

Query Match 0.7%; Score 27; DB 10; Length 189;
 Best Local Similarity 100.0%; Pred. No. 0.47;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 3112 aaagtgcacacagacgagcagcagc 3138
 |||||

Db 125 AAAGTCATCCACAGACCTGGCTGC 151
 RESULT 30
 BG656884
 LOCUS
 DEFINITION

BF656884
 df25g11.y1 Wellcome CRC PRN3 St10 5 Xenopus laevis cDNA clone
 IMAGE:3558357 5' similar to TR:Q91897 Q91897 FIBROBLAST GROWTH
 FACTOR RECEPTOR PRECURSOR. ; mRNA sequence.

ACCESSION
 BG656884
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 African clawed frog.

REFERENCE
 AUTHORS
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
 Xenopodinae; Xenopus.
 1 (bases 1 to 514)
 Clifton, S., Johnson, S.L., Blumberg, B., Song, J., Hillier, L., Pape, D.,
 Martin, J., Wylie, T., Underwood, K., Theising, B., Bowers, Y., Person
 , B., Gibbons, M., Harvey, N., Ritter, E., Jackson, Y., McCann, R.,
 Waterston, R. and Wilson, R.
 Washu Xenopus EST project, 1999
 Unpublished (1999)
 Other ESTs: df25g11.x1
 Contact: Sandy Clifton, Ph.D.
 Washu Xenopus EST project, 1999
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810

FEATURES
 source
 1. .514
 /organism="Xenopus laevis"
 /db_xref="taxon:8355"
 /clone="IMAGE:3558357"
 /clone_lib="Wellcome CRC PRN3 St10 5"
 /tissue_type="embryo, stage 10.5"
 /lab_host="DH10B (phage-resistant)"
 /note="Vector: pBSRN3; Site_1: NotI; Site_2: EcoRI; cDNAs
 were oligo-dT primed and directionally cloned. Staging
 according to Nieuwkoop and Faber. Library was constructed
 by N. Garrett, P. LeMaire, A.M. Zorn, and J.B. Gurdon
 (Wellcome/CRC Institute)."
 148 a 110 c 141 g 114 t 1 others

Query Match 0.7%; Score 27; DB 10; Length 514;
 Best Local Similarity 100.0%; Pred. No. 0.55;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3112 aaagtgcacacagacgagcagcagc 3138
 |||||

RESULT 31
 AA637964
 LOCUS
 DEFINITION
 AA637964
 vr30a02.r1 Barstead mouse myotubes MB1R95 Mus musculus cDNA clone
 IMAGE:1122122 5' similar to gb:M84489 EXTRACELLULAR
 SIGNAL-REGULATED KINASE 2 (HUMAN); gb:X58712 Mouse MAPK mRNA for
 mitogen-activated protein kinase (MOUSE);, mRNA sequence.
 AA637964

```

AA637964.1 GI:2561552
EST.
house mouse
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 525)
REFERENCE
AUTHORS
Marta, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
Waterston, R.
The WashU-HMI Mouse EST Project
Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:611458
Seq primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 313.
Location/Qualifiers
1..525
/organism="Mus musculus"
/strain="C3H"
/db_xref="taxon:10090"
/clone="IMAGE:112212"
/clone.lib="Barstead mouse myotubes MPLR5"
/cell_line="C2C12"
/lab_host="DH10B"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: EcoRI; Site_2: NotI; 1st strand cDNA
was primed with a Not I - oligo(dT) primer [5',
TGTTACGAATCTGAAGTGGAGCGCGCCCTTTTCTTTTCTTTTCTTTT
3']; Double-stranded cDNA was ligated to Eco RI adaptors
[AAATCGATCCTTG], digested with Not I and cloned into the
Not I and Eco RI sites of the modified pT7T3 vector.
Library constructed by Bob Barstead. The C2C12 cell line
(available from ATCC, catalog # CRL-1772) differentiates
rapidly, forming contractile myotubes and producing
characteristic muscle proteins."
BASE COUNT 143 a 125 c 115 g 142 t
ORIGIN

Query Match 0.6%; Score 26; DB 9; Length 525;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3173 aagatctgtgacttggccttgcgcg 3198
|||||
Db 232 AAGATCTGTGACTTTGGCCTTGCCCG 257

RESULT 32
AW911950
LOCUS
DEFINITION
ur89e03.y1 NCI_CGAP_Mam6 Mus musculus cDNA clone IMAGE:3157468 5'
similar to gb:X58712 Mouse MAPK mRNA for mitogen-activated protein
kinase (MOUSE);, mRNA sequence.
ACCESSION
AW911950
VERSION
AW911950.1 GI:8077468
EST.
house mouse.
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 542)
REFERENCE

AA637964.1 http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP).
Tumor Gene Index
Unpublished (1997)
Other ESTs: ur89e03.x1
Contact: Robert Strausberg, Ph.D.
Email: cgapsb-remail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
cDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
image.llnl.gov/image/html/iresources.shtml

MGI:1060224
Seq primer: -40RP from Gibco
High quality sequence stop: 423.
Location/Qualifiers
1..542
/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:3157468"
/clone.lib="NCI_CGAP_Mam6"
/sex="female, virgin"
/tissue_type="infiltrating ductal carcinoma"
/dev_stage="5 months"
/lab_host="DH10B"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Jeffrey Green, M.D., NIH"
BASE COUNT 150 a 133 c 113 g 145 t
ORIGIN

Query Match 0.6%; Score 26; DB 9; Length 542;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3173 aagatctgtgacttggccttgcgcg 3198
|||||
Db 98 AAGATCTGTGACTTTGGCCTTGCCCG 123

RESULT 33
AZ645762/c
LOCUS
DEFINITION
Jm0511E24F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0511E24 F, DNA sequence.
ACCESSION
AZ645762
VERSION
AZ645762.1 GI:11775570
KEYWORDS
GSS.
SOURCE
house mouse.
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 589)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Rellly
, M., Rose, M., Rose, R., Stokes, R., Tinney, A., von Niederhausen, A.
and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177

```

Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0511 row: E column: 24
 Seq primer: CTTGTAAACGACGCGCCAGT
 Class: plasmid ends
 High quality sequence stop: 589.
 Location/Qualifiers
 1. .589

FEATURES

source
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUCG140511E24"
 /clone_lib="Mouse 10Kb plasmid UUCG1M library"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (g1147321141gb1AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 133 a 149 c 161 g 146 t
 ORIGIN

Query Match 0.6%; Score 26; DB 12; Length 589;
 Best Local Similarity 100.0%; Pred. No. 1.6;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3122 cacagagacctgcctcggaacat 3147
 |||||||||||||||||||||||||||||

Db 257 CACAGAGACCTGCCTCGGAACAT 232

RESULT 34

LOCUS BG518797 748 bp mRNA linear EST 02-APR-2001
 DEFINITION 602578390F1 NCI_CGAP_Lu29 Mus musculus cDNA clone IMAGE:3491663 5', mRNA sequence.

ACCESSION BG518797.1 GI:13514016

VERSION BG518797

KEYWORDS EST.

SOURCE house mouse.

ORGANISM

Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 1 (bases 1 to 748)
 NIH-MGC http://mgc.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Gilbert Smith, Ph.D.
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLAM8536 row: c column: 24

High quality sequence stop: 735.

Location/Qualifiers

1. .748
 /organism="Mus musculus"
 /strain="CZECH II (feral)"
 /db_xref="taxon:10090"
 /clone="IMAGE:3491663"
 /clone_lib="NCI_CGAP_Lu29"
 /tissue_type="spontaneous tumor, metastatic to mammary."
 Stem cell origin.
 /lab_host="DH10B"
 /note="Organ: lung; Vector: pCMV-SPORT6; Site_1: SalI;
 Site_2: NotI; Cloned unidirectionally. Primer: Oligo dt.
 Library constructed by Life Technologies. Investigator
 providing samples: Gilbert Smith, NIH"

BASE COUNT 215 a 180 c 156 g 197 t
 ORIGIN

Query Match 0.6%; Score 26; DB 10; Length 748;
 Best Local Similarity 100.0%; Pred. No. 1.6;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3173 aagatctgtgactttggccttgcccg 3198
 |||||||||||||||||||||||||||||

Db 185 AAGATCTGTGACTTTGGCCTTGCCCG 210

RESULT 35

LOCUS B1112246 763 bp mRNA linear EST 26-JUN-2001
 DEFINITION 602899921F1 NCI_CGAP_Mam5 Mus musculus cDNA clone IMAGE:5029733 5', mRNA sequence.

ACCESSION B1112246 GI:14563147

VERSION B1112246.1

KEYWORDS EST.

SOURCE house mouse.

ORGANISM

Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 1 (bases 1 to 763)
 NIH-MGC http://mgc.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov

Plate: LLAM1083 row: j column: 06
 High quality sequence stop: 761.

Location/Qualifiers

1. .763
 /organism="Mus musculus"
 /strain="C57/B6"
 /db_xref="taxon:10090"
 /clone="IMAGE:5029733"
 /clone_lib="NCI_CGAP_Mam5"
 /tissue_type="tumor, gross tissue"
 /dev_stage="7 months"
 /lab_host="DH10B"
 /note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI;
 Site_2: NotI; Cloned unidirectionally. Primer: Oligo dt.
 Library constructed by Life Technologies. Investigators
 providing samples: Lothar Hennighausen/Robin Humphreys,
 NIH"

BASE COUNT 222 a 179 c 159 g 203 t
 ORIGIN

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Query Match      0.6%; Score 26; DB 10; Length 763;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3173 aagatctgtgacttggccttgcccg 3198
|||||
Db 200 AAGATCTGTGACTTTGGCCTTGCCCG 225

RESULT 36
B1158214
LOCUS
DEFINITION 789 bp mRNA linear EST 05-JUL-2001
602920679F1 NIH_CGAP_Mam3 Mus musculus cDNA clone IMAGE:5060946 5',
mRNA sequence.
B1158214
B1158214.1 GI:14618215
VERSION
KEYWORDS
SOURCE EST.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 789)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
TITLE
AUTHORS
JOURNAL
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs@email.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia Deng Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arranged by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Place: LLNL1164 row: n column: 19
High quality sequence start: 3
High quality sequence stop: 672.
Location/Qualifiers
1..789
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="IMAGE:5060946"
/clone_lib="NIH_CGAP_Mam3"
/tissue_type="tumor, gross tissue"
/lab_host="DH10B"
/Note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert 2 kb. Library constructed by Life
Technologies, catalog #12017-018. Investigators providing
samples: Lothar Hennighausen/Chu-Xia Deng, NIH Reference
for transgenic model: Xu et al., Nature Genetics 22, 37-43
(1999). Note: this is a NCI_CGAP Library."
BASE COUNT 221 a 187 c 176 g 205 t
ORIGIN

Query Match      0.6%; Score 26; DB 10; Length 789;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3173 aagatctgtgacttggccttgcccg 3198
|||||
Db 33 AAGATCTGTGACTTTGGCCTTGCCCG 58

RESULT 37
A1746873
LOCUS
DEFINITION 827 bp mRNA linear EST 22-JUN-1999
ul08e07.y1 Sugano mouse embryo mewa Mus musculus cDNA clone
IMAGE:2076228 5', similar to db:X58712 Mouse MAPK mRNA for
mitogen-activated protein kinase (MOUSE);, mRNA sequence.
A1746873

```

```

VERSION
KEYWORDS
SOURCE
ORGANISM

REFERENCE
AUTHORS

TITLE
JOURNAL
COMMENT

FEATURES
source
1..827
/organism="Mus musculus"
/strain="C57BL"
/db_xref="taxon:10090"
/clone="IMAGE:2076228"
/clone_lib="Sugano mouse embryo mewa"
/dev_stage="embryo, 14 dpc"
/lab_host="DH10B"
/Note="Vector: pME18S-FL3; Site_1: DraIII (CACTGCTGTG);
Site_2: DraIII (CACCATGTG); 1st strand cDNA was primed
with an oligo(dT) primer [ATGCGCCCTTTTCTTTTCTTTT];
double-stranded cDNA was ligated to a draIII adaptor
[GTGTGCCCTACTGG], digested and cloned into distinct draIII
sites of the pME18S-FL3 vector (5' site CACTGCTGTG, 3' site
CACCATGTG). XhoI should be used to isolate the cDNA
insert. Size selection was performed to exclude fragments
<1.5kb. Library constructed by Dr. Sumio Sugano
(University of Tokyo Institute of Medical Science).
Custom primers for sequencing: 5' end primer
CTTCTGCTCTAAAGCTGCG and 3' end primer
CGACCTGCAGCTCAGCACA."
BASE COUNT 199 a 226 c 223 g 179 t
ORIGIN

Query Match      0.6%; Score 26; DB 9; Length 827;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3173 aagatctgtgacttggccttgcccg 3198
|||||
Db 698 AAGATCTGTGACTTTGGCCTTGCCCG 723

RESULT 38
BE279830
LOCUS
DEFINITION 846 bp mRNA linear EST 13-JUL-2000
601157156F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3140604 5',
mRNA sequence.
ACCESSION BE279830
VERSION BE279830.1 GI:9154825
KEYWORDS
SOURCE EST.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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REFERENCE
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM108 row: p column: 13
High quality sequence stop: 85.
Location/Qualifiers
FEATURES
source
1..846
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3140604"
/clone_lib="NIH_MGC_21"
/tissue_type="choriocarcinoma"
/lab_host="DH10B (phage-resistant)"
/Note="Organ: placenta; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
```

BASE COUNT	149 a	263 c	200 g	233 t	1 others
ORIGIN					

```

Query Match
Best Local Similarity 0.6%; Score 26; DB 10; Length 846;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3479 ggagaccaccaaggcgagactgcatt 3504
|||||
Db 32 CGAGACCCCAAGCGAGACCTGCATT 57

RESULT 39
BG870441
LOCUS BG870441
DEFINITION BG870441.1 GI:14220981
ACCESSION BG870441
VERSION BG870441.1 GI:14220981
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
1 (bases 1 to 869)
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:4922605"
/clone_lib="NCI_CGAP_SG2"
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM10842 row: j column: 14
High quality sequence stop: 709.
Location/Qualifiers
FEATURES
source
1..869
/organism="Mus musculus"
```

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/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:4922605"
/clone_lib="NCI_CGAP_SG2"
/lab_host="DH10B (TI phage-resistant)"
/Note="Organ: salivary gland; Vector: pCMV-SPORT6; Site_1:
NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo
dT. Average insert size 1.3 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
BASE COUNT 248 a 229 c 184 g 208 t
ORIGIN

Query Match
Best Local Similarity 0.6%; Score 26; DB 10; Length 869;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3173 aagatctgtgactttggccttgccc 3198
|||||
Db 482 AAGATCTGTGACTTTGGCCTTGCCG 507

RESULT 40
BG923284
LOCUS BG923284
DEFINITION BG923284.1 GI:14303760
ACCESSION BG923284
VERSION BG923284.1 GI:14303760
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
1 (bases 1 to 876)
/NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM10914 row: i column: 12
High quality sequence stop: 716.
Location/Qualifiers
FEATURES
source
1..876
/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:4954067"
/clone_lib="NCI_CGAP_Mam6"
/sex="female, virgin"
/tissue_type="infiltrating ductal carcinoma"
/dev_stage="5 months"
/lab_host="DH10B"
/Note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Jeffrey Green, M.D., NIH"
BASE COUNT 219 a 250 c 224 g 183 t
ORIGIN

Query Match
Best Local Similarity 0.6%; Score 26; DB 10; Length 876;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3173 aagatctgtgactttggccttgccc 3198
```

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Db 583 AAGATCTGTGACTTTGGCCTTGCCCG 608
|||||
RESULT 41
BF780935 916 bp mRNA linear EST 12-JAN-2001
LOCUS 602105450F1 NCI_CGAP_Kid14 Mus musculus cDNA clone IMAGE:4223556
DEFINITION 5', mRNA sequence.
ACCESSION BF780935
VERSION BF780935.1 GI:12085968
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 916)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LAM9812 row: c column: 13
High quality sequence stop: 677.
FEATURES
Location/Qualifiers
1..916
/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:4223556"
/lab_host="NCI_CGAP_Kid14"
/notes="Organ: kidney; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.75 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library. 1"
BASE COUNT 238 a 228 c 215 g 235 t
ORIGIN
Query Match 0.6%; Score 26; DB 10; Length 916;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3173 aagatctgtgactttggccttgcccg 3198
|||||
Db 158 AAGATCTGTGACTTTGGCCTTGCCCG 183
|||||

RESULT 42
BF140383 1002 bp mRNA linear EST 24-OCT-2000
LOCUS 60178789F1 NCI_CGAP_Lu30 Mus musculus cDNA clone IMAGE:4015703 5',
DEFINITION mRNA sequence.
ACCESSION BF140383
VERSION BF140383.1 GI:10979423
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 1002)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.

Email: cgabbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LAM9812 row: n column: 24
High quality sequence stop: 556.
FEATURES
Location/Qualifiers
1..1002
/organism="Mus musculus"
/strain="CZECH II"
/db_xref="taxon:10090"
/clone="IMAGE:4015703"
/clone_lib="NCI_CGAP_Lu30"
/tissue_type="tumor, metastatic to mammary"
/lab_host="DH10B"
/notes="Organ: lung; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; transgenic model WNT-1, expression driven by
MMTV-LTR enhancer; Cloned unidirectionally. Primer: Oligo
dT. Library constructed by Life Technologies.
Investigator providing samples: Gilbert Smith, NIH"
BASE COUNT 287 a 245 c 231 g 239 t
ORIGIN
Query Match 0.6%; Score 26; DB 10; Length 1002;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3173 aagatctgtgactttggccttgcccg 3198
|||||
Db 79 AAGATCTGTGACTTTGGCCTTGCCCG 104
|||||

RESULT 43
BF320636 722 bp mRNA linear EST 29-DEC-2000
LOCUS u555b06.y1 NCI_CGAP_Mam6 Mus musculus cDNA clone IMAGE:3672947 5',
DEFINITION similar to SM:MK01_MOUSE P27703 MITOGEN-ACTIVATED PROTEIN KINASE 1
; mRNA sequence.
ACCESSION BF320636
VERSION BF320636.1 GI:11269633
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 722)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Other_ESTs: u555b06.x1
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
cDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
image.llnl.gov/image/html/iresources.shtml
MGI:1433715
High quality sequence stop: 460.
FEATURES
Location/Qualifiers
1..722
/organism="Mus musculus"
/strain="FVB/N"

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/db_xref="taxon:10090"
/clone="IMAGE:3672947"
/clone_lib="NCI_CCAP_Mam6"
/sex="female, virgin"
/tissue_type="infiltrating ductal carcinoma"
/dev_stage="5 months"
/lab_host="DH10B"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: Sali;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Jeffrey Green, M.D., NIH"
168 a 201 c 196 g 154 t 3 others

BASE COUNT 168 a 201 c 196 g 154 t 3 others

ORIGIN

Query Match 0.6%; Score 25; DB 10; Length 722;
Best Local Similarity 100.0%; Pred. No. 4.5;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3174 agatctgtgaacttggccttgcccg 3198
|||||

Db 685 ACATCTGCACTTGGCCTTGCCCG 709

RESULT 44

LOCUS R86582 233 bp mRNA linear EST 17-AUG-1995

DEFINITION RABEST157T Rabbit Osteoclast, Dennis Sakai Oryctolagus cuniculus

ACCESSION R86582

VERSION R86582.1 GI:947236

KEYWORDS EST,

SOURCE rabbit.

ORGANISM Oryctolagus cuniculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.

AUTHORS Sakai, D., Tong, H.-S. and Minkin, C.

TITLE Osteoclast Molecular Phenotyping by Random cDNA Sequencing

JOURNAL Bone 17 (2), 111-119 (1995)

MEDLINE 96021365

COMMENT Other_ESTs: RABEST035T, RABEST040T, RABEST075T
Contact: Sakai D
Basic Sciences
University of Southern California
USC School of Dentistry, 925 West 34th Street, DEN-4220, Los
Angeles, CA 90089-0641
Tel: 2137405563
Fax: 2137407560
Email: sakai@molbio.usc.edu
Seq primer: T7 promoter.

FEATURES Location/Qualifiers

source 1..233
/organism="Oryctolagus cuniculus"
/strain="New Zealand White"
/db_xref="taxon:9986"
/clone="pRABOC157"
/clone_lib="Rabbit Osteoclast, Dennis Sakai"
/lab_host="E. coli DH12S"
/note="Vector: pSPORT1; Site_1: Sali; Site_2: NotI; Poly(A
) RNA was purified from a 97% pure population of
osteoclasts prepared from the long bones of 10 day old
rabbits. First strand cDNA was synthesized by priming
with an oligo(dT)-NotI anchor-primer and second strand
cDNA was synthesized by replacement synthesis as described
by Gubler and Hoffman (Gene 25:283, 1983). Following the
addition of Sali adaptors and NotI digestion, the cDNA was
cloned between the Sali (50) and NotI (30) sites of the
pSPORT1 (BRL) plasmid vector."

BASE COUNT 53 a 61 c 79 g 40 t

ORIGIN

Query Match 0.6%; Score 24; DB 10; Length 233;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2578 cggcgcttcgggaaggtgggtgga 2601
|||||

Db 75 CGCGCCTTCGGAAGGTGGTGA 98

RESULT 45

LOCUS AQ939636 234 bp DNA linear GSS 23-AUG-2000

DEFINITION NR3-110R Human NotI clones Homo sapiens genomic, DNA sequence.

ACCESSION AQ939636

VERSION AQ939636.1 GI:7216014

KEYWORDS GSS.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS 1 (bases 1 to 234)
Zabarovskiy, E.R., Gizatullin, R., Podowski, R.M., Zabarovska, V.V., Xie
, L., Muravenko, O.V., Kozyrev, S., Petrenko, L., Skobeleva, N., Li, J.,
Protopopov, A., Kashuba, V., Ernberg, I., Winberg, G. and Wahlstedt, C.

TITLE NotI clones in the analysis of the human genome

JOURNAL Nucleic Acids Res. 28 (7), 1635-1639 (2000)

MEDLINE 20175728

COMMENT Contact: Podowski RM
Center for Genomics Research
Karolinska Institute
17177 Stockholm, Sweden
Tel: +46-8-728-6372
Fax: +46-8-337983
Email: Raf.Podowski@cgr.ki.se
Class: NotI site.

FEATURES Location/Qualifiers

source 1..234
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="Human NotI clones"

BASE COUNT 42 a 71 c 75 g 38 t 8 others

ORIGIN

Query Match 0.6%; Score 24; DB 12; Length 234;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 560 caggaggtggtgtgggtgacgg 583
|||||

Db 93 CAGGAGGTGGTGGGATCACCG 116

Search completed: July 15, 2002, 20:07:24
Job time: 14482 sec

Db 181 gacccccctcgagtgggcttggccagagctcaggagggccagccaccggagagacaaagga 240

QY 241 cagcgagagacacgggggtgtgtcgagactcgagagggcacagagccagggccctactgcaa 300

Db 241 cagcgagagacacgggggtgtgtcgagactcgagagggcacagagccagggccctactgcaa 300

QY 301 ggtgttgtctgtcgacagagttacatgccaacgacacacagcagctacgtctgtctactcaa 360

Db 301 ggtgttgtctgtcgacagagttacatgccaacgacacacagcagctacgtctgtctactcaa 360

QY 361 gtacatcaaggacgcgcatcgagggcacacggccggccagctcctaacgtgtgtgtgagaga 420

Db 361 gtacatcaaggacgcgcatcgagggcacacggccggccagctcctaacgtgtgtgtgagaga 420

QY 421 ctttgagcagccattcatcaacaagctgcacgctcttgggtcaacaaggagagcgccat 480

Db 421 ctttgagcagccattcatcaacaagctgcacgctcttgggtcaacaaggagagcgccat 480

QY 481 gtgggtgccccgtgtgtgtgtccatccccggcctcaatgtgtacagctgcgtctgcgaagctc 540

Db 481 gtgggtgccccgtgtgtgtgtccatccccggcctcaatgtgtacagctgcgtctgcgaagctc 540

QY 541 ggtgtgtgtgcccagacgggcagaggtggtgtgggatgacccggcggggcatgctgtgtc 600

Db 541 ggtgtgtgtgcccagacgggcagaggtggtgtgggatgacccggcggggcatgctgtgtc 600

QY 601 cagcgaactgtgcagagtgacctgtacctgtcagtgcgagacacaccttggggagaccagga 660

Db 601 cagcgaactgtgcagagtgacctgtacctgtcagtgcgagacacaccttggggagaccagga 660

QY 661 cttccctttccaaccccttccctggtgcacatcacaggcaacgagctctatgacatccagct 720

Db 661 cttccctttccaaccccttccctggtgcacatcacaggcaacgagctctatgacatccagct 720

QY 721 gttgcccaggaatcgctggagctgctggttaggggagaagctgggtcctgaactgcaccgt 780

Db 721 gttgcccaggaatcgctggagctgctggttaggggagaagctgggtcctgaactgcaccgt 780

QY 781 gtgggtcgagttaacttcaggtgtcaccttttaactggagctacccaggaagcagcagaga 840

Db 781 gtgggtcgagttaacttcaggtgtcaccttttaactggagctacccaggaagcagcagaga 840

QY 841 gcggggtlaagtgggtggtggtggtggtggtggtggtggtggtggtggtggtggtggtggt 900

Db 841 gcggggtlaagtgggtggtggtggtggtggtggtggtggtggtggtggtggtggtggtggt 900

QY 901 cctgacatcccaaaagtcagccagcacgacctggggtcgatgtgtgtgcaaggcccaacaa 960

Db 901 cctgacatcccaaaagtcagccagcacgacctggggtcgatgtgtgtgcaaggcccaacaa 960

QY 961 cgggcatccagcgatttcggggagagcaccgaggtcattgtgcatgaaaaatcccttcatcag 1020

Db 961 cgggcatccagcgatttcggggagagcaccgaggtcattgtgcatgaaaaatcccttcatcag 1020

QY 1021 cgtcgagtggtgtcaaaaggaccatcctgtgagggccacggcagagagcagctggtgaagct 1080

Db 1021 cgtcgagtggtgtcaaaaggaccatcctgtgagggccacggcagagagcagctggtgaagct 1080

QY 1081 gcccggtgaagctggtgagcgtatcccccccgcccgagttccagtggttacaaggatggaaggc 1140

Db 1081 gcccggtgaagctggtgagcgtatcccccccgcccgagttccagtggttacaaggatggaaggc 1140

QY 1141 actgtccggggccacagttccacatgccctggtgtcgaaggaggtgacagagggccagcac 1200

Db 1141 actgtccggggccacagttccacatgccctggtgtcgaaggaggtgacagagggccagcac 1200

QY 1201 agggacctacacccctcgccctgtgaaactcgcgtgtggtcgtgagggcgcaacatcagcct 1260

Db 1201 agggacctacacccctcgccctgtgaaactcgcgtgtggtcgtgagggcgcaacatcagcct 1260

QY 1261 ggagctggtgtggaatgtgcccccccgatatacatgagaaggagggcctcctccccagcat 1320

Db 1261 ggagctggtgtggaatgtgcccccccgatatacatgagaaggagggcctcctccccagcat 1320

QY 1321 ctactcggttcacagccgcccagggccctcacctgcacggcctacggggtgccccctgcctct 1380

Db 1321 ctactcggttcacagccgcccagggccctcacctgcacggcctacggggtgccccctgcctct 1380

QY 1381 cagcatccagtggaactggtggccctggacacccctgcaagatgtttgcccagcgtagctct 1440

Db 1381 cagcatccagtggaactggtggccctggacacccctgcaagatgtttgcccagcgtagctct 1440

QY 1441 ccggcgcgccgacagacaagacctatgccacagtccgtgactgagggcggtgaccac 1500

Db 1441 ccggcgcgccgacagacaagacctatgccacagtccgtgactgagggcggtgaccac 1500

QY 1501 gcagggtgcccgtgaaccccccatcgagagcctggacacctggaccgagtttctgtgagggaaa 1560

Db 1501 gcagggtgcccgtgaaccccccatcgagagcctggacacctggaccgagtttctgtgagggaaa 1560

QY 1561 gaataagactgtgagcaagctggtgatccagaatgccaacgtgtctgccatgtacaagtctg 1620

Db 1561 gaataagactgtgagcaagctggtgatccagaatgccaacgtgtctgccatgtacaagtctg 1620

QY 1621 tgtgtgtctccaaacaggtgggcccaggtgagcgggtcacttacttctatgtgaccacct 1680

Db 1621 tgtgtgtctccaaacaggtgggcccaggtgagcgggtcacttacttctatgtgaccacct 1680

QY 1681 ccccgagggcttcaccatcgaaatcccaagccatcccaggagctactagagggccagccggt 1740

Db 1681 ccccgagggcttcaccatcgaaatcccaagccatcccaggagctactagagggccagccggt 1740

QY 1741 gctcctgagctgccaaagccgaacgtacaaagtacagatctctgcgtgtgacggcctcaa 1800

Db 1741 gctcctgagctgccaaagccgaacgtacaaagtacagatctctgcgtgtgacggcctcaa 1800

QY 1801 cctgtccacgtctgcacgatgcgcacgggaacccgcttctgtctcgactgcaagaacgtgca 1860

Db 1801 cctgtccacgtctgcacgatgcgcacgggaacccgcttctgtctcgactgcaagaacgtgca 1860

QY 1861 tctgttgcacacccctctggccggccagcctggagaggttggcacctggggcgccacgc 1920

Db 1861 tctgttgcacacccctctggccggccagcctggagaggttggcacctggggcgccacgc 1920

QY 1921 cagcgtcagctgagatatacccccgctgcgcccagacagcagagggccactatgtgtgcga 1980

Db 1921 cagcgtcagctgagatatacccccgctgcgcccagacagcagagggccactatgtgtgcga 1980

QY 1981 agtgcaagaccggcgacgcatgacaagcactgccaagaagtacacctgtcgggtgcaggc 2040

Db 1981 agtgcaagaccggcgacgcatgacaagcactgccaagaagtacacctgtcgggtgcaggc 2040

QY 2041 cctggaaacccctcggtctcagcagaacttgaccgacctcctggtgaaactgtgagcgactc 2100

Db 2041 cctggaaacccctcggtctcagcagaacttgaccgacctcctggtgaaactgtgagcgactc 2100

QY 2101 gctggagatgagtgctgtgtggcgagcgacgcgcgcacggccacgcatcgtgtgtacaaaga 2160

Db 2101 gctggagatgagtgctgtgtggcgagcgacgcgcgcacggccacgcatcgtgtgtacaaaga 2160

QY 2161 cgagaggtgctggaggaaaagtctggagtcgacttggcgactcccaaccagaaagctgag 2220

Db 2161 cgagaggtgctggaggaaaagtctggagtcgacttggcgactcccaaccagaaagctgag 2220

QY 2221 catccagcgctgcgcgagggaggtgcggggacgctatctgtgcagcgctgtgcaacgcgcaa 2280

Db 2221 catccagcgctgcgcgagggaggtgcggggacgctatctgtgcagcgctgtgcaacgcgcaa 2280

QY 2281 gggctgggtcaactcctcccgccagcgtggccgtggaaggctcccgagataaaggcagcat 2340

Db 2281 gggctgggtcaactcctcccgccagcgtggccgtggaaggctcccgagataaaggcagcat 2340

QY 2341 ggagatcgtgtatccttctcgtgataccgctcgcgtcgcgtcgcgtcgcgtcgcgtcgcgtc 2400

Db 2341 ggagatcgtgtatccttctcgtgataccgctcgcgtcgcgtcgcgtcgcgtcgcgtcgcgtc 2400

```
QY 2401 cctcatcttctgtaacatgagagccgcccacagacatcaagagcggtactgtc 2460
|||||
Db 2401 cctcatcttctgtaacatgagagccgcccacagacatcaagagcggtactgtc 2460
QY 2461 catcatcatggagcccgagggtgctctgagagcaatgcgaatacctctctacaga 2520
|||||
Db 2461 catcatcatggagcccgagggtgctctgagagcaatgcgaatacctctctacaga 2520
QY 2521 tgcacagcagtggaatttcccccagagcggtgcacctggggagagtgcctggctacgg 2580
|||||
Db 2521 tgcacagcagtggaatttcccccagagcggtgcacctggggagagtgcctggctacgg 2580
QY 2581 cgctctcgagaaagtgtggaagcctccgcttctcgatcccaagggcagcagctgtga 2640
|||||
Db 2581 cgctctcgagaaagtgtggaagcctccgcttctcgatcccaagggcagcagctgtga 2640
QY 2641 caccgtggcgtgaaatgctgaaagaggcgccacagcgccagcagcgcgctgat 2700
|||||
Db 2641 caccgtggcgtgaaatgctgaaagaggcgccacagcgccagcagcgcgctgat 2700
QY 2701 gtccgagctcaagatcctcatcacaatcggaacacacctcaacgttgtcaacctctcgg 2760
|||||
Db 2701 gtccgagctcaagatcctcatcacaatcggaacacacctcaacgttgtcaacctctcgg 2760
QY 2761 ggcgtgcacaaagccagggccccctcatggtgatcgtggagtctctcaagtacggcaa 2820
|||||
Db 2761 ggcgtgcacaaagccagggccccctcatggtgatcgtggagtctctcaagtacggcaa 2820
QY 2821 cctctccaaattcctgcgcgccaagggagcgccttcagccccgcggagaaagtctcc 2880
|||||
Db 2821 cctctccaaattcctgcgcgccaagggagcgccttcagccccgcggagaaagtctcc 2880
QY 2881 cgagcagcggagcgttccgcgcctatggtgagctcgcagagctggatcggagcgggcc 2940
|||||
Db 2881 cgagcagcggagcgttccgcgcctatggtgagctcgcagagctggatcggagcgggcc 2940
QY 2941 ggggagcagcagaggttctcttcgcggttcttcgaagaccgagggcgagcgagggcg 3000
|||||
Db 2941 ggggagcagcagaggttctcttcgcggttcttcgaagaccgagggcgagcgagggcg 3000
QY 3001 ggcttccagaccgaagagctgaggaacctgtggtctgagcccgctgacctggaagatct 3060
|||||
Db 3001 ggcttccagaccgaagagctgaggaacctgtggtctgagcccgctgacctggaagatct 3060
QY 3061 tctctctacagcttccaggtgagcagagggatggaagttccttggttcccgaaagtgc 3120
|||||
Db 3061 tctctctacagcttccaggtgagcagagggatggaagttccttggttcccgaaagtgc 3120
QY 3121 ccacagagacctggctgcggaacattctgctgcggaagcgacgtggtgaaagatctg 3180
|||||
Db 3121 ccacagagacctggctgcggaacattctgctgcggaagcgacgtggtgaaagatctg 3180
QY 3181 tgactttggccttggccgggacatctacaaagacctgactacgtlcccgaaaggcagtcg 3240
|||||
Db 3181 tgactttggccttggccgggacatctacaaagacctgactacgtlcccgaaaggcagtcg 3240
QY 3241 ccgggtcggccctgaaagtgcagagccctgaaagcatcttcgacaaggtgtacacacgca 3300
|||||
Db 3241 ccgggtcggccctgaaagtgcagagccctgaaagcatcttcgacaaggtgtacacacgca 3300
QY 3301 gagtgacgtgtggttcccttgggggtgcttctctggagagatcttctctgggggacctcccc 3360
|||||
Db 3301 gagtgacgtgtggttcccttgggggtgcttctctggagagatcttctctgggggacctcccc 3360
QY 3361 gtaccttgggttgcagatcaatgagagttctgcgagcggtgagagcggcacaaagat 3420
|||||
Db 3361 gtaccttgggttgcagatcaatgagagttctgcgagcggtgagagcggcacaaagat 3420
QY 3421 gaggccccgagagctggccaatcccgccatacgcgcgcatcatgctgaactgctgtccgg 3480
|||||
Db 3421 gaggccccgagagctggccaatcccgccatacgcgcgcatcatgctgaactgctgtccgg 3480
QY 3481 agacccccagcgagacctgcattctctcgagctggtggagatctctgggggacctgctcca 3540
```

```
|||||
Db 3481 agacccccagcgagacctgcattctcgagctggtcgagatccttggggacctgctcca 3540
QY 3541 gggcaggggcttgcagaagagagaggtctgcattggccccgcgcagctctcagagctc 3600
|||||
Db 3541 gggcaggggcttgcagaagagagaggtctgcattggccccgcgcagctctcagagctc 3600
QY 3601 aqaagagggcgagcttctcgaggtgtccacatggtccctacacatcgccccggctgacgc 3660
|||||
Db 3601 aqaagagggcgagcttctcgaggtgtccacatggtccctacacatcgccccggctgacgc 3660
QY 3661 tgagacagcccgcaagcctgcagcgccacagcctgccccaggtattacaactgggt 3720
|||||
Db 3661 tgagacagcccgcaagcctgcagcgccacagcctgccccaggtattacaactgggt 3720
QY 3721 gtcttctcccggtgctcgccagaggggtcgagaccctggttctccagagatgaagac 3780
|||||
Db 3721 gtcttctcccggtgctcgccagaggggtcgagaccctggttctccagagatgaagac 3780
QY 3781 atttgaggaattccccatgaccccccaacacacacataaaaggtctgtggacaaccagacaga 3840
|||||
Db 3781 atttgaggaattccccatgaccccccaacacacacataaaaggtctgtggacaaccagacaga 3840
QY 3841 cagtgaggtggtgctcgccgagaggtttgagcagatagagcagcgcatagacaaga 3900
|||||
Db 3841 cagtgaggtggtgctcgccgagaggtttgagcagatagagcagcgcatagacaaga 3900
QY 3901 aagcggtctcag 3912
|||||
Db 3901 aagcggtctcag 3912
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RESULT 2

```
US-09-442-384B-447
; Sequence 447, Application US/09442384B
; GENERAL INFORMATION:
; APPLICANT: Chenchik, Alex
; APPLICANT: Lukashiev, Matvey
; TITLE OF INVENTION: Hematology/Immunology Array
; FILE REFERENCE: CLON-006CIP15
; CURRENT APPLICATION NUMBER: US/09/442.384B
; CURRENT FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: 09/053,375
; PRIOR FILING DATE: 1998-03-31
; NUMBER OF SEQ ID NOS: 830
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 447
; LENGTH: 4416
; TYPE: DNA
; ORGANISM: homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 4243
; OTHER INFORMATION: n = A,T,C or G
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 4243
; OTHER INFORMATION: n = A,T,C or G
US-09-442-384B-447
```

```
Query Match 95.2%; Score 3912; DB 5; Length 4416;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3912; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 ccacgcgcagcgccgcgagatgcagcgggcgccgcgcgtgtgcctgcgactgtgctctg 60
Db 1 ccacgcgcagcgccgcgagatgcagcgggcgccgcgcgtgtgcctgcgactgtgctctg 60
QY 61 cctgggactcctggacggcctgggtgagtggtactctccatgaccccccgacctgaacat 120
Db 61 cctgggactcctggacggcctgggtgagtggtactctccatgaccccccgacctgaacat 120
```



```
QY 2231 gtgcgcgaggagatgcgggacgctatctgtgcagctgtgtcacaagccaaaggctgcctc 2290
|||||
Db 121 gtgcgcgaggagatgcgggacgctatctgtgcagctgtgtcacaagccaaaggctgcctc 180
|||||
QY 2291 aactcctccgcagcgtgcgcgtgaagcctccagagataaaggcagcagatgagatcgtg 2350
|||||
Db 181 aactcctccgcagcgtgcgcgtgaagcctccagagataaaggcagcagatgagatcgtg 240
|||||
QY 2351 atccttgcgttacgcggcgtcatcgtctcttctcttctgggtccctcctcctcatcttc 2410
|||||
Db 241 a'ccttgcgttacgcggcgtcatcgtctcttctcttctgggtccctcctcctcatcttc 300
|||||
QY 2411 ttaacatgaggagccgcccacgcagacatcaagacggcgtacctgtccatcatcgtg 2470
|||||
Db 301 tgaacatgaggagccgcccacgcagacatcaagacggcgtacctgtccatcatcgtg 360
|||||
QY 2471 gaccccgggaggtgcctctgagagcaatcgaaatcctgtctctacgatgccagccag 2530
|||||
Db 361 gaccccgggaggtgcctctgagagcaatcgaaatcctgtctctacgatgccagccag 420
|||||
RESULT 4
US-09-918-995-21977
; Sequence 21977, Application US/09918995
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 21977
; LENGTH: 463
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-918-995-21977

Query Match 5.4%; Score 223; DB 5; Length 463;
Best Local Similarity 100.0%; Pred. No. 4e-98;
Matches 223; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3605 gagggcagcttctcagaggtgtccaccatggccctacacatcgcccaggctgacgctgag 3664
|||||
Db 45 gagggcagcttctcagaggtgtccaccatggccctacacatcgcccaggctgacgctgag 104
|||||
QY 3665 gacagccgcgaagcctgcagcgcacacagcctgcccaggtattacaactgggtgtcc 3724
|||||
Db 105 gacagccgcgaagcctgcagcgcacacagcctgcccaggtattacaactgggtgtcc 164
|||||
QY 3725 ttcccgggtgcctggccagagggtgtagaccctggttctcctcagatgaagacattt 3784
|||||
Db 165 ttcccgggtgcctggccagagggtgtagaccctggttctcctcagatgaagacattt 224
|||||
QY 3785 gaggaattccccatgaccccaacacctacaaagctctgtgg 3827
|||||
Db 225 gaggaattccccatgaccccaacacctacaaagctctgtgg 267
|||||
RESULT 5
US-09-918-995-23705
; Sequence 23705, Application US/09918995
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
```

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; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 23705
; LENGTH: 477
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc_feature
; LOCATION: (1)_(477)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-23705

Query Match 3.5%; Score 145; DB 5; Length 477;
Best Local Similarity 100.0%; Pred. No. 4.3e-60;
Matches 145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3768 ccaggatgaagacatttgaggaaattccccatgaccccaacgacctacaaaggctctgtg 3827
|||||
Db 40 ccaggatgaagacatttgaggaaattccccatgaccccaacgacctacaaaggctctgtg 99
|||||
QY 3828 acaaccagacagacagtgggatggtgctgcctcgaggaggtttgacagatagagaca 3887
|||||
Db 100 acaaccagacagacagtgggatggtgctgcctcgaggaggtttgacagatagagaca 159
|||||
QY 3888 ggcatagacaagaagcggtctcag 3912
|||||
Db 160 ggcatagacaagaagcggtctcag 184
|||||
RESULT 6
US-10-027-632-20120
; Sequence 20120, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20120
; LENGTH: 770
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-20120

Query Match 3.1%; Score 127; DB 6; Length 770;
Best Local Similarity 100.0%; Pred. No. 2.5e-51;
Matches 127; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1441 ccggcggcgagcagcagaacacctcatgccacagtcgcgtgactgagggcggtgaccac 1500
|||||
Db 379 ccggcggcgagcagcagaacacctcatgccacagtcgcgtgactgagggcggtgaccac 438
|||||
```

QY 1501 gcagatgccgtgaacccatcgagagcctggacacctggaccgagttgtggaaggaaa 1560
Db 439 gcagatgccgtgaacccatcgagagcctggacacctggaccgagttgtggaaggaaa 498
QY 1561 gaataag 1567
Db 499 gaataag 505

RESULT 7
US-10-027-632-144519/C
; Sequence 144519, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027.632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 144519
; LENGTH: 671
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-144519

Query Match 3.0%; Score 123; DB 6; Length 671;
Best Local Similarity 100.0%; Pred. No. 2.3e-49;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3585 gcagctctcagagctcagaagaggcagcttctcgagggtgtccaccatggccctacaca 3644
Db 123 GCAGCTCTCAGAGCTCAGAAGAGGGCAGCTTCTCGCAGGTGTCCACCATGGCCCTACACA 64
QY 3645 tcgcccaggctgacgctgagagcagcccgccaaagcctgcagcgccacagcctggccgcca 3704
Db 63 TCGCCAGGCTGACGCTGAGGACAGCCGCCCAAGCCCTGCAGCGCCACAGGCTGGCCGCCCA 4
QY 3705 ggt 3707
Db 3 GGT 1

RESULT 8
US-10-027-632-144520/C
; Sequence 144520, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027.632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676

; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 144520
; LENGTH: 671
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-144520

Query Match 3.0%; Score 123; DB 6; Length 671;
Best Local Similarity 100.0%; Pred. No. 2.3e-49;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3585 gcagctctcagagctcagaagaggcagcttctcgagggtgtccaccatggccctacaca 3644
Db 123 GCAGCTCTCAGAGCTCAGAAGAGGGCAGCTTCTCGCAGGTGTCCACCATGGCCCTACACA 64
QY 3645 tcgcccaggctgacgctgagagcagcccgccaaagcctgcagcgccacagcctggccgcca 3704
Db 63 TCGCCAGGCTGACGCTGAGGACAGCCGCCCAAGCCCTGCAGCGCCACAGGCTGGCCGCCCA 4
QY 3705 ggt 3707
Db 3 GGT 1

RESULT 9
US-09-539-331D-34177
; Sequence 34177, Application US/09539331D
; GENERAL INFORMATION:
; APPLICANT: Sellhamer, Jeffrey J.
; APPLICANT: Deleageane, Angelo M.
; APPLICANT: Stuart, Susan G.
; APPLICANT: Stuve, Laura L.
; APPLICANT: Mullany, Sara J.
; APPLICANT: Naughton, Rebecca E.
; TITLE OF INVENTION: POLYNUCLEOTIDES OF CARDIOVASCULAR SYSTEM TISSUE
; FILE REFERENCE: PD-1022 CIP
; CURRENT APPLICATION NUMBER: US/09/539,331D
; CURRENT FILING DATE: 2000-03-30
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 40961
; SOFTWARE: PERL Program
; SEQ ID NO 34177
; LENGTH: 476
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: hu01173578
US-09-539-331D-34177

Query Match 2.3%; Score 96; DB 5; Length 476;
Best Local Similarity 100.0%; Pred. No. 3.4e-36;
Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3085 cacagagatggagttcctgcttcccgaaagtgcatccacagagacctggtgctcgaa 3144
Db 24 cacagagatggagttcctgcttcccgaaagtgcatccacagagacctggtgctcgaa 83
QY 3145 cattctgctcgaaagcgacgtggtgaagatctg 3180

; APPLICANT: SILVER, MARCY
; APPLICANT: ISNER, JEFFREY M.
; APPLICANT: YOON, YOUNG-SUP
; TITLE OF INVENTION: USE OF LYMPHANGIOGENIC AGENTS TO TREAT LYMPHATIC
; FILE REFERENCE: 71417/55062
; CURRENT APPLICATION NUMBER: US/09/970,088
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: 60/237,171
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 8
; LENGTH: 420
; TYPE: DNA
; ORGANISM: Bos sp.
US-09-970-088-8

Query Match 0.8%; Score 32; DB 5; Length 420;
Best Local Similarity 100.0%; Pred. No. 5.5e-05;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2457 tgcctcatcatcatgaccgccggggaggtgcct 2488
|||||
DB 347 tgcctcatcatcatgaccgccggggaggtgcct 378

RESULT 15
US-09-704-167A-7
; Sequence 7, Application US/09704167A
; GENERAL INFORMATION:
; APPLICANT: Havemann, Klaus
; TITLE OF INVENTION: Production and Use of Endothelial-like Cells
; FILE REFERENCE: BPD-100
; CURRENT APPLICATION NUMBER: US/09/704.167A
; CURRENT FILING DATE: 2000-11-01
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc.feature
; OTHER INFORMATION: VEGFR-3 5'-primer for RT-PCR, VEGFR-3 GenBank accession no. NM002
US-09-704-167A-7

Query Match 0.6%; Score 23; DB 5; Length 23;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2794 gatcgtgaggtctcgaagtacg 2816
|||||
DB 1 gatcgtgaggtctcgaagtacg 23

RESULT 16
US-09-539-331D-34177/c
; Sequence 34177, Application US/09539331D
; GENERAL INFORMATION:
; APPLICANT: Seilhamer, Jeffrey J.
; APPLICANT: Delegeane, Angelo M.
; APPLICANT: Stuart, Susan G.
; APPLICANT: Stuve, Laura L.
; APPLICANT: Mullahy, Sara J.
; APPLICANT: Naughton, Rebecca E.
; TITLE OF INVENTION: POLYNUCLEOTIDES OF CARDIOVASCULAR SYSTEM TISSUE
; FILE REFERENCE: PD-1022 CIP
; CURRENT APPLICATION NUMBER: US/09/539,331D
; CURRENT FILING DATE: 2000-03-30

; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 40961
; SOFTWARE: PERL Program
; SEQ ID NO 34177
; LENGTH: 476
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; OTHER INFORMATION: Incyte ID No: hu01173578
US-09-539-331D-34177

Query Match 0.6%; Score 23; DB 5; Length 476;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3063 tctgtcacagcttcacagtgccc 3085
|||||
DB 27 TCTGTACAGCTTCCAGGTGCC 5

RESULT 17
US-10-027-400-1
; Sequence 1, Application US/10027400
; GENERAL INFORMATION:
; APPLICANT: WILLIAMS, Lewis T.
; TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR RECEPTORS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market, Steuart Street Tower, 20th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/027,400
; FILING DATE: 19-Dec-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/461,917
; FILING DATE: 05-JUN-1995
; APPLICATION NUMBER: US 07/151,414
; FILING DATE: 02-FEB-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Dow, Karen B.
; REGISTRATION NUMBER: 29,684
; REFERENCE/DOCKET NUMBER: 2307K-267-2-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/326-2400
; TELEFAX: 415/326-2422
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6373 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 129..3398
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-027-400-1

Query Match 0.6%; Score 23; DB 6; Length 6373;

Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3170 gtgaagatctgtgacttggcct 3192
|||||
Db 2622 GTCAAGATCTGTGACTTTGGCCT 2644

RESULT 18

US-09-053-375B-419
; Sequence 419, Application US/09053375B
; GENERAL INFORMATION:
; APPLICANT: Chenchik, Alex
; APPLICANT: Bibilashvili, Robert
; TITLE OF INVENTION: Nucleic Acid Arrays
; FILE REFERENCE: CLON-006
; CURRENT APPLICATION NUMBER: US/09/053,375B
; CURRENT FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 1543
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 419
; LENGTH: 6378
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-053-375B-419

Query Match 0.6%; Score 23; DB 5; Length 6378;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3170 gtgaagatctgtgacttggcct 3192
|||||
Db 2633 gtgaagatctgtgacttggcct 2655

RESULT 19

US-09-704-167A-8/c
; Sequence 8, Application US/09704167A
; GENERAL INFORMATION:
; APPLICANT: Havemann, Klaus
; TITLE OF INVENTION: Production and Use of Endothelial-like Cells
; FILE REFERENCE: BPD-100
; CURRENT APPLICATION NUMBER: US/09/704,167A
; CURRENT FILING DATE: 2000-11-01
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: VEGFR-3 3'-primer for RT-PCR, VEGFR-3 GenBank accession no. NM002
US-09-704-167A-8

Query Match 0.5%; Score 22; DB 5; Length 22;
Best Local Similarity 100.0%; Pred. No. 4.9;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3160 aagcagctgtgaagatctgt 3181
|||||
Db 22 AAGCAGCTGTGAAGATCTGT 1

RESULT 20

US-10-116-712-166/c
; Sequence 166, Application US/10116712
; GENERAL INFORMATION:
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Switzer, Ann

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.568
; CURRENT APPLICATION NUMBER: US/10/116,712
; CURRENT FILING DATE: 2002-04-07
; NUMBER OF SEQ ID NOS: 670
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 166
; LENGTH: 501
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 488
; OTHER INFORMATION: n = A,T,C or G
US-10-116-712-166

Query Match 0.5%; Score 22; DB 6; Length 501;
Best Local Similarity 100.0%; Pred. No. 4.1;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2391 tctctctctctcatctcttg 2412
|||||
Db 377 TCCTCCTCCTCCTCATCTCTG 356

RESULT 21

US-10-099-926-644
; Sequence 644, Application US/10099926
; GENERAL INFORMATION:
; APPLICANT: King, Gordon E.
; APPLICANT: Meagher, Madeleine Joy
; APPLICANT: Xu, Jiangchun
; APPLICANT: Secrist, Heather
; APPLICANT: Jiang, Yuqiu
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
; FILE REFERENCE: 210121.547C2
; CURRENT APPLICATION NUMBER: US/10/099,926
; CURRENT FILING DATE: 2002-03-17
; NUMBER OF SEQ ID NOS: 1982
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 644
; LENGTH: 517
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-099-926-644

Query Match 0.5%; Score 22; DB 6; Length 517;
Best Local Similarity 100.0%; Pred. No. 4.1;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2391 tctctctctctcatctcttg 2412
|||||
Db 209 tcctctctctctcatctcttg 230

RESULT 22

US-10-143-883-83/c
; Sequence 83, Application US/10143883
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PM029C1N
; CURRENT APPLICATION NUMBER: US/10/143,883
; CURRENT FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 09/758,459
; PRIOR FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: 60/179,065
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/180,628

; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 406
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 83
; LENGTH: 1078
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (106)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1047)
; OTHER INFORMATION: n equals a,t,g, or c
US-10-143-883-83

Query Match 0.5%; Score 22; DB 6; Length 1078;
Best Local Similarity 100.0%; Pred. No. 4;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2391 tcctctctctctctctctctg 2412
Db 764 TCCTCTCTCTCTCTCTCTG 743

RESULT 23
US-09-053-375B-724
; Sequence 724, Application US/09053375B
; GENERAL INFORMATION:
; APPLICANT: Chenchik, Alex
; APPLICANT: Bibilashvili, Robert
; TITLE OF INVENTION: Nucleic Acid Arrays
; FILE REFERENCE: CLON-006
; CURRENT APPLICATION NUMBER: US/09/053,375B
; CURRENT FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 1543
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 724
; LENGTH: 4479
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-053-375B-724

Query Match 0.5%; Score 22; DB 5; Length 4479;
Best Local Similarity 100.0%; Pred. No. 3.6;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3126 gagactggtctgctcggaacat 3147
Db 2309 gagactggtctgctcggaacat 2330

RESULT 24
US-09-918-995-31410/c
; Sequence 31410, Application US/09918995
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 31410
; LENGTH: 471
; TYPE: DNA
; ORGANISM: Homo sapiens

; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(471)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-31410

Query Match 0.5%; Score 21; DB 5; Length 471;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2379 tcttcttctgggtctctctcc 2399
Db 120 TCTTCTTCTGGGTCTCTCTCC 100

RESULT 25
US-60-382-445-1176/c
; Sequence 1176, Application US/60382445
; GENERAL INFORMATION:
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Gaiger, Alexander
; APPLICANT: Gordon, Brian
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF BLADDER CANCER
; FILE REFERENCE: 210121.573P1
; CURRENT APPLICATION NUMBER: US/60/382,445
; CURRENT FILING DATE: 2002-05-20
; NUMBER OF SEQ ID NOS: 2900
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1176
; LENGTH: 523
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-382-445-1176

Query Match 0.5%; Score 21; DB 7; Length 523;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2379 tcttcttctgggtctctctcc 2399
Db 23 TCTTCTTCTGGGTCTCTCTCC 3

RESULT 26
US-10-027-632-104255
; Sequence 104255, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 104255
; LENGTH: 583
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-104255

Query Match 0.5%; Score 21; DB 6; Length 583;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2391 tctctctctctctctctctct 2411
|||||
Db 300 tctctctctctctctctctct 320

RESULT 27
US-10-027-632-325232
; Sequence 325232, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027.632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 325232
; LENGTH: 583
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-325232

Query Match 0.5%; Score 21; DB 6; Length 583;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2391 tctctctctctctctctctct 2411
|||||
Db 300 tctctctctctctctctctct 320

RESULT 28
US-60-377-240-6245/c
; Sequence 6245, Application US/60377240
; GENERAL INFORMATION:
; APPLICANT: Diggans, James C.
; APPLICANT: Porter, Mark
; APPLICANT: Wei, Tao
; TITLE OF INVENTION: Canine Gene Microarrays for Molecular Toxicology Modeling
; FILE REFERENCE: 44921-5116-PR
; CURRENT APPLICATION NUMBER: US/60/377,240
; CURRENT FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 11109
; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 6245
; LENGTH: 598
; TYPE: DNA
; ORGANISM: Canis familiaris
; FEATURE:
; OTHER INFORMATION:
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(598)
; OTHER INFORMATION: n = a or c or g or t
US-60-377-240-6245

Query Match 0.5%; Score 21; DB 7; Length 598;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2391 tctctctctctctctctctct 2411
|||||
Db 143 TCCTCCTCCTCCTCATCTTCT 123

RESULT 29
US-60-377-240-1586
; Sequence 1586, Application US/60377240
; GENERAL INFORMATION:
; APPLICANT: Diggans, James C.
; APPLICANT: Porter, Mark
; APPLICANT: Wei, Tao
; TITLE OF INVENTION: Canine Gene Microarrays for Molecular Toxicology Modeling
; FILE REFERENCE: 44921-5116-PR
; CURRENT APPLICATION NUMBER: US/60/377,240
; CURRENT FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 11109
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1586
; LENGTH: 641
; TYPE: DNA
; ORGANISM: Canis familiaris
; FEATURE:
; OTHER INFORMATION:
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(641)
; OTHER INFORMATION: n = a or c or g or t
US-60-377-240-1586

Query Match 0.5%; Score 21; DB 7; Length 641;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2478 gggaggtgcctctggaggagc 2498
|||||
Db 154 gggaggtgcctctggaggagc 174

RESULT 30
US-10-155-881-17468/c
; Sequence 17468, Application US/10155881
; GENERAL INFORMATION:
; APPLICANT: Dotson, Stanton B.
; APPLICANT: Kovalic, David K.
; APPLICANT: Liu, Jingdong
; APPLICANT: Lutfiyva, Linda L.
; APPLICANT: McIninch, James
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
; FILE REFERENCE: 38-21(15300)J
; CURRENT APPLICATION NUMBER: US/10/155,881
; CURRENT FILING DATE: 2002-05-22


```

; NUMBER OF SEQ ID NOS: 37595
; SEQ ID NO 17468
; LENGTH: 674
; TYPE: DNA
; ORGANISM: Glycine max
US-10-155-881-17468

```

Query Match 0.5%; Score 21; DB 6; Length 674;
Best Local Similarity 100.0%; Pred. NO. 12;
Matches 21; Conservative 0; Mismatches 0; Indels

Qy 2391 tccctcctcctcctcattct 2411
 |||||
 Db 194 tccctcctcctcctcattct 174

RESULT 31
US-10-027-632-15064/c
: Sequence 15064. Application US/10027632

```

: GENERAL INFORMATION:
: APPLICANT: Wang, David G.
: TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
: TITLE OF INVENTION: Polymorphisms in the Human Genome
: FILE REFERENCE: 108827.129
: CURRENT APPLICATION NUMBER: US/10/027,632
: CURRENT FILING DATE: 2002-04-30
: PRIOR APPLICATION NUMBER: US 60/218,006
: PRIOR FILING DATE: 2000-07-12
: PRIOR APPLICATION NUMBER: US 60/198,676
: PRIOR FILING DATE: 2000-04-20
: PRIOR APPLICATION NUMBER: US 60/193,483
: PRIOR FILING DATE: 2000-03-29
: PRIOR APPLICATION NUMBER: US 60/185,218
: PRIOR FILING DATE: 2000-02-24
: PRIOR APPLICATION NUMBER: US 60/167,363
: PRIOR FILING DATE: 1999-11-23
: PRIOR APPLICATION NUMBER: US 60/156,358
: PRIOR FILING DATE: 1999-09-28
: PRIOR APPLICATION NUMBER: US 60/146,002
: PRIOR FILING DATE: 1999-08-09
: NUMBER OF SEQ ID NOS: 325720
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 15064
: LENGTH: 744
: TYPE: DNA
: ORGANISM: Human
: US-10-027-632-15064

```

```
Query Match      0.5%; Score 21; DB 6; Length 744;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 21; Conservative 0; Mismatches 0; Indels
```

Qy 3079 ggtggccagaggatggagt 3099
 |||||
Db 275 GGTGGCCAGAGCGATGGAGTT 255

RESULT 32
US-10-027-632-30946/c
: Sequence 30946, Application US/10027632

```

: GENERAL INFORMATION:
: APPLICANT: Wang, David G.
: TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
: POLYMORPHISMS IN THE HUMAN GENOME
: TITLE OF INVENTION: Polymorphisms in the Human Genome
: FILE REFERENCE: 108827.129
: CURRENT APPLICATION NUMBER: US/10/027,632
: CURRENT FILING DATE: 2002-04-30
: PRIOR APPLICATION NUMBER: US 60/218,006
: PRIOR FILING DATE: 2000-07-12
: PRIOR APPLICATION NUMBER: US 60/198,676
: PRIOR FILING DATE: 2000-04-20

```

```

; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30946
; LENGTH: 997
; TYPE: DNA
; ORGANISM: Human
; US-10-027-632-30946

```

```
Query Match      0.5%; Score 21; DB 6; Length 997;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 21: Conservative 0; Mismatches 0; Indels
```

Qy 3079 ggtggccagagggatggagtt 3099
|||||
Db 604 GGTGGCCAGAGGGATGGAGTT 584

```

RESULT 33
US-10-045-428A-2
: Sequence 2, Application US/10045428A
: GENERAL INFORMATION:
: APPLICANT: Mano, Hiroyuki
: APPLICANT: Sakata, Tsunekai
: APPLICANT: Hasegawa, Mamoru
: APPLICANT: Tabata, Toshiaki
: TITLE OF INVENTION: Promoter
: FILE REFERENCE: 50026/011003
: CURRENT APPLICATION NUMBER: US/10/045,428A
: PRIOR FILING DATE: 2002-04-15
: PRIOR APPLICATION NUMBER: 09/735,103
: PRIOR FILING DATE: 2000-12-12
: PRIOR APPLICATION NUMBER: 09/142,529
: PRIOR FILING DATE: 1999-08-12
: PRIOR APPLICATION NUMBER: PCT/JP97/00741
: PRIOR FILING DATE: 1997-03-10
: PRIOR APPLICATION NUMBER: JP 8/54294
: PRIOR FILING DATE: 1996-03-12
: NUMBER OF SEQ ID NOS: 16
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 2
: LENGTH: 2574
: TYPE: DNA
: ORGANISM: Mus musculus
US-10-045-428A-2

```

Query Match 0.5%; Score 21; DB 6; Length 2574;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 21; Conservative 0; Mismatches 0; Indels

Qy	3118	catccacagagacctggctgc	3138
Db	1566	catccacagagacctggctgc	1586

RESULT 34
US-10-172-118-1257
; Sequence 1257, Application US/10172118
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yudong
; APPLICANT: Linsley, Peter

```
; APPLICANT: Mao, Mao
; APPLICANT: Roberts, Chris
; APPLICANT: Van 't Veer, Laura
; APPLICANT: Van de Vijver, Marc
; APPLICANT: Bernards, Rene
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 9301-175-999
; CURRENT APPLICATION NUMBER: US/10/172,118
; CURRENT FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: 60/380,770
; PRIOR FILING DATE: 2002-05-14
; NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 1257
; LENGTH: 3314
; TYPE: DNA
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: NM_006235
; DATABASE ENTRY DATE: 2001-06-18
US-10-172-118-1257

Query Match          0.5%; Score 21; DB 6; Length 3314;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 661 cttctttccaccctctct 681
      |||||
Db 1516 cttctttccaccctctct 1536

RESULT 35
US-09-053-375B-733
; Sequence 733, Application US/09053375B
; GENERAL INFORMATION:
; APPLICANT: Chenchik, Alex
; APPLICANT: Bibilashvili, Robert
; TITLE OF INVENTION: Nucleic Acid Arrays
; FILE REFERENCE: CLON-006
; CURRENT APPLICATION NUMBER: US/09/053,375B
; CURRENT FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 1543
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 733
; LENGTH: 5470
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-053-375B-733

Query Match          0.5%; Score 21; DB 5; Length 5470;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 382 ccagacagacagtggtggtggt 3852
      |||||
Db 4047 ccagacagacagtggtggtggt 4057

RESULT 36
US-09-540-210B-10654/c
; Sequence 10654, Application US/09540210B
; GENERAL INFORMATION:
; APPLICANT: Seilhamer, Jeffrey J.
; APPLICANT: Delegeane, Angelo M.
; APPLICANT: Stuart, Susan G.
; APPLICANT: Stuve, Laura L.
; APPLICANT: Mullahy, Sara J.
; APPLICANT: Naughton, Rebecca E.
; TITLE OF INVENTION: POLYNUCLEOTIDES OF URINARY TRACT TISSUE
; FILE REFERENCE: PD-1037 CIP
; CURRENT APPLICATION NUMBER: US/09/540,210B
; CURRENT FILING DATE: 2002-04-03
; PRIOR APPLICATION NUMBER: 08/972,899
; PRIOR FILING DATE: November 18, 1997
; PRIOR APPLICATION NUMBER: 08/395,244
; PRIOR FILING DATE: February 27, 1995
; PRIOR APPLICATION NUMBER: 08/722,922
; PRIOR FILING DATE: September 27, 1996
; PRIOR APPLICATION NUMBER: 60/005,526
; PRIOR FILING DATE: September 29, 1995
; PRIOR APPLICATION NUMBER: 08/824,029
; PRIOR FILING DATE: March 25, 1997
; PRIOR APPLICATION NUMBER: 60/014,010
; PRIOR FILING DATE: March 25, 1996
; PRIOR APPLICATION NUMBER: 08/826,847
; PRIOR FILING DATE: April 10, 1997
; PRIOR APPLICATION NUMBER: 60/015,533
; PRIOR FILING DATE: April 10, 1996
; PRIOR APPLICATION NUMBER: 08/903,555
; PRIOR FILING DATE: July 31, 1997
; PRIOR APPLICATION NUMBER: 60/023,308
; PRIOR FILING DATE: July 31, 1996
; PRIOR APPLICATION NUMBER: 08/862,178
; PRIOR FILING DATE: May 22, 1997
; PRIOR APPLICATION NUMBER: 60/018,217
; PRIOR FILING DATE: May 23, 1996
; PRIOR APPLICATION NUMBER: 08/881,589
; PRIOR FILING DATE: June 24, 1997
; PRIOR APPLICATION NUMBER: 60/021,275
; PRIOR FILING DATE: June 25, 1996
; PRIOR APPLICATION NUMBER: 08/903,802
; PRIOR FILING DATE: July 31, 1997
; PRIOR APPLICATION NUMBER: 60/023,308
; PRIOR FILING DATE: July 31, 1996
; PRIOR APPLICATION NUMBER: 08/905,881
; PRIOR FILING DATE: August 1, 1997
; PRIOR APPLICATION NUMBER: 60/025,204
; PRIOR FILING DATE: August 1, 1996
; PRIOR APPLICATION NUMBER: 08/903,471
; PRIOR FILING DATE: July 30, 1997
; PRIOR APPLICATION NUMBER: 60/025,478
; PRIOR FILING DATE: July 31, 1996
; PRIOR APPLICATION NUMBER: 08/903,556
; PRIOR FILING DATE: July 31, 1997
; PRIOR APPLICATION NUMBER: 60/025,217
; PRIOR FILING DATE: August 22, 1996
; PRIOR APPLICATION NUMBER: 08/937,142
; PRIOR FILING DATE: September 23, 1997
; PRIOR APPLICATION NUMBER: 60/026,598
; PRIOR FILING DATE: September 24, 1996
; PRIOR APPLICATION NUMBER: 08/960,746
; PRIOR FILING DATE: October 29, 1997
; PRIOR APPLICATION NUMBER: 60/030,144
; PRIOR FILING DATE: October 30, 1996
; PRIOR APPLICATION NUMBER: 08/826,847
; PRIOR FILING DATE: April 10, 1997
; PRIOR APPLICATION NUMBER: 60/015,533
; PRIOR FILING DATE: April 10, 1996
; PRIOR APPLICATION NUMBER: 08/755,524
; PRIOR FILING DATE: November 22, 1996
; PRIOR APPLICATION NUMBER: 60/007,495
; PRIOR FILING DATE: November 22, 1995
; PRIOR APPLICATION NUMBER: 09/021,031
; PRIOR FILING DATE: February 10, 1998
; PRIOR APPLICATION NUMBER: 60/039,325
; PRIOR FILING DATE: February 13, 1997
; PRIOR APPLICATION NUMBER: 09/035,172
; PRIOR FILING DATE: March 4, 1998
; PRIOR APPLICATION NUMBER: 60/040,431
; PRIOR FILING DATE: March 5, 1997
; PRIOR APPLICATION NUMBER: 09/041,894
; PRIOR FILING DATE: March 12, 1998
; PRIOR APPLICATION NUMBER: 60/040,199
; PRIOR FILING DATE: March 14, 1997
; PRIOR APPLICATION NUMBER: 09/050,817
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; PRIOR FILING DATE: March 30, 1998
; PRIOR APPLICATION NUMBER: 60/043,792
; PRIOR FILING DATE: April 11, 1997
; PRIOR APPLICATION NUMBER: 09/074,999
; PRIOR FILING DATE: May 8, 1998
; PRIOR APPLICATION NUMBER: 60/048,431
; PRIOR FILING DATE: May 29, 1997
; PRIOR APPLICATION NUMBER: 09/107,592
; PRIOR FILING DATE: June 30, 1998
; PRIOR APPLICATION NUMBER: 60/052,751
; PRIOR FILING DATE: July 1, 1997
; PRIOR APPLICATION NUMBER: 09/094,079
; PRIOR FILING DATE: June 9, 1998
; PRIOR APPLICATION NUMBER: 60/049,975
; PRIOR FILING DATE: June 13, 1997
; NUMBER OF SEQ ID NOS: 35654
; SOFTWARE: PERL Program
; SEQ ID NO 10654
; LENGTH: 226
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: hu00301736
US-09-540-210B-10654

Query Match 0.5%; Score 20; DB 5; Length 226;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1303 ggcctctctccccagcatct 1322
|||||
Db 207 GGCCTCCTCCCCAGCATCT 188

RESULT 37
US-09-721-544-17764/c
; Sequence 17764, Application US/09721544
; GENERAL INFORMATION:
; APPLICANT: Arterburn, Matthew
; APPLICANT: Asghari, Vida
; APPLICANT: Damavandi, Simin
; APPLICANT: Dickson, Mark
; APPLICANT: Drake, Jim
; APPLICANT: Drmanac, Radoje
; APPLICANT: Engleman, Brandie
; APPLICANT: Faulkner, Brandy
; APPLICANT: Garcia, Veronica
; APPLICANT: Giedt, Gretchen
; APPLICANT: Hunter, Kelly
; APPLICANT: Jones, Aaron
; APPLICANT: Jones, Lee
; APPLICANT: Kita, David
; APPLICANT: Labat, Ivan
; APPLICANT: Laroya, Mimi
; APPLICANT: Lomelli, Michelle
; APPLICANT: Nguyen, Phuong
; APPLICANT: Nogra, Margie
; APPLICANT: Palencia, Servando
; APPLICANT: Raisi, Fariba
; APPLICANT: Smith, Benjamin
; APPLICANT: Tkach, Joe
; APPLICANT: Tran, Lien
; APPLICANT: Verna, Ron
; APPLICANT: Yang, Fei
; APPLICANT: Yim, Kenneth
; TITLE OF INVENTION: Novel Nucleic Acid Sequences Obtained
; FILE REFERENCE: 728CIP
; CURRENT APPLICATION NUMBER: US/09/721,544
; CURRENT FILING DATE: 2000-11-21
; PRIOR APPLICATION NUMBER: 09/515,128
; PRIOR FILING DATE: 1998-02-13
; NUMBER OF SEQ ID NOS: 24489
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 17950
; LENGTH: 366
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-721-544-17950

Query Match 0.5%; Score 20; DB 5; Length 366;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: 09/034,341
; PRIOR FILING DATE: 1998-02-13
; NUMBER OF SEQ ID NOS: 24489
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 17764
; LENGTH: 356
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-721-544-17764

Query Match 0.5%; Score 20; DB 5; Length 356;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1303 ggcctctctccccagcatct 1322
|||||
Db 211 GGCCTCCTCCCCAGCATCT 192

RESULT 38
US-09-721-544-17950
; Sequence 17950, Application US/09721544
; GENERAL INFORMATION:
; APPLICANT: Arterburn, Matthew
; APPLICANT: Asghari, Vida
; APPLICANT: Damavandi, Simin
; APPLICANT: Dickson, Mark
; APPLICANT: Drake, Jim
; APPLICANT: Drmanac, Radoje
; APPLICANT: Engleman, Carrie
; APPLICANT: Faulkner, Brandy
; APPLICANT: Garcia, Veronica
; APPLICANT: Giedt, Gretchen
; APPLICANT: Hunter, Kelly
; APPLICANT: Jones, Aaron
; APPLICANT: Jones, Lee
; APPLICANT: Kita, David
; APPLICANT: Labat, Ivan
; APPLICANT: Laroya, Mimi
; APPLICANT: Lomelli, Michelle
; APPLICANT: Nguyen, Phuong
; APPLICANT: Nogra, Margie
; APPLICANT: Palencia, Servando
; APPLICANT: Raisi, Fariba
; APPLICANT: Smith, Benjamin
; APPLICANT: Tkach, Joe
; APPLICANT: Tran, Lien
; APPLICANT: Verna, Ron
; APPLICANT: Yang, Fei
; APPLICANT: Yim, Kenneth
; TITLE OF INVENTION: Novel Nucleic Acid Sequences Obtained
; FILE REFERENCE: 728CIP
; CURRENT APPLICATION NUMBER: US/09/721,544
; CURRENT FILING DATE: 2000-11-21
; PRIOR APPLICATION NUMBER: 09/515,128
; PRIOR FILING DATE: 1998-02-13
; NUMBER OF SEQ ID NOS: 24489
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 17950
; LENGTH: 366
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-721-544-17950

Query Match 0.5%; Score 20; DB 5; Length 366;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3173 aagatctgtgactttggcct 3192
|||||
Db 73 aagatctgtgactttggcct 92

RESULT 39
US-60-382-445-2302/c
; Sequence 2302, Application US/60382445
; GENERAL INFORMATION:
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Gaiger, Alexander
; APPLICANT: Gordon, Brian
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.573P1
; CURRENT APPLICATION NUMBER: US/60/382.445
; CURRENT FILING DATE: 2002-05-20
; NUMBER OF SEQ ID NOS: 2900
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2302
; LENGTH: 456
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-382-445-2302

Query Match 0.5%; Score 20; DB 7; Length 456;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2391 tctctctctctcatcttc 2410
|||||
Db 141 TCCTCTCTCTCATCTTC 122

RESULT 40
US-09-721-544-7766
; Sequence 7766, Application US/09721544
; GENERAL INFORMATION:
; APPLICANT: Arterburn, Matthew
; APPLICANT: Asghari, Vida
; APPLICANT: Damavandi, Simin
; APPLICANT: Dickson, Mark
; APPLICANT: Drake, Jim
; APPLICANT: Drmanac, Radoje
; APPLICANT: Engleman, Carrie
; APPLICANT: Faulkner, Brandy
; APPLICANT: Garcia, Veronica
; APPLICANT: Hunter, Kelly
; APPLICANT: Jessen, Aaron
; APPLICANT: Jones, Lee
; APPLICANT: Klita, David
; APPLICANT: Labat, Ivan
; APPLICANT: Laroya, Mimi
; APPLICANT: Lomelli, Michelle
; APPLICANT: Nguyen, Phuong
; APPLICANT: Nogra, Margie
; APPLICANT: Palencia, Servando
; APPLICANT: Raisi, Fariba
; APPLICANT: Smith, Benjamin
; APPLICANT: Tkach, Joe
; APPLICANT: Tran, Lien
; APPLICANT: Verna, Ron
; APPLICANT: Yang, Fei
; APPLICANT: Yim, Kenneth
; TITLE OF INVENTION: Novel Nucleic Acid Sequences Obtained
; FILE REFERENCE: 728C1P
; CURRENT APPLICATION NUMBER: US/09/721,544
; CURRENT FILING DATE: 2000-11-21

; PRIOR APPLICATION NUMBER: 09/515,128
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: 09/034,341
; PRIOR FILING DATE: 1998-02-13
; NUMBER OF SEQ ID NOS: 24489
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 7766
; LENGTH: 461
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(461)
; OTHER INFORMATION: n = A,T,C or G
US-09-721-544-7766

Query Match 0.5%; Score 20; DB 5; Length 461;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3173 aagatctgtgactttggcct 3192
|||||
Db 170 aagatctgtgactttggcct 189

RESULT 41
US-09-918-995-24204
; Sequence 24204, Application US/09918995
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 24204
; LENGTH: 462
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(462)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-24204

Query Match 0.5%; Score 20; DB 5; Length 462;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3173 aagatctgtgactttggcct 3192
|||||
Db 91 aagatctgtgactttggcct 110

RESULT 42
US-09-721-544-7765
; Sequence 7765, Application US/09721544
; GENERAL INFORMATION:
; APPLICANT: Arterburn, Matthew
; APPLICANT: Asghari, Vida
; APPLICANT: Damavandi, Simin
; APPLICANT: Dickson, Mark
; APPLICANT: Drake, Jim
; APPLICANT: Drmanac, Radoje
; APPLICANT: Engleman, Carrie
; APPLICANT: Faulkner, Brandy
; APPLICANT: Garcia, Veronica

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; APPLICANT: Giedt, Gretchen
; APPLICANT: Hunter, Kelly
; APPLICANT: Jessen, Aaron
; APPLICANT: Jones, Lee
; APPLICANT: Kita, David
; APPLICANT: Labat, Ivan
; APPLICANT: Laroya, Mimi
; APPLICANT: Lomelli, Michelle
; APPLICANT: Nguyen, Phuong
; APPLICANT: Nogra, Margie
; APPLICANT: Palencia, Servando
; APPLICANT: Raisi, Fariba
; APPLICANT: Smith, Benjamin
; APPLICANT: Tkach, Joe
; APPLICANT: Tran, Lien
; APPLICANT: Verna, Ron
; APPLICANT: Yang, Fel
; APPLICANT: Yim, Kenneth
; TITLE OF INVENTION: Novel Nucleic Acid Sequences Obtained
; TITLE OF INVENTION: From a cDNA Library of Fetal Liver-Spleen
; FILE REFERENCE: 728CIP
; CURRENT APPLICATION NUMBER: US/09/721,544
; CURRENT FILING DATE: 2000-11-21
; PRIOR APPLICATION NUMBER: 09/515,128
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: 09/034,341
; PRIOR FILING DATE: 1998-02-13
; NUMBER OF SEQ ID NOS: 24489
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7765
; LENGTH: 484
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(484)
; OTHER INFORMATION: n = A,T,C or G
US-09-721-544-7765
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Query Match 0.5%; Score 20; DB 5; Length 484;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 3173 aagatctgtgacttggcct 3192
|||||
Db 200 aagatctgtgacttggcct 219
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```
RESULT 43
US-09-918-995-37258
; Sequence 37258, Application US/09918995
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38034
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 37258
; LENGTH: 518
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(518)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-37258
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Query Match 0.5%; Score 20; DB 5; Length 518;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2391 tcctctctctctcatcttc 2410
|||||
Db 314 tcctctctctctcatcttc 333

RESULT 44
US-60-377-240-3743/c
; Sequence 3743, Application US/60377240
; GENERAL INFORMATION:
; APPLICANT: Digheans, James C.
; APPLICANT: Porter, Mark
; APPLICANT: Wei, Tao
; TITLE OF INVENTION: Canine Gene Microarrays for Molecular Toxicology Modeling
; FILE REFERENCE: 44921-5116-PR
; CURRENT APPLICATION NUMBER: US/60/377,240
; CURRENT FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 11109
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3743
; LENGTH: 575
; TYPE: DNA
; ORGANISM: Canis familiaris
; FEATURE:
; OTHER INFORMATION:
; NAME/KEY: misc_feature
; LOCATION: (1)...(575)
; OTHER INFORMATION: n = a or c or g or t
US-60-377-240-3743
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Query Match 0.5%; Score 20; DB 7; Length 575;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 2391 tcctctctctctcatcttc 2410
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Db 418 TCCTCCTCCTCCTCATCTTC 399
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RESULT 45
US-10-027-632-142575
; Sequence 142575, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
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; SEQ ID NO 142575
; LENGTH: 627
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-142575

Query Match 0.5%; Score 20; DB 6; Length 627;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2391 tctctctctctctcttc 2410
|||||
Db 596 tctctctctctctcttc 615

Search completed: July 16, 2002, 02:56:38
Job time: 24536 sec

**ORIGINAL
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OM nucleic - nucleic search, using sw model

Run on: July 15, 2002, 18:09:07 ; Search time 12941.8 Seconds
(without alignments)
6872.393 Million cell updates/sec

Title: US-09-375-248-1
Perfect score: 4111
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Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 21979536 seqs, 10817449327 residues

Word size : 0
Total number of hits satisfying chosen parameters: 43959072

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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SUMMARIES

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2	4111	100.0	4111	17	US-09-375-248-1
3	4111	100.0	4795	3	US-07-959-951A-3
4	4111	100.0	4795	6	US-08-257-754-3
5	4111	100.0	4795	15	US-09-169-079-3
6	3912	95.2	4195	3	US-07-959-951A-1
7	3912	95.2	4195	6	US-08-257-754-1
8	3912	95.2	4195	15	US-09-169-079-1
9	3912	95.2	4416	10	US-08-601-132-36
10	3912	95.2	4416	10	US-08-671-573A-36
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12	3912	95.2	4416	17	US-09-355-700-1
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37 440 10.7 575 60 US-60-213-847-55 Sequence 55, Appl
38 401 9.8 415 60 US-60-213-178-1247 Sequence 1247, Ap
39 388 9.4 535 28 US-09-716-953-1245 Sequence 1245, Ap
40 340 8.3 1575 56 US-60-172-373-15761 Sequence 15761, A
41 339 8.2 340 60 US-60-213-847-1271 Sequence 1271, Ap
42 310 7.5 724 57 US-60-184-770-470 Sequence 470, App
43 309 7.5 576 31 US-09-823-241-233 Sequence 233, App
44 253 6.2 256 62 US-60-233-937-796 Sequence 796, App
45 233 5.7 644 18 US-09-474-434-807 Sequence 807, App

ALIGNMENTS

RESULT 1
PCT-US99-06133-1
: SEQUENCE 1: Application PC/TUS9906133
: GENERAL INFORMATION:
: APPLICANT: Ferrelli, Robert E
: APPLICANT: Alitalo, Kari
: APPLICANT: Finegold, David N
: APPLICANT: Karkkainen, Marika
: TITLE OF INVENTION: SCREENING AND THERAPY FOR LYMPHATIC DISORDERS INVOLVING
: FILE OF INVENTION: THE FLT4 RECEPTOR TYROSINE KINASE (VEGFR-3)
: CURRENT APPLICATION NUMBER: PCT/US99/06133
: CURRENT FILING DATE: 1999-03-26
: NUMBER OF SEQ ID NOS: 18
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 1
: LENGTH: 4111
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (20)..(4111)
: OTHER INFORMATION: Human Flt4 (VEGFR-3) long form cDNA
PCT-US99-06133-1

Query Match 100.0%: Score 4111; DB 1: Length 4111;
Best Local Similarity 100.0%: Pred. No. 0;
Matches 4111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT      3
: US-07-959-951A-3
: Sequence 3, Application US/07959951A
: GENERAL INFORMATION:
: APPLICANT: Alitalo, Karl, et al.
: TITLE OF INVENTION: FL74, A NOVEL RECEPTOR TYROSIN KINASE
: NUMBER OF SEQUENCES: 10
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
: STREET: 6300 Sears Tower, 233 South Wacker Drive
: CITY: Chicago
: STATE: Illinois
: COUNTRY: United States
: ZIP: 60606-6402
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/07/959,951A

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: FILING DATE: 19921009
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Gruber, Lewis S.
: REGISTRATION NUMBER: 30,060
: REFERENCE/DOCKET NUMBER: 28113/31104
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 312/474-6300
: TELEFAX: 312/474-0448
: TELEX: 25-3856
: INFORMATION FOR SEQ ID NO: 3:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 4795 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: cdna
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 20..4111
: US-07-959-951A-3

Query Match 100.0%; Score 4111; DB 3; Length 4795;
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Matches 4111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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: GENERAL INFORMATION:				
: APPLICANT: Alitalo, Karl				
: APPLICANT: Kaipainen, Arja				
: APPLICANT: Valtola, Reija				
: APPLICANT: Jussila, Lotta				
: TITLE OF INVENTION: File4 (VEGFR-3) as a Target for Tumor Imaging and Ant				
: FILE REFERENCE: 28113/34891				
: CURRENT APPLICATION NUMBER: US/09/169,079				
: CURRENT FILING DATE: 1998-10-09				
: EARLIER APPLICATION NUMBER: 08/901,710				
: EARLIER FILING DATE: 1997-07-28				
: EARLIER APPLICATION NUMBER: 08/340,011				
: EARLIER FILING DATE: 1994-11-14				
: EARLIER APPLICATION NUMBER: 08/257,754				
: EARLIER FILING DATE: 1994-07-09				

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: EARLIER APPLICATION NUMBER: 07/959,951
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: EARLIER FILING DATE: 1992-10-09
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QY 3181 tgactttggcctTgcccgggacatctacaagaacctgactacgtctccgaaggcagtgcc 3240
Db 3181 TGACTTTGGCCTTGGCCGGGACATCTACAAGACCTGACTACGTCCGCAAGGGCAGTGC 3240
QY 3241 ccggctgccccTgaagtggatggccccctgaaagcattctcgacaagggtgtacacacgca 3300
Db 3241 CCGGCTGCCCTTGAAGTGGATGGCCCTGAAAGCATCTTTCGACAAGGTGTACACCACGCA 3300
QY 3301 gagtgcgtgtggtctcttgggggtgctctctctgggagatacttctctLgggggctcccc 3360
Db 3301 GAGTGACGTGTGCTTGTGGGGTCTTCTCTGCGAGATCTTCTCTCTGCGGGGCTCTCCC 3360
QY 3361 gtacctggggTgcagataaaLtgaggagtctctgcccagcgctgagagcggcacaggat 3420
Db 3361 GTACCTTGGGTGACAGTCAATGAGGAGTTCTGCGAGGGCTGAGAGCGGCACCAAGAT 3420
QY 3421 gaggcccccgagctggccactccccccataacgcgcgcatcatgtgaaactggtctcgg 3480
Db 3421 GAGGGCCCGGAGCTGGCCACTTCCCGCCATACGCCGATCATGCTGAACTGCTGTGTCGG 3480
QY 3481 agacccccaggcgagacctgcatctctcgagctggtLggagatacctgggggacctctcca 3540
Db 3481 AGACCCCAAGGCGAGACCTGCATTCTCGAGCTGTGTGAGATCTCTGCGGGGACCTGCTCCA 3540
QY 3541 gggcgagggtcctgcagaaggaaggaggtctgcatggtccccgcgcagctctcagagctc 3600
Db 3541 GGGCAGGGGCTGCAAGAGGAAGAGGAGGTGTGATGGCCCCCGCGCAGCTCTCTAGAGCTC 3600
QY 3601 agaaagggcgagcttctcgaggggtgtccacctggccctacacatcgcccagggtgacgc 3660

Db 3121 CCACAGAGACCTGGCTGCTCGGAACATTTCTGCTTCGGAAGCCAGCTGGTCAAGATCTG 3180
QY 3181 tgactttggccttgcccgagacatctacaaagacctgactcgtccgcaagcgagtg 3240
Db 3181 TGACTTTGGCCTTGCCCGGACATCTACAAAGACCTGACTAGCTCCGCAAGCGCAAGTCG 3240
QY 3241 ccggctgccccctgaatgagtgatggccccctgaaagcatcttcgacaaggtgtacacacgcga 3300
Db 3241 CCGCTGCCCTCAAGTGGATGCCCTGAAAGCATTTTCGACAAGGTGTACACCAACGCA 3300
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QY 3421 gaggccccggagctggccactccccccataacgcccatcatctgtaaaactgtggtccgg 3480
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RESULT 8
US-09-169-079-1
: GENERAL INFORMATION:
: APPLICANT: Alitalo, Kari
: APPLICANT: Kaipainen, Arja
: APPLICANT: Vaitola, Relfa
: APPLICANT: Jussila, Lotta
: TITLE OF INVENTION: Fil4 (VEGFR-3) as a Target for Tumor Imaging and Anti-Tumor Thera
: FILE REFERENCE: 28113/34891
: CURRENT APPLICATION NUMBER: US/09/169,079
: CURRENT FILING DATE: 1998-10-09
: EARLIER APPLICATION NUMBER: 08/901,710
: EARLIER FILING DATE: 1997-07-28
: EARLIER APPLICATION NUMBER: 08/340,011
: EARLIER FILING DATE: 1994-11-14
: EARLIER APPLICATION NUMBER: 08/257,754
: EARLIER FILING DATE: 1994-07-09

: EARLIER APPLICATION NUMBER: 07/959,951
: EARLIER FILING DATE: 1992-10-09
: NUMBER OF SEQ ID NOS: 22
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 1
: LENGTH: 4195
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (20)..(3913)
US-09-169-079-1

Query Match 95.2%: Score 3912; DB 15; Length 4195;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3912; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 ccacgcgcagcggcggagatgcagcggggcgccgcgctgtgctcgagactgtgctctg 60
QY 61 cctgggactcctggacggcctggtgagtggtctactcatgaccccccccgaccttgaacat 120
Db 61 cctgggactcctggacggcctggtgagtggtctactcatgaccccccccgaccttgaacat 120
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Db 121 cagcgaagagtcacacgtcatcgacacccggtgacagcctgtccatctcctgcaggggaca 180
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Db 3481 agaccccaaggcgagacctgcatctctcggaactggttgagatcctctggggacctgtctcca 3540
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Qy 3661 tgaggacagcccgccagctgagccgacagcctgagcccgccaggtatcacactgggt 3720
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Qy 3841 cagtggatggtgtggtgctcgaggaggtttgagcagatagagagcaggtacagacaaga 3900
Db 3841 cagtggatggtgtggtgctcgaggaggtttgagcagatagagagcaggtacagacaaga 3900
Qy 3901 aagcggttcag 3912
Db 3901 aagcggttcag 3912
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RESULT 9

US-08-601-132-36

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: Sequence 36, Application US/08601132
: GENERAL INFORMATION:
: APPLICANT: Allitalo, Karl
: APPLICANT: Joukov, Vladimir
: TITLE OF INVENTION: Receptor Ligand
: NUMBER OF SEQUENCES: 41
: CORRESPONDENCE ADDRESS:
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: ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
: STREET: 6300 Sears Tower, 233 South Wacker Drive
: CITY: Chicago
: STATE: Illinois
: COUNTRY: United States of America
: ZIP: 60606-6402
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: FILING DATE: US/08/601,132
: CLASSIFICATION: 530
: ATTORNEY/AGENT INFORMATION:
: NAME: Gass, David A.
: REGISTRATION NUMBER: 38,153
: REFERENCE/DOCKET NUMBER: 28113/33118
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 312/474-6300
: TELEFAX: 312/474-0448
: TELEX: 25-3856
: INFORMATION FOR SEQ ID NO: 36:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 4416 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: US-08-601-132-36
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Query Match 95.2%; Score 3912; DB 10; Length 4416;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 3912; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 CCACGGCAGCGCGCGAGATGCAGCGGGCGCGCGCTGTGCTGCTGCTGCTGCTGCTG 60
Qy 61 cctgggactcctggagcggcctgtgagtggtggtactccatgacccccccgacctgaacat 120
Db 61 CCTGGGACTCCTGGAGCGGCTTGGTGAGTGGCTACTCATGACCCCGCCGACCTTGAACAT 120
Qy 121 ccagggaggatcacacgtcatcacaccggtgacagcctgtccatctcctgcaggagaca 180
Db 121 CACGGAGGAGTCAACGTATCATGACACCGGTGACACGCTGTCCATCTCTCTGAGGGACA 180
Qy 181 gacccccctcagtgggcttggccaggagctcaggaggcgccagccaccggagacaagga 240
Db 181 GCACCCCTCGAGTGGGCTTGGCCAGGAGCTCAGGAGCGCCAGCCAGCCAGGACAAGGA 240
Qy 241 cagcaggacacgggggtgtgtgcgaactgcgagggcacagagcgcagccctactgcaa 300
Db 241 CACGAGGACACGGGGGTGTGTGCGACTGCGAGGCGACAGCGCCAGGCCCTTACTGCAA 300
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Qy 361 gtacatcaaggcagcagcatcaggggaccacgcccagctcctcactcgttctcgtgagaga 420
Db 361 GTACATCAAGGACCGCATCGAGGGCACACGCGCGCCAGCTCTCTAGCTTCTGCTGAGAGA 420
Qy 421 ctttgagcagcatctcatcaaacgctgacagcctcttgggtcaacaggaagacgacct 480
Db 421 CTTTGAGCAGCCATTCTCAACAGCCTGACACGCTTTGGTCAACAGAGAGAGCGCCAT 480
Qy 481 gtgggtgcctgtctgtgtgtccatccccggcctcaatgtcacgctgcgctcgcaagctc 540
Db 481 GTGGGTGCCCTCTCTGTGGTGTCCATCCCCGGCCTCAATGTACGCTGCGCTCGCAAGCTC 540
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Db 601 CAGCCCACTCTGACAGATGCCCTGTACCTGCACTGCGAGACCACCTGGGGAGACCAGGA 660
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QY 961 cggcatccagcgtattcgggagagcaccgaggtcattgtgcatgaaaaacccttcatcag 1020
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Qy 2041 ctugaagacccctcggctcagcagaacttgaccgaacctctcctggtgaacgTlgagcgactc 2100
Db 2041 CCTGAAGACCCCTCGGCTCACGCGAAGACTTTCAGCGACTCTCTGTGAACCTGAGCGCACTC 2100
Qy 2101 qctgaagatcagTgcttggtggccgagcgacgcccagcatcgTgTgTlacaaga 2160
Db 2101 GCTGCAATCAGACTGCTTGGTGGCCGAGCGACGCCGCCAGCATCTGTGTGTACAAGA 2160
Qy 2161 caqaggrTgtcTgaagaaagtctgagTcgactTggcgactccaacccagaagctlgag 2220
Db 2161 CGAGAGGCTGCTGAGGAAAGTCTGGAGTCGACTTGGCGGACTCCAAACCAGAAAGCTGAG 2220
Qy 2221 catccagcgctcgcgagagagatgcgggacgctatctgtgcagcgtTgtgcaacgccaa 2280
Db 2221 CATCCAGCGCTGCGGAGAGATGCGGACGCTATCTGTGAGCGTGTGTCAACGCCAA 2280
Qy 2281 gggctgcTcaactctccgcccagcgtTggcgtTggcgactccaacccagaagctlgag 2340
Db 2281 GGCTGCGTCACTCTCCGCCAGCGTGGCCGTGGAAAGGCTCCGAGGATAAAGGGCAGCAT 2340
Qy 2341 ggaatcgtgatactgtcgtggtaccggcgtcatcgtcgtgtcttcttctgggtcctcct 2400
Db 2341 GGAGATCGTATCTTCTGCTGCTACCGGCGTATCGTGTCTTCTTGGGTCTCTCTCT 2400
Qy 2401 cctcatctctgtTaaatgagagggccgcccacgacacatcaagcggcTtacctgtc 2460
Db 2401 CCTCATCTTCTGTAAATGATGAGGAGCGCGGCCACGACAGATCAAGACGGGTACCTGT 2460
Qy 2461 caLcatatgaccccgaggagTgctctTggaggaagcaatgcgaLaacctgtcctacga 2520
Db 2461 CATCATCATGACCCCGGAGGTGCTCTGGAGAGCAATGCGAATACCTGTCTTACGA 2520
Qy 2521 tgcagcagTggaaatcccccgagagcgtgacacctggggagagTgctcggctacgg 2580
Db 2521 TGGCAGCAGTGGGAATTCGCCCGGAGAGGGCTGCACCTGGGGAGAGTGTCTGGCTACGG 2580
Qy 2581 cgcctTcggaagTggtggaagcctccgcttctcggcatcccaagggcagcagctgtga 2640
Db 2581 CGCTTCGGGAAGGTGTTGGAAGCCCTCCCGCTTTCGGCATCCACAAAGGGCAGCAGCTGTGA 2640
Qy 2641 caccgtTggcgtgaaaatgctgaaagaggcgccacgycagcgagcagcgcgctgat 2700
Db 2641 CACCGTGGCGGTCAAAATGCTGAAGAGGGCGCACGGCCAGCGACACCGCGCGCTGAT 2700
Qy 2701 gtcggagctcaagatcctcatcatcgcggaacacctcaacgtTggtcaacctcctcg 2760
Db 2701 GTCGGAGCTCAAGATCCTATTACATCGCAACACCCTCAACGTGCTCAACCTCTCTCGG 2760
Qy 2761 ggcgtcaccaagccagggccctcatgTgTgTgagTctgTgagTctgcaagTaccgaa 2820
Db 2761 GGCTGCACCAAGCCCGAGGGCCCCCTCATGTGTGATCTGTGGAGTTCGTCAAGTACGGCAA 2820
Qy 2821 cctctcaactctcgtcgcgaagcggaagcgtcttcagccccctcgcggagaaagctctcc 2880
Db 2821 CCTCTCAACTTCTTGGCGCCAAAGCGGACGCCCTTCAGCCCCCTGGCGGAGAAAGTCTCC 2880
Qy 2881 cgaagacgcgagcgtctccgcacatgTgagctcgcagcgtTgagTcggagcgcc 2940
Db 2881 CGAGCAGCGGACGCTTCGGGCCATGTGTGGAGCTCGCAGGCTGGATCGGAGCGGCC 2940
Qy 2941 gggagcagcagcagggctcctcgcgctcTcgaagaccgagggcgagcagcg 3000
Db 2941 GGGAGCAGCGACAGGGTCTCTTCGCGCGGTCTTCTGAAAGCCGAGGGCGGAGCGGCG 3000

RESULT 12

US-09-355-700-1

; Sequence 1, Application US/09355700

; GENERAL INFORMATION:

; APPLICANT: Ludwig Institute for Cancer Research

; Helsinki University Licensing

; Alitalo, Kari(U.S. only)

Qy 3001 ggcttctccagaccaagaagctgaggacctgtgctgagcccgcctgaccatggaagatct 3060
Db 3001 GGCTTCTCCAGACCAAGAAGCTGAGGACCTGTGGCTTGAGCCCGCTGACCATGGAAGATCT 3060
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Db 3061 TGCTCTGTACAGCTTCCAGGTGCCAGAGGGATGGAGTTCTCTGGCTTCGGAAGTGCAT 3120
Qy 3121 ccacagagacctggctgctcggaaacttctgctgTcggaagcgagctggTgaagatctg 3180
Db 3121 CCACAGAGACCTGGCTGCTCGGAACATTTCTGCTGTCGGAAGCGACGTGCTGAAGATCTG 3180
Qy 3181 tgactttggccttgcccgggacatctacaaaagacctgactacgtccgcaagggcgagtgc 3240
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Qy 3481 agaccccaaggcgagacctgcattctcggagctggTggagatcctgggggacctgctca 3540
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Qy 3661 tgagagaccccgcaagcctgcagcgccacagcctggcgcaggtattacaactgggt 3720
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Qy 3721 gtcctttccgggtgcctggccagaggggctgagaccgtggttctcctcagagatgaagac 3780
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Db 3781 ATTTGAGGAATTTCCCATGATGACCCCAACGACCTTACAAAGGCTCTGTGGACAACACACAGA 3840
Qy 3841 cagTggagTggtgctcgtcggcggaggtttgagcagatagagagcagagcatagacaaga 3900
Db 3841 CAGTGGGATGTTGCTTGGCTCGGCTCGGAGAGTTCGAGCAGATAGAGAGCAGCATAGACAAGA 3900
Qy 3901 aagcggttcaag 3912
Db 3901 AAGCGGCTTCAG 3912

RESULT 12

US-09-355-700-1

; Sequence 1, Application US/09355700

; GENERAL INFORMATION:

; APPLICANT: Ludwig Institute for Cancer Research

; Helsinki University Licensing

; Alitalo, Kari(U.S. only)

OY 1321 ctactcgcgtcaagccgcccagcctcacctgcacggcctacggtgccccctcctct 1380
DB 1321 CTACTCGCGTCAACGCCAGCCCTCACCTGCACGGCTACGGGGTCCCCCTCCT 1380
OY 1381 cagatcaagtggactggcgccctgacaccctgcaagatggttggccagctagtcct 1440
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OY 1441 ccggcgagcagcagcaagcctcatcccacagtgcccgatgcccgtgagggcggtgaccac 1500
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Db 3541 GGCAGGGCCCTGCAAGAGAAAGAGAGGTCTGCAATGGCCCGCCGAGCTCTCAGAGCTC 3600
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QY 3901 aagcggttcag 3912
Db 3901 AAGCGGCTTCAG 3912

RESULT 13

US-09-440-302A-1035
; Sequence 1035, Application US/09440302A
; GENERAL INFORMATION:
; APPLICANT: Chenchik, Alex
; TITLE OF INVENTION: Human Neurobiology Array
; FILE REFERENCE: CLON-006CIP11
; CURRENT APPLICATION NUMBER: US/09/440.302A
; PRIOR FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: 09/053,375
; PRIOR FILING DATE: 1998-03-31
; NUMBER OF SEQ ID NOS: 1193
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1035
; LENGTH: 4416
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 4243
; OTHER INFORMATION: n = A,T,C or G
US-09-440-302A-1035

Query Match 95.2%; Score 3912; DB 18; Length 4416;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3912; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 ccacgcagcagcggcggagatgacggggcgccgctgtgctgcgactgtggctctg 60
QY 61 cctgggactcctggacggcctgtgagtgctgactctcatgaccccccgacctgaacat 120
Db 61 cctgggactcctggacggcctgtgagtgctgactctcatgaccccccgacctgaacat 120
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: APPLICANT: Lukashiev, Matvey
: TITLE OF INVENTION: Hematology/Immunology Array
: FILE REFERENCE: CLON-006CIP15
: CURRENT FILING DATE: US/09/442.384A
: PRIOR FILING DATE: 1999-11-17
: PRIOR APPLICATION NUMBER: 09/053,375
: NUMBER OF SEQ ID NOS: 830
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 447
: LENGTH: 4416
: TYPE: DNA
: ORGANISM: homo sapiens
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: 4243
: OTHER INFORMATION: n = A,T,C or G
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US-09-442-384A-447
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 3912; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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O	y	1501	gcagatgcgttgaaaccccatcgagagcctggacaaccttgacgcaggtttgttgagggaaa	1560
D	b	1501	gcagatgcgttgaaaccccatcgagagcctggacaaccttgacgcaggtttgttgagggaaa	1560
O	y	1561	gaalagaactgtgagcaagctggctgatccagaatgccaaactgtctgccatgacaaagt	1620
D	b	1561	gaalagaactgtgagcaagctggctgatccagaatgccaaactgtctgccatgacaaagt	1620
O	y	1621	tgctgttccacaaggttgggccagatgagcggctcatctactctctatgtgaccacat	1680
D	b	1621	tgctgttccacaaggttgggccagatgagcggctcatctactctctatgtgaccacat	1680
O	y	1681	ccccgcagcgtctcaccatcgaaatccaaagccatccgagagctactagagggccagccgt	1740
D	b	1681	ccccgcagcgtctcaccatcgaaatccaaagccatccgagagctactagagggccagccgt	1740
O	y	1741	gctcctgagctgcgaagccgacagctacaagtcagagacatctgcgctggacgcctcaa	1800
D	b	1741	gctcctgagctgcgaagccgacagctacaagtcagagacatctgcgctggacgcctcaa	1800
O	y	1801	ccgtgccagctgcagatgagcagcggaacccgctctcgtcgaactgcagaacatgtgca	1860
D	b	1801	ccgtgccagctgcagatgagcagcggaacccgctctcgtcgaactgcagaacatgtgca	1860
O	y	1861	tcgtctgcacacccctctggccgcagcctgagagagatgcacctggggcgcccaagc	1920
D	b	1861	tcgtctgcacacccctctggccgcagcctgagagagatgcacctggggcgcccaagc	1920
O	y	1921	cacgctcagcctgagtatcccccgctgcgcccgcagcagcggaagggccacatgtgtgcga	1980
D	b	1921	cacgctcagcctgagtatcccccgctgcgcccgcagcagcggaagggccacatgtgtgcga	1980
O	y	1981	agtgcgaagaccggcgagccatgcagaagcacttgccaaagaatctcctgttcgttgagcgc	2040
D	b	1981	agtgcgaagaccggcgagccatgcagaagcacttgccaaagaatctcctgttcgttgagcgc	2040
O	y	2041	ccttggaagcccttcggtctcacgaacttgaccgaacctctcgtgaactgagcgaactc	2100
D	b	2041	ccttggaagcccttcggtctcacgaacttgaccgaacctctcgtgaactgagcgaactc	2100
O	y	2101	gctggagatgcagtgtctggctggcggaagcgacgcgccagcatctgttggacaaaga	2160
D	b	2101	gctggagatgcagtgtctggctggcggaagcgacgcgccagcatctgttggacaaaga	2160
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RESULT 19

US-08-770-449-31

; Sequence 31, Application US/08770449

; GENERAL INFORMATION:

; APPLICANT: Bennett, Brian D.

; APPLICANT: Goeddel, David

; APPLICANT: Lee, James M.

; APPLICANT: Matthews, William

; APPLICANT: Tsai, Siao Ping

; APPLICANT: Wood, William I.

; TITLE OF INVENTION: PROTEIN TYROSINE KINASE AGONIST ANTIBODIES

; NUMBER OF SEQUENCES: 42

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Genentech, Inc.

; STREET: 460 Point San Bruno Blvd

; CITY: South San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94080

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: WinPatIn (Genentech)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/770,449

; FILING DATE: 20-Dec-1996

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:


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: APPLICATION NUMBER: PCT/US93/00586
: FILING DATE: 22-JAN-1993
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 07/826935
: FILING DATE: 22-JAN-1992
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/222616
: FILING DATE: 04-APR-1994
: ATTORNEY/AGENT INFORMATION:
: NAME: Lee, Wendy M.
: REGISTRATION NUMBER: 40,378
: REFERENCE/DOCKET NUMBER: P0821P2D1
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 415/225-1994
: TELEFAX: 415/952-9881
: TELEX: 910/371-7168
: INFORMATION FOR SEQ ID NO: 31:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 4425 base pairs
: TYPE: Nucleic Acid
: STRANDEDNESS: Single
: TOPOLOGY: Linear
: US-08-770-449-31

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RESULT 22

US-08-446-648-45

; Sequence 45, Application US/08446648

; GENERAL INFORMATION:

; APPLICANT: Genentech, Inc.

; APPLICANT: Bennett, Brian D.

; APPLICANT: Goeddel, David

; APPLICANT: Lee, James M.

; APPLICANT: Matthews, William

; APPLICANT: Tsai, Siao Ping

; APPLICANT: Wood, William I.

; TITLE OF INVENTION: PROTEIN TYROSINE KINASE AGONIST ANTIBODIES

; NUMBER OF SEQUENCES: 45

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Genentech, Inc.

; STREET: 460 Point San Bruno Blvd

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; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,648
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/222616
; FILING DATE: 04-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0821P3PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 45:
; LENGTH: 9108 base pairs
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; US-08-446-648-45
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Query Match 95.2%; Score 3912; DB 8; Length 9108;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 3912; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 24
US-10-081-126-1
; Sequence 1, Application US/10081126
; GENERAL INFORMATION:
; APPLICANT: De Vries, Gerald W.
; TITLE OF INVENTION: Methods of Extending Corneal Graft
; TITLE OF INVENTION: Survival
; FILE REFERENCE: P-AR 4951
; CURRENT APPLICATION NUMBER: US/10/081,126
; CURRENT FILING DATE: 2002-02-22
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 4113
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (22)...(4110)
US-10-081-126-1

Query Match 82.6%; Score 3397; DB 37; Length 4113;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 4097; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

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RESULT 25

PCT-US99-08079-1
; Sequence 1, Application PC/TUS9908079
; GENERAL INFORMATION:
; APPLICANT: Northwest Biotherapeutics, Inc.
; TITLE OF INVENTION: METHODS FOR THE DIAGNOSIS AND TREATMENT OF METASTATIC
; TITLE OF INVENTION: PROSTATE TUMORS
; FILE REFERENCE: 8511-025-228
; CURRENT APPLICATION NUMBER: PCT/US99/08079
; CURRENT FILING DATE: 1999-04-13
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 4450
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (22) .. (3915)
PCT-US99-08079-1

Query Match 77.8% Score 3198; DB 1; Length 4450;

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RESULT 26

US-10-012-214-1
; Sequence 1, Application US/10012214
; GENERAL INFORMATION:
; APPLICANT: Sai L. Su
; TITLE OF INVENTION: METHODS FOR THE DIAGNOSIS AND TREATMENT OF METASTATIC
; TITLE OF INVENTION: PROSTATE TUMORS
; FILE REFERENCE: 20093-001000US
; CURRENT APPLICATION NUMBER: US/10/012,214
; PRIOR FILING DATE: 2001-11-06
; PRIOR APPLICATION NUMBER: PCT/US99/08079
; PRIOR FILING DATE: 1999-04-13
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 4450
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (22)..(3915)
US-10-012-214-1

[illegible]

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RESULT 27

US-60-167-943-103

; Sequence 103, Application US/60167943

; GENERAL INFORMATION:

; APPLICANT: Hodgson, David M.

; APPLICANT: Lincoln, Stephen E.

; APPLICANT: Russo, Frank D.

; APPLICANT: Spito, Peter A.

; APPLICANT: Banville, Steve C.

; APPLICANT: Bratcher, Shawn R.

; APPLICANT: Dufour, Gerard E.

; APPLICANT: Cohen, Howard J.

; APPLICANT: Rosen, Bruce

; APPLICANT: Shah, Purvi

; APPLICANT: Chalup, Michael S.

; APPLICANT: Hillman, Jennifer L.

; TITLE OF INVENTION: RECEPTOR MOLECULES

; FILE REFERENCE: PT-0093 P

; CURRENT APPLICATION NUMBER: US/60/167,943

; CURRENT FILING DATE: 1999-11-29

; NUMBER OF SEQ. ID NOS: 244

; SOFTWARE: PERL Program

; SEQ. ID NO 103

Jones, Anissa L.

Yu, Jimmy Y.

Greenawalt, Lila B.

Panzer, Scott R.

Roseberry, Ann M.

Wright, Rachel J.

Chen, Wensheng

Liu, Tommy

Yap, Pierre E.

Amshey, Stefan

Fong, Willy Tuen


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: LENGTH: 4461
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc_feature
: OTHER INFORMATION: Incyte ID No: 902563.1
: FEATURE:
: NAME/KEY: unsure
: LOCATION: 2402-2421
: OTHER INFORMATION: a, t, c, g, or other
US-60-167-943-103

Query Match      66.2%; Score 2721; DB 55; Length 4461;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 3891; Conservative 0; Mismatches 21; Indels 1; Gaps 1;

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QY 61 cctgggactcctgacggcctgtgagtgcgtactcatgaacccccgcgaccttgaaat 120
Db 72 cctgggactcctgacggcctgtgagtgcgtactcatgaacccccgcgaccttgaaat 131

QY 121 caccggaggatcacagctatcgacaccggtgacagcctgtccatctcctgcaggggaca 180
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Db 192 gcacccccctcagtggtggtccaggagctcaggaggcccgccaccggagacaagga 251

QY 241 cagcggagacacggggtggtgcgaactgcagaggacacagacgcaggccctactgcga 300
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QY 361 gtacataaaggcagcatcagaggaccacgcgcgcagctcctactcgttgagaga 420
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: FILE REFERENCE: GX-0019-1 P
: CURRENT APPLICATION NUMBER: US/60/324,185
: CURRENT FILING DATE: 2001-09-21
: NUMBER OF SEQ ID NOS: 35862
: SOFTWARE: PERL Program
: SEQ ID NO 4274
: LENGTH: 4459
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc_feature
: OTHER INFORMATION: Incyte ID No: 1082992.1
: NAME/KEY: unsure
: LOCATION: 2402-2421
: OTHER INFORMATION: a, t, c, g, or other
: US-60-324-185-4274

Query Match	62.6%	Score 2573	DB 71	Length 4459
Best Local Similarity	99.4%	Pred. No. 0		
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Qy 278 acagacgcccagggccctactcgaagggtgtgtctgtcgacagaggtacatgccaaacgacaca	337			
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Db 1189 aaggaggtgacagagggccagcagcactacacccctcgccctgtggaaactccctgct	1248
Qy 1238 ggcctgagggcgaacatcagcctggagctggtgtgaaatgtgccccccagatacatgag	1297
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Qy 1298 aaggagggcctctcccagcaactctactcgcgtcacagcggcagggccctcaccctgcag	1357
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Qy 1358 gctacgggggtgcccctgctctcagcatccagtggtggtggtggcctggacacccctgc	1417
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Qy 1958 cacgagggccactgtgtgcgaagtgcgaagccgagcagcctgacaaagcactgcca	2017
Db 1969 cacgagggccactgtgtgcgaagtgcgaagccgagcagcctgacaaagcactgcca	2028
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OY 2258 ctgtgcagcgttgtaaacgccaaaggcctgctcaactctcccgccagcgtggccctggaaa 2317
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DB 2329 ggtccgaagataaaggcagcagtgagatcgtgataccttctgctgacggcgctatcgct 2388
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DB 2389 gtctctctctggnn 2448
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DB 2449 gacataaagacgggtacactgtccatcatcatatggaccccggggagtgctctctggaggag 2508
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DB 2509 caatgcgaatacctctctacatgccagcagtgaggatcccccggagagcggtgcac 2568
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DB 2629 atcccaaaaggcagcagctgtgacacccctggccgtgaaaatgctgaaaagagggcgccacgc 2688
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OY 2678 gccagcgagcacgcgcgctgctgagctcagagctcaagatccctcatcaccatcggaaccac 2737
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DB 2689 gccagcgagcacgcgcgctgctgagctcagagctcaagatccctcatcaccatcggaaccac 2748
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OY 2738 ctcaacgttggtcaaacctctcctggcgctgacaaagccgacgggccctctcatggtgac 2797
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DB 2749 ctcaacgttggtcaaacctctcctggcgctgacaaagccgacgggccctctcatggtgac 2808
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DB 2809 tggaggtctgcaagtagcgaacacctctccaaactcctgcgcccaagcggaagccttc 2868
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DB 2869 agccctctcgcgagagaagctctcccgagcagcgcgacgcttccgcgccatggtggagctc 2928
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OY 2918 gccaggtcggatcgagcgccggggagcagcgacagggtctcttcgcgcggttctcg 2977
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DB 2929 gccaggtcggatcgagcgccggggagcagcgacagggtctcttcgcgcggttctcg 2988
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DB 2989 aagaccggggcgagcagcgagcgggcctctccagaccagaagctgaggaacctgtggtcg 3048
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DB 3169 gaaagcgacgtggtgaaagatctgtgacttbgccttgcccgggagacatctacaaagacctc 3228
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OY 3218 gactacgtcccgcaaggcgagtgcccggtgccccctgaagtggatggccccctgaaagcactc 3277
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DB 3229 gactacgtcccgcaaggcgagtgcccggtgccccctgaagtggatggccccctgaaagcactc 3288
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OY 3278 ttcaacaagggtgtacaccacacagagtgacgtggttctcttgggtgcttctctctggag 3337
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DB 3289 ttcaacaagggtgtacaccacacagagtgacgtggttctcttgggtgcttctctctggag 3348
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OY 3338 atcttctctctgggggctcccccgtacccctgggtgcagatcaaatgagagagttcttgccag 3397
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DB 3349 atcttctctctgggggctcccccgtacccctgggtgcagatcaaatgagagagttcttgccag 3408
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DB 3409 cggctgagagcggccaaagatgaggcccccgagctggccactcccgccatcacgcgcgc 3468
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DB 3529 gagatctctgggggacctgctccaggcgagggtcctgcaaggaggaaggaggtctgcatg 3588
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DB 3589 gccccgcgacgtctcagagctcagaagagagggcagcttctcgagggtgtccaccatggcc 3648
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OY 3638 ctacacatcgcccgaggtgacgctgagacagcccgccaaagccttgacgcccacagcctg 3697
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DB 3649 ctacacatcgcccgaggtgacgctgagagacagcccgccaaagccttgacgcccacagcctg 3708
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OY 3698 gccccaggtattacaactgggttctcttcccggtgcttggccagaggggctgagacc 3757
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DB 3709 gccgcaagttatacaactgggtgctcttctcccggtgcttggccagaggggctgagacc 3768
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DB 3829 ggcctgtgggaacaccagacagacagtggtggtgcttggcctcgaggaggtttgagcag 3888
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RESULT 29

US-60-172-373-15763
; Sequence 15763, Application US/60172373
; GENERAL INFORMATION:

; APPLICANT: Morris, MacDonald
; APPLICANT: Lal, Preeti
; APPLICANT: Diep, Dinh
; TITLE OF INVENTION: Method for the Identification of Sequence Polymorphisms Using
; FILE REFERENCE: GX-0006 P
; CURRENT APPLICATION NUMBER: US/60/172,373
; CURRENT FILING DATE: 1999-12-16
; NUMBER OF SEQ ID NOS: 25,772
; SOFTWARE: PERL Program
; SEQ ID NO 15763
; LENGTH: 4462
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: 902563.2

US-60-172-373-15763
; Sequence 15763, Application US/60172373
; GENERAL INFORMATION:

; APPLICANT: Morris, MacDonald
; APPLICANT: Lal, Preeti
; APPLICANT: Diep, Dinh
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; CURRENT APPLICATION NUMBER: US/60/172,373
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; NUMBER OF SEQ ID NOS: 25,772
; SOFTWARE: PERL Program
; SEQ ID NO 15763
; LENGTH: 4462
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: 902563.2

; FEATURE:									
; NAME/KEY: unsure									
; LOCATION: 2402-2421, 2907, 3602									
; OTHER INFORMATION: a, t, c, g, or other									
US-60-172-373-15763									
Query Match 58.1%; Score 2390; DB 56; Length 4462;									
Best Local Similarity 100.0%; Pred. No. 0;									
Matches 2390; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
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Db	12	ccacgcgcagcggccggaagatgcagcggggcgccgcgtgctgcgtgcgactgtggtctcg	71						
QY	61	ctcggaactcttgagcggcctggtgagtggtctactccatgacccccccacaccttgaaat	120						
Db	72	ctcggaactcttgagcggcctggtgagtggtctactccatgacccccccacaccttgaaat	131						
QY	121	cacggaggagtacacgtctacacccggtgacagcctgtccatctctgcaggggaca	180						
Db	132	cacggaggagtacacgtctacacccggtgacagcctgtccatctctgcaggggaca	191						
QY	181	gaacccccctgagtggttggccagagctcaaggaggccacccacccggagacaaga	240						
Db	192	gaacccccctgagtggttggccagagctcaaggaggccacccacccggagacaaga	251						
QY	241	cagcgaggacacgggggtggtgcgagactgcgagggcacagacgcgcagccctactgc	300						
Db	252	cagcgaggacacgggggtggtgcgagactgcgagggcacagacgcgcagccctactgc	311						
QY	301	gggtgtgctgctgcagaggtacatgccaacgacacaggcagctactgctgctactaca	360						
Db	312	gggtgtgctgctgcagaggtacatgccaacgacacaggcagctactgctgctactaca	371						
QY	361	gtacatcaaggcacgcacgcagggcaccacgcgcgcagctcaactcaactgttcgtgaga	420						
Db	372	gtacatcaaggcacgcacgcagggcaccacgcgcgcagctcaactcaactgttcgtgaga	431						
QY	421	ctttgagcagccattcatcaacaagcctgacacgcctcttggtcaacaggaagacgccat	480						
Db	432	ctttgagcagccattcatcaacaagcctgacacgcctcttggtcaacaggaagacgccat	491						
QY	481	gtgggtgacctgtcgtggttccatccccggcctcaatgtcaagctgcgtgcgtcgaagctc	540						
Db	492	gtgggtgacctgtcgtggttccatccccggcctcaatgtcaagctgcgtgcgtcgaagctc	551						
QY	541	ggtgctgtgagccagcggcgagaggtggtgtgggatgaccggcggggcgtgctcgtgtc	600						
Db	552	ggtgctgtgagccagcggcgagaggtggtgtgggatgaccggcggggcgtgctcgtgtc	611						
QY	601	cacgcactgtgcacgatgccctgtacctgcagtcgcagacacacctggggagaccagga	660						
Db	612	cacgcactgtgcacgatgccctgtacctgcagtcgcagacacacctggggagaccagga	671						
QY	661	cttcctttccaaacccctctcgtgtgcacatcacaggcaacgactctatgaatccagct	720						
Db	672	cttcctttccaaacccctctcgtgtgcacatcacaggcaacgactctatgaatccagct	731						
QY	721	gttgccacgaagctcgtgagctgctggttaggggagagctggttcttgaactgcacct	780						
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QY	781	gtggctgagtttaactcagggtgtaacctttgactgggactaccagggaaagcaggcaga	840						
Db	792	gtggctgagtttaactcagggtgtaacctttgactgggactaccagggaaagcaggcaga	851						
QY	841	gcggggttaagtgggtgccgagcagcgtcccgagacacccacacagaactctcagcat	900						
Db	852	gcggggttaagtgggtgccgagcagcgtcccgagacacccacacagaactctcagcat	911						
QY	901	ctcgacatcccaacgctcagcagcagcagcctgggctcgtatgtgtcgaaggccaaca	960						
Db	992	agtgcgaagaccggcgagcccatgacaagcactgcacaagaagtacctgtcgtgtgcaagg	2051						

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QY	1561	gaataagactgtgacaagctggtgatccagaatgccaaactgctctgcatagtacaagt	1620						
Db	1572	gaataagactgtgacaagctggtgatccagaatgccaaactgctctgcatagtacaagt	1631						
QY	1621	tgtgtctccaaacaggtggcgccagatgagcggctcctactctactctgtgaccacat	1680						
Db	1632	tgtgtctccaaacaggtggcgccagatgagcggctcctactctactctgtgaccacat	1691						
QY	1681	ccccgacggcttcaccatcgaaatccaaagcctccgagagctactagagggcgccagcgg	1740						
Db	1692	ccccgacggcttcaccatcgaaatccaaagcctccgagagctactagagggcgccagcgg	1751						
QY	1741	gctcctgagctgcgaagcgcgacagctacaagtacagacatctgcgctggtaccgctcaa	1800						
Db	1752	gctcctgagctgcgaagcgcgacagctacaagtacagacatctgcgctggtaccgctcaa	1811						
QY	1801	ctgttccacgctgcacgatgcgcacggaaacccgctctgtctcgactcaagaacgtgca	1860						
Db	1812	ctgttccacgctgcacgatgcgcacggaaacccgctctgtctcgactcaagaacgtgca	1871						
QY	1861	tctgttccacccctctgcccgcagcctggagaggtggcacctggggcgccgacgc	1920						
Db	1872	tctgttccacccctctgcccgcagcctggagaggtggcacctggggcgccgacgc	1931						
QY	1921	cacgctcagctgagatcccccccgctgcgcccgcagcagcagggggccactatgtgtgcga	1980						
Db	1932	cacgctcagctgagatcccccccgctgcgcccgcagcagcagggggccactatgtgtgcga	1991						
QY	1981	agtgcgaagaccggcgagccatgacaagcactgccacaagaagtacctgtcgggtgcaggc	2040						
Db	1992	agtgcgaagaccggcgagccatgacaagcactgccacaagaagtacctgtcgggtgcaggc	2051						

Db	1381	aaagcggttcacgtgtaaaaggacctggccagaatgtggctgtgacaggcgacacctg	1440
Qy	3860	actcccaaggagcgcgccgctgagcgggggcccgagagggcccgagagccaggtgtttaca	4019
Db	1441	actcccaaggagcgcgccgctgagcgggggcccgagagccaggtgtttaca	1500
Qy	4020	acagcgagtagtgggagctgtcggagccaaagcgagaggagaccactgctccccgtgccc	4079
Db	1501	acagcgagtagtgggagctgtcggagccaaagcgagaggagaccactgctccccgtgccc	1560
Qy	4080	gcgtgactttcttcacagacaacagctactaa	4111
Db	1561	gcgtgactttcttcacagacaacagctactaa	1592
RESULT 31			
US-60-213-360-951			
: Sequence 951, Application US/60213360			
: GENERAL INFORMATION:			
: APPLICANT: Morris, MacDonald			
: APPLICANT: Lal, Preeti			
: APPLICANT: Diep, Dinh			
: TITLE OF INVENTION: Method for the Identification of Sequence Polymorphisms Using			
: TITLE OF INVENTION: Polynucleotide Sequence Databases, and Single Nucleotide Polymor			
: FILE REFERENCE: GX-0014 P			
: CURRENT APPLICATION NUMBER: US/60/213,360			
: CURRENT FILING DATE: 2000-06-21			
: NUMBER OF SEQ ID NOS: 8347			
: SOFTWARE: PERL Program			
: SEQ ID NO 951			
: LENGTH: 3277			
: TYPE: DNA			
: ORGANISM: Homo sapiens			
: FEATURE:			
: NAME/KEY: misc_feature			
: OTHER INFORMATION: lncyte ID No: 1084493.6			
US-60-213-360-951			
Query Match 30.4%; Score 1248; DB 60; Length 3277;			
Best Local Similarity 99.7%; Pred. No. 0;			
Matches 1588; Conservative 0; Mismatches 2; Indels 2; Gaps 2;			
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Db	1	gccagccagtgggaattccccgagagcgctgcacctggaggagagtgctcggtctacggc	60
Qy	2582	gccttcgggaaggtggtggaagcctccgcttccgcatccacaaggcgagcgagctgtgac	2641
Db	61	gccttcgggaaggtggtggaagcctccgcttccgcatccacaaggcgagcgagctgtgac	120
Qy	2642	accgtgcccgtgaaatgctgaaagagcgccacggccagcgagcaocgcgcgtgatg	2701
Db	121	accgtgcccgtgaaatgctgaaagagcgccacggccagcgagcgagcgcgctgatg	180
Qy	2702	tcggagctcaagatcctcattcacatcgcaaccacctcaacgtggtcaacctctcggg	2761
Db	181	tcggagctcaagatcctcattcacatcgcaaccacctcaacgtggtcaacctctcggg	240
Qy	2762	gcgtgcaccaagcccgagggcccccct-catggtgatcgtggagttctcgaatcagcgcaa	2820
Db	241	gcgtgcaccaagcccgagggcccccctgcattggtgatcgtggagttctcgaatcagcgcaa	300
Qy	2821	cctctccaaactcctgcgcgcgaacgcggga-cgccttcagccccctgcgcggaagagtc	2879
Db	301	cctctccaaactcctgcgcgcgaacgcgggaacgccttcagccccctgcgcggaagagtc	360
Qy	2880	ccgagcagcgagcagctcccgccatggtgagctcgcaggtcgatcggaagcgcc	2939
Db	361	ccgagcagcgagcagctcccgccatggtgagctcgcaggtcgatcggaagcgcc	420
Qy	2940	cggggagcagcagacagggttcctcttcgcgcggttcttcgaagaccgagggcgagcgaggc	2999

Db	421	cggggagcagcgacagggtccctcttcgcgcggttctcgaagaccgagggcgagcgagcg	480
Qy	3000	gggcttctccacagacaagaagctgaggacctgtgctgagccccgctgaccttggaagatc	3059
Db	481	gggcttctccacagacaagaagctgaggacctgtgctgagccccgctgaccttggaagatc	540
Qy	3060	tigtctgtcacagcttccaggctggccagagggatggagttccttggcttctccgaaagtga	3119
Db	541	tigtctgtcacagcttccaggctggccagagggatggagttccttggcttctccgaaagtga	600
Qy	3120	tcacagagacctggtgctcggaaattctctgtcggaaagcgacgtgggtgaagatct	3179
Db	601	tcacagagacctggtgctcggaaattctctgtcggaaagcgacgtgggtgaagatct	660
Qy	3180	gtgactttggccttggccgggacatctacaaagaccctgacctacgtccgcaaggcgagtg	3239
Db	661	gtgactttggccttggccgggacatctacaaagaccctgacctacgtccgcaaggcgagtg	720
Qy	3240	cccggctgcccctgaagtggatggccccctgaaagcatcttcgacaagggtgtacacacgc	3299
Db	721	cccggctgcccctgaagtggatggccccctgaaagcatcttcgacaagggtgtacacacgc	780
Qy	3300	agagtgaagtggtgctcttgggggtgcttctctctggagatcttctctctgggggctccc	3359
Db	781	agagtgaagtggtgctcttgggggtgcttctctctggagatcttctctctgggggctccc	840
Qy	3360	cgtacccctgggtgcagatcaatgagagttctgccagcgctgagagcgacgcaaaaga	3419
Db	841	cgtacccctgggtgcagatcaatgagagttctgccagcgctgagagcgacgcaaaaga	900
Qy	3420	tgaggggcccgagctggccactcccgccatcacgcccgcacatcatgctgaactgctggtccg	3479
Db	901	tgaggggcccgagctggccactcccgccatcacgcccgcacatcatgctgaactgctggtccg	960
Qy	3480	gagaccccaaggcgagacctgcattctcggagctggtggagatcctctgggggacctgcctc	3539
Db	961	gagaccccaaggcgagacctgcattctcggagctggtggagatcctctctgggggacctgcctc	1020
Qy	3540	agggcaggggcgctgcaagaggaaggaggtctgcatggcccccgcgagcctctcagagct	3599
Db	1021	agggcaggggcgctgcaagaggaaggaggtctgcatggcccccgcgagcctctcagagct	1080
Qy	3600	cagaagagggcagcttctcgaggtgtccacatggccctacacatcgccccaggtgacg	3659
Db	1081	cagaagagggcagcttctcgaggtgtccacatggccctacacatcgccccaggtgacg	1140
Qy	3660	ctgagagcagcccgcacagcctgcagcgccacagcctggcccgccaggtattacaactggg	3719
Db	1141	ctgagagcagcccgcacagcctgcagcgccacagcctggcccgccaggtattacaactggg	1200
Qy	3720	tgctcttcccgggtgctggccagaggggtgagacccgtgggttctctccaggaatgaaga	3779
Db	1201	tgctcttcccgggtgctggccagaggggtgagacccgtgggttctctccaggaatgaaga	1260
Qy	3780	catttgaggaattccccatgaccaccaacgcactacaaaggctctgtggacaaccagacag	3839
Db	1261	catttgaggaattccccatgaccaccaacgcactacaaaggctctgtggacaaccagacag	1320
Qy	3840	acagtggagatggtgctggcctcgagaggtttgagcagatagagagcaggtatagacaag	3899
Db	1321	acagtggagatggtgctggcctcgagaggtttgagcagatagagagcaggtatagacaag	1380
Qy	3900	aaagcgggttcagctgtaaaaggacctggccagaatgtggctgtgacaggggcacacctg	3959
Db	1381	aaagcgggttcagctgtaaaaggacctggccagaatgtggctgtgacaggggcacacctg	1440
Qy	3960	actcccaaggagggcgcgccgctgagcggggggcccgaggaggccaggtgtttaca	4019
Db	1441	actcccaaggagggcgcgcgccgctgagcggggggcccgaggaggccaggtgtttaca	1500
Qy	4020	acagcgagtagtgggagctgcggagccaagcgagggagggaccactgctccccctctccc	4079

1
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; FILING DATE: US/08/446, 648
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/222616
; FILING DATE: 04-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0821P3PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6827 base pairs
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; US-08-446-648-17

Query Match 23.1%; Score 950; DB 8; Length 6827;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1000; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2869 ggagaaagtctccagacgagcgagcgtctccgaccattggtgagctccagagctgga 2928
DB 2924 GGAGAAGTCTCCGACACGCGGGACCTTCCGCGCATGGTGGAGCTGCCAGGCTGGA 2865
QY 2929 tcggagggcgccgggagcagcagaggggtcctctcttcgcccgggtctctcgaagaccgaggg 2988
DB 2864 TCGGAGCGCGCGGGAGCAGGACAGAGGTCTCTTCCGCGCGGTCTCTCGAAGACCCGAGGG 2805
QY 2989 cggagcgagcgggctctccagaccagaaagactgagagactgtggctgagcccgctgac 3048
DB 2804 CGGAGCGAGCGGGCTTCTCCAGACCAGAGCTGAGGACCTTGGCTGAGCCCGCTGAC 2745
QY 3049 catggaagattctgtctgtatagcttcnaggtggccagagggatggagttcctggtcttc 3108
DB 2744 CATGGAAGATCTTGTCTGCTACAGCTTCCAGCTTCCAGCTGGCCAGAGGGATGCGAGTCTCTGCTTC 2685
QY 3109 ccgaaagtcatccacagagacactggctgtcctcggaacattctgtctcggaaagcgactg 3168
DB 2684 CCGAAAGTGCATCCACAGAGACCTGGCTGCTCGGAACATTTCTGTCGGAAGGCGACGT 2625
QY 3169 ggtgaagatctgtgactttggccttggccgggagacatctacaagaccctgactacgtccg 3228
DB 2624 GGTGAAGATCTGTGACTTTGGCTTTGCCCGGACATCTACAAGACCCCGACTACGTCCG 2565
QY 3229 caagggcagtcgccggctccctgaagtggatggccccctgaaagcatcttcgcacaaggt 3288
DB 2564 CAAGGCGAGTGCCTGCCCTCAAGTGGATGGCCCTGAAAGCATCTTCGACAAGGT 2505
QY 3289 gtacaccacgagatgacgtgtgtctttgggtgtctctctctctctctctctctctctct 3348
DB 2504 GTACACACGCGAGGTGACGTGTGGTGTCTTTCGGGTGCTTCTCTGGAGATCTTCTCTCT 2445
QY 3349 gggggcctcccgtaacctggggtgcaataatgagagttcttcgagcggtgagaga 3408
DB 2444 GGGGGCTCTCCCGTACCTTGGGGTGCATATCAATGAGGAGTTCTCCGACGGCTGAGAGA 2385
QY 3409 cggcacaaggatgagggcccgagctggccactcccgccatcccgccatcatctgaa 3468
DB 2384 CGGCAAGGATGAGGGCCCGGAGCTGGCCACTCCCGCCATACGCCGCATCATGCTCAA 2325
QY 3469 ctgctggtccggagagaccccaaggcgagacacctgcatctctcggagctggtggagatcctggg 3528

DB 2324 CTGCTGGTCCGGAGACCCCAAGCGGAGACTTGCATTCTCGGAGCTGGTGGAGATCCTGGG 2265
QY 3529 ggaactgtctccagggcaggggctcagaagagaagagaggtctcagatggcccgccgag 3588
DB 2264 GGACCTGTCTCCAGGCGAGGGGCTTCAAGAGGAAGAGGAGGTCTGCATGGGCCCCCGGAG 2205
QY 3589 ctctcagagctcagaagaggggagcttctcgcaggtgtctccaccatggccctacacatcgc 3648
DB 2204 CTCTCAGAGCTCAGAAAGAGGGGAGCTTCTCGCAGGTGTCCACCATGGCCCTACACATCGC 2145
QY 3649 ccaggtgacgtgagagcagagcccgcccaagcctgagcgccacagcctggccgcccaggtla 3708
DB 2144 CCAGGCTGACGCTGAGGACAGCCCGCCCAAGCCTGCGAGGCCACAGCTTGGCCCGCAGGTA 2085
QY 3709 ttacaactgggtgtctcttcccggtgctggtggtggtggtggtggtggtggtggtggtggt 3768
DB 2084 TTACAACCTGGGTGTCTTTTCCCGGGTGCTTGGCCAGAGGGGTGAGACCCGTGGTTCCTC 2025
QY 3769 caggatgaagacatttgaggaattcccccatgacccccacacacacacacacacacacacac 3828
DB 2024 CAGGATGAAGACATTTGAGGAATTTCCCATGACCCCAACAGACTACAAAGGCTCTCTGGA 1965
QY 3829 caaccagacagacagtggatggtgctggtggtggtggtggtggtggtggtggtggtggtggt 3869
DB 1964 CAACCAGACAGACAGTGGATGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1924

RESULT 35
US-08-770-449-17/c
; Sequence 17, Application US/08770449
; GENERAL INFORMATION:
; APPLICANT: Bennett, Brian D.
; APPLICANT: Goeddel, David
; APPLICANT: Lee, James M.
; APPLICANT: Matthews, William
; APPLICANT: Tsai, Siao Ping
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: PROTEIN TYROSINE KINASE AGONIST ANTIBODIES
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/770.449
; FILING DATE: 20-Dec-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/00586
; FILING DATE: 22-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/826935
; FILING DATE: 22-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/222616
; FILING DATE: 04-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0821P2D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168

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: INFORMATION FOR SEQ ID NO: 17:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 6827 base pairs
: TYPE: Nucleic Acid
: STRANDEDNESS: Single
: TOPOLOGY: Linear
: US-08-770-449-17

Query Match      23.1%; Score 950; DB 11; Length 6827;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1000; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2869 ggagaagctcccgagacagcagcagcgttccgcgccatggtgagagctcgccaggtgga 2928
Db 2924 GGAGAAGTCTCCCGAGCAGCGCGAGCGCTTCCGCGCCATGGTGGAGCTCGCCAGGCTGA 2865

Qy 2929 tcggagggccggggagcagcagcaggggtccctcttcgcgcggtttctcgaagaccgagg 2988
Db 2864 TCGAGGCGCGCGGGAGCAGCAGCAGGCTCTTCCGCGCGTCTTCGAGACCCAGGG 2805

Qy 2989 cggagcgagcgggctctccagaccagaaagctgaggacctgtggtgagcccgctgac 3048
Db 2804 CGGAGCGAGCGGGCTCTCCAGACCAGAGCTGAGGACCTGTGGCTGAGCCCGCTGAC 2745

Qy 3049 catggaagatctgtctgtacagcttcaggtgcccagaggaatgagttcctggtctc 3108
Db 2744 CATGGAAGATCTTGTCTGTCTACAGCTTCCAGGTGGCCAGAGGATGGATTCCTGGCTTC 2685

Qy 3109 ccgaaagtgcaccagagacctggtctcgcggaacattctgtctcgaaagcagcgt 3168
Db 2684 CCGAAAGTGCATCCACAGAGACCTGGCTGCTCGGAACATTTCTGCTCGGAAGCGACGT 2625

Qy 3169 ggtgaagatctgtactttgaccttccgcgggacatctcacaagaccctgactacgtccg 3228
Db 2624 GTGGAAGATCTGTGACTTTGGCTTTCGCCGGGACATCTCAAAGACCCCGACTACGTCCG 2565

Qy 3229 caagggcagtgcccggtcgccctgaagtggatggatggccctgaagcatcttcgaagat 3288
Db 2564 CAAGGCGAGTGCCCGCTGCCCTGAAGTGGATGGCGCCCTGAAAGCATCTTCGACAAAGT 2505

Qy 3289 gtacacacgacagagtacgtgtggttcctttgggtgtctctcttggagatctctctct 3348
Db 2504 GTACACACGACAGTAGCTGTGTGTCTTGGGTGCTTCTCTGGAGATCTTCTCTCT 2445

Qy 3349 gggggcctcccgatccctggggtgcagatcaatgagagatctcgccagcgtctgagaga 3408
Db 2444 GGGGGCTCCCCGTACCCGTGGGTGCAGATCAATGAGAGATTCTGCGACGCGCTGAGAGA 2385

Qy 3409 cggcacaaggatgagggcccgagctggccactccgcacatacgcgcgcacatcatgctgaa 3468
Db 2384 CGGCACAAGGATCAGGGCCCGGAGCTGGCCACTCCCCGCCATACGCCGATCATGCTGAA 2325

Qy 3469 ctgctggtccggagaccacaaaggcagacactgcattctcggagctggtgagatcctggg 3528
Db 2324 CTGCTGCTCCGGAGACCCCAAGCGGAGACTGCAATCTCGAGCTGCTGGAGATCCTGGG 2265

Qy 3529 ggacctctccagggcagggcctcgaagaggaagagaggtctgcatggcccccgag 3588
Db 2264 GGACCTGCTCCAGGCGAGGGGCTGCAAGAGAAAGAGAGGAGTCTGCATGGCCCCCGGAG 2205

Qy 3589 ctctcagagctcagaagaggcagctctctcgaggtgtccacattggccctacacatcgc 3648
Db 2204 CTCTCAGAGCTCAGAAGAGGGCAGCTTCTCGCAGGTGTCCACCATGGCCCTACACATCGC 2145

Qy 3649 ccagctgacgctgagacagcccgccaaagcctgcagcgccacagcctgcccaggtga 3708
Db 2144 CCAGGCTGACGCTGAGGAGAGCCCGCCAAAGCTTGAGCGGCCACAGCCCTGGCCGCGAGGTA 2085

Qy 3709 ttacaactgggtgtctctttcccggtgtgcttggccagaggggctgagaccgtggttcctc 3768
Db 2084 TTACAACCTGGGTGTCTTTTCCCGGGTGCCTTGCCACAGAGGGGCTGAGACCCGGTTCCTC 2025
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Qy 3769 caggatgaagacatttgaggaattccccatgaccaccaagcactacaaaggctctgtgga 3828
Db 2024 CAGGATGAAGACATTTGAGGAATTTCCCATGACCCCAAGCAGCTACAAAGGCTCTGTGGA 1965

Qy 3829 caaccagacagacagtggtgctggtcctcgagggagt 3869
Db 1964 CAACCAGACAGACAGTGGGATGGTGTGCTGCGCTCGGAGGAGT 1924

RESULT 36
US-09-982-610-17/c
: Sequence 17, Application US/09982610
: GENERAL INFORMATION:
: APPLICANT: Genentech, Inc.
: Bennett, Brian D.
: Goeddel, David
: Lee, James M.
: Matthews, William
: Tsai, Siao Ping
: Wood, William I.
: TITLE OF INVENTION: PROTEIN TYROSINE KINASE AGONIST ANTIBODIES
: NUMBER OF SEQUENCES: 45
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Genentech, Inc.
: STREET: 460 Point San Bruno Blvd
: CITY: South San Francisco
: STATE: California
: COUNTRY: USA
: ZIP: 94080
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: WinPatIn (Genentech)
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/982,610
: FILING DATE: 17-Oct-2001
: CLASSIFICATION: <Unknown>
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/446,648
: FILING DATE: 1996-MAY-23
: APPLICATION NUMBER: 08/222616
: FILING DATE: 04-APR-1994
: ATTORNEY/AGENT INFORMATION:
: NAME: Lee, Wendy M.
: REGISTRATION NUMBER: 40,378
: REFERENCE/DOCKET NUMBER: P0821P3PCT
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 415/225-1994
: TELEFAX: 415/952-9881
: TELEX: 910/371-7168
: INFORMATION FOR SEQ ID NO: 17:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 6827 base pairs
: TYPE: Nucleic Acid
: STRANDEDNESS: Single
: TOPOLOGY: Linear
: SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-09-982-610-17

Query Match      23.1%; Score 950; DB 36; Length 6827;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1000; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2869 ggagaagctcccgagcagcagcagcgttccgcgccatggtgagagctcgccaggtgga 2928
Db 2924 GGAGAAGTCTCCCGAGCAGCGCGAGCCTTCCGCGCCATGGTGGAGCTCGCCAGGCTGA 2865

Qy 2929 tcggagcgcgccggggagcagcagcaggggtccctcttcgcgcggtttctcgaagaccgagg 2988
Db 2864 TCGAGGCGCGCGGGAGCAGCAGCAGGCTCTTCCGCGCGTCTTCGAGACCCAGGG 2805

Qy 2989 cggagcgagcgggctctccagaccagaaagctgaggacctgtggtgagcccgctgac 3048
Db 2804 CGGAGCGAGCGGGCTCTCCAGACCAGAGCTGAGGACCTGTGGCTGAGCCCGCTGAC 2745

Qy 3049 catggaagatctgtctgtacagcttcaggtgcccagaggaatgagttcctggtctc 3108
Db 2744 CATGGAAGATCTTGTCTGTCTACAGCTTCCAGGTGGCCAGAGGATGGATTCCTGGCTTC 2685

Qy 3109 ccgaaagtgcaccagagacctggtctcgcggaacattctgtctcgaaagcagcgt 3168
Db 2684 CCGAAAGTGCATCCACAGAGACCTGGCTGCTCGGAACATTTCTGCTCGGAAGCGACGT 2625

Qy 3169 ggtgaagatctgtactttgaccttccgcgggacatctcacaagaccctgactacgtccg 3228
Db 2624 GTGGAAGATCTGTGACTTTGGCTTTCGCCGGGACATCTCAAAGACCCCGACTACGTCCG 2565

Qy 3229 caagggcagtgcccggtcgccctgaagtggatggatggccctgaagcatcttcgaagat 3288
Db 2564 CAAGGCGAGTGCCCGCTGCCCTGAAGTGGATGGCGCCCTGAAAGCATCTTCGACAAAGT 2505

Qy 3289 gtacacacgacagagtacgtgtggttcctttgggtgtctctcttggagatctctctct 3348
Db 2504 GTACACACGACAGTAGCTGTGTGTCTTGGGTGCTTCTCTGGAGATCTTCTCTCT 2445

Qy 3349 gggggcctcccgatccctggggtgcagatcaatgagagatctcgccagcgtctgagaga 3408
Db 2444 GGGGGCTCCCCGTACCCGTGGGTGCAGATCAATGAGAGATTCTGCGACGCGCTGAGAGA 2385

Qy 3409 cggcacaaggatgagggcccgagctggccactccgcacatacgcgcgcacatcatgctgaa 3468
Db 2384 CGGCACAAGGATCAGGGCCCGGAGCTGGCCACTCCCCGCCATACGCCGATCATGCTGAA 2325

Qy 3469 ctgctggtccggagaccacaaaggcagacactgcattctcggagctggtgagatcctggg 3528
Db 2324 CTGCTGCTCCGGAGACCCCAAGCGGAGACTGCAATCTCGAGCTGCTGGAGATCCTGGG 2265

Qy 3529 ggacctctccagggcagggcctcgaagaggaagagaggtctgcatggcccccgag 3588
Db 2264 GGACCTGCTCCAGGCGAGGGGCTGCAAGAGAAAGAGAGGAGTCTGCATGGCCCCCGGAG 2205

Qy 3589 ctctcagagctcagaagaggcagctctctcgaggtgtccacattggccctacacatcgc 3648
Db 2204 CTCTCAGAGCTCAGAAGAGGGCAGCTTCTCGCAGGTGTCCACCATGGCCCTACACATCGC 2145

Qy 3649 ccagctgacgctgagacagcccgccaaagcctgcagcgccacagcctgcccaggtga 3708
Db 2144 CCAGGCTGACGCTGAGGAGAGCCCGCCAAAGCTTGAGCGGCCACAGCCCTGGCCGCGAGGTA 2085

Qy 3709 ttacaactgggtgtctctttcccggtgtgcttggccagaggggctgagaccgtggttcctc 3768
Db 2084 TTACAACCTGGGTGTCTTTTCCCGGGTGCCTTGCCACAGAGGGGCTGAGACCCGGTTCCTC 2025
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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 55
; LENGTH: 575
; TYPE: DNA
; ORGANISM: HUMAN
US-60-213-847-55

Query Match      10.7%; Score 440; DB 60; Length 575;
Best Local Similarity 100.0%; Pred. No. 5e-199;
Matches 440; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2989 cggagcagcgggcttctccagaccagaagaagctgagacctgtgctgagcccgctaac 3048
      |||||||
DB 2804 CGGAGCGAGCGGGCTTCTCCAGACCAAGAAAGCTGAGGACCTGTGGCTGAGCCCGCTGAC 2745

QY 3049 catggaagatctgtgtctacagcttccaggtggtccagagggatggagttcctggtctc 3108
      |||||||
DB 2744 CATGGAAGATCTTGTCTGTCTACAGCTTCCAGGTGGCCAGAGGGATGGAGTTCTCGCTTC 2685

QY 3109 cgaagaagtcattccacagagacctgctgctcggaacattctgctcggaagcagct 3168
      |||||||
DB 2684 CGGAAGTGCATCCACAGAGACCTGGCTCTCGGAACATCTCTGTCGGAAGGACGCT 2625

QY 3169 ggtgaagatctgtgactttggccttggccgggagacattacaaagaccctgactacgtccg 3228
      |||||||
DB 2624 GGTGAAGATCTGTGACTTTGGCCTTGGCCGGGACATCTACAAAGACCCGACTAGCTCCG 2565

QY 3229 caaggcagtgcccggctcccctgaagtggatggccccctgaaacatctcttgacaaggt 3288
      |||||||
DB 2564 CAAGGCGAGTGGCCGGCTGCCCTGAAAGTGGATGGGCCCTGAAGACATCTTCCACAAGGT 2505

QY 3289 gtacaccacgacagtgacgtgtgcttctggggtgcttctctggagatcttctctct 3348
      |||||||
DB 2504 GTACACCACGACAGTGACGTGTGGTCTTCTGGGTGCTTCTCTGGAGATCTTCTCTCT 2445

QY 3349 gggggcctcccgctacccctggggtgcagatcaatgaggagttcttccagcggctgagaga 3408
      |||||||
DB 2444 GGGGGCTTCCCGTACCTTGGGGTGCAGATCAATGAGGAGTTCTGCCAGCGCTCAGAGA 2385

QY 3409 cggcacaagaatgagggccccggagctggcgaactcccgcatccagccgcatcgtgaa 3468
      |||||||
DB 2384 CGGCAACAGAGATGAGGGCCCCGGAGCTGGCCACTCCCGCATACGCCCGCATCATGCTGAA 2325

QY 3469 ctgctggtccggagaccccaaggcgagacctgacttctcgagctggtggagatcctggg 3528
      |||||||
DB 2324 CTGCTGCTCGGAGACCCCAAGCCGACACCTGCATTTCTGGAGCTGTGTGGAGATCCTGG 2265

QY 3529 ggaactgtctccggcaggggctcgaagaggaagagaggttctgcatggtgcccccgag 3588
      |||||||
DB 2264 GGACCTGTCTCCAGGCGAGGGGCTGCAAGAGGAGAGAGGTCTGCATGTGCCCGCCGCGAG 2205

QY 3589 ctctcagagctcagaagaggcagcttctcgaggtgtccaccatggccctacacatgac 3648
      |||||||
DB 2204 CTCTCAGACTCAGAAGAGGGGAGGCTTCTGCGAGGTGTCCACATGGGCCCTACACATGCG 2145

QY 3649 ccaggtgacgtgagcagagcccgccagcctgcagcgccacagcctggccgcccagta 3708
      |||||||
DB 2144 CCAGGCTGACGCTGAGGACAGCCCGCCAGCCTGCAGGCCACACACCTTGGCGCCAGGTA 2085

QY 3709 ttacaactgggtgtctcttcccggtgctggtggtccagaggggctgagaccccggttctctc 3768
      |||||||
DB 2084 TTACAACCTGGGTGTCTTCTCCCGGTGCTTGGCCAGAGGGGCTGAGACCCGTTGTTCTCTC 2025

QY 3769 caggtatgaacatttgaggaattcccatgaccccaacgacctcaaaagcctctgtgga 3828
      |||||||
DB 2024 CAGGATGAAGACATTTGAGGAATTTCCCATGATACCCCAACGACCTACAAAGGCTCTGTGGA 1965

QY 3829 caaccagacagacagtggatggtgtgctggcctcgagagagt 3869
      |||||||
DB 1964 CAACCTGACAGACACTGGGATGCTGCTGGCCTCGGAGGAGT 1924

RESULT 37
US-60-213-847-55
; Sequence 55, Application US/60213847
; GENERAL INFORMATION:
; APPLICANT: Beasley, Ellen
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS OF THE
; TITLE OF INVENTION: SER/THR AND TYR FAMILY OF KINASES, NUCLEIC ACID MOLECULES
; TITLE OF INVENTION: ENCODING THESE HUMAN KINASE PROTEINS, AND USES THEREOF
; FILE REFERENCE: CL000704
; CURRENT APPLICATION NUMBER: US/60/213,847
; CURRENT FILING DATE: 2000-06-23
; NUMBER OF SEQ ID NOS: 1824
```

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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 55
; LENGTH: 575
; TYPE: DNA
; ORGANISM: HUMAN
US-60-213-847-55

Query Match      9.8%; Score 401; DB 60; Length 415;
Best Local Similarity 100.0%; Pred. No. 2.4e-180;
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3672 cgcgaagcctcagcgccacacagcctggcgccaggtattacaactggtgtcccttcccg 3731
      |||||||
DB 32 cgcgaagcctcagcgccacacagcctggcgccaggtattacaactggtgtcccttcccg 91

QY 3732 ggtgctggccagaggggctgagaccctggttctctccaggtatgaagacatttgaggaa 3791
      |||||||
DB 92 ggtgctggccagaggggctgagaccctggttctctccaggtatgaagacatttgaggaa 151

QY 3792 tccccatgaccccaacagacctacaaggctctgtggacaaccagacagacagcagtggtg 3851
      |||||||
DB 152 tccccatgaccccaacagacctacaaggctctgtggacaaccagacagacagcagtggtg 211

QY 3852 tgctggcctcgagagagtttgagcagatagagcaggcatagacaagaagcgcgttca 3911
      |||||||
DB 212 tgcggccctcgagagagtttgagcagatagagcaggcatagacaagaagcgcgttca 271

QY 3912 gctgtaaaggacctggccagaatgtggtgtgacagggcacacccctgactcccaaggga 3971
      |||||||
DB 272 gctgtaaaggacctggccagaatgtggtgtgacagggcacacccctgactcccaaggga 331

QY 3972 ggcggcgccgctgagcgggggggggggggggggggggggggggggggggggggggggg 4031
      |||||||
DB 332 ggcggcgccgctgagcgggggggggggggggggggggggggggggggggggggggggg 391

QY 4032 gggagctgctggagcgaagcgagagagaccactgctccccgtctgcccgcgtgactttct 4091
      |||||||
DB 392 gggagctgctggagcgaagcgagagagaccactgctccccgtctgcccgcgtgactttct 451

QY 4092 tcacagacaacagctactaa 4111
      |||||||
DB 452 tcacagacaacagctactaa 471

RESULT 38
US-60-213-178-1247
; Sequence 1247, Application US/60213178
; GENERAL INFORMATION:
; APPLICANT: Beasley, Ellen
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL000689
; CURRENT APPLICATION NUMBER: US/60/213,178
; CURRENT FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 1425
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1247
; LENGTH: 415
; TYPE: DNA
; ORGANISM: Human
US-60-213-178-1247

Query Match      9.8%; Score 401; DB 60; Length 415;
Best Local Similarity 100.0%; Pred. No. 2.4e-180;
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3114 agtgcattccacagacagacctggctgctcggaacattctgctcggaagcagcagtggtga 3173
      |||||||
DB 15 agtgcattccacagacagacctggctgctcggaacattctgctcggaagcagcagtggtga 74
```

QY 3174 agatctgtgactttgacctgcccggagacatctacaaagaccctgactaogtccgcaagg 3233
Db 75 agatctgtgactttgacctgcccggagacatctacaaagaccctgactaogtccgcaagg 134
QY 3234 gcagtgcccggctgcccctgaagtgaagtggccctgaagcatcttcgacaaggtatata 3293
Db 135 gcagtgcccggctgcccctgaagtgaagtggccctgaagcatcttcgacaaggtatata 194
QY 3294 ccacgcagagtgacgtgtgtctcttgggggtgtctctctggagatcttctctctggggg 3353
Db 195 ccacgcagagtgacgtgtgtctcttgggggtgtctctctggagatcttctctctggggg 254
QY 3354 cctcccgcctaccctgggtgacagatcaatgagaggttctgcacggctgagagacggca 3413
Db 255 cctcccgcctaccctgggtgacagatcaatgagaggttctgcacggctgagagacggca 314
QY 3414 caaggatgaggggcccggagctggccactcccgcctacacgcgcacatctgctgaactgct 3473
Db 315 caaggatgaggggcccggagctggccactcccgcctacacgcgcacatctgctgaactgct 374
QY 3474 ggtccggagaccccaaggcgagacctgcattcttcggagctg 3514
Db 375 ggtccggagaccccaaggcgagacctgcattcttcggagctg 415

RESULT 39

US-09-716-953-1245

; Sequence 1245, Application US/09716953

; GENERAL INFORMATION:

; APPLICANT: Gearing, David P.

; APPLICANT: Holtzman, Douglas A.

; APPLICANT: McCarthy, Sean

; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES

; TITLE OF INVENTION: THEREFOR

; FILE REFERENCE: 1600.2044-001

; CURRENT APPLICATION NUMBER: US/09/716,953

; CURRENT FILING DATE: 2000-11-21

; PRIOR APPLICATION NUMBER: 60/167,413

; PRIOR FILING DATE: 1999-11-24

; NUMBER OF SEQ ID NOS: 2620

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 1245

; LENGTH: 535

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: (1)...(535)

; OTHER INFORMATION: n = A,T,C or G

US-09-716-953-1245

Query Match 9.4%; Score 388; DB 28; Length 535;

Best Local Similarity 99.8%; Pred. No. 4e-174;

Matches 438; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3281 gacaaaggtgtacaccacgcagagtgacgtgtgtctcttgggtgtctctctcggagatc 3340

Db 15 gacaaaggtgtacaccacgcagagtgacgtgtgtctcttgggtgtctctcggagatc 74

QY 3341 ttctctctgggggctcccgctacccctgggtgcagatcaatgagagttcttgcacgcgg 3400

Db 75 ttctctctgggggctcccgctacccctgggtgcagatcaatgagagttcttgcacgcgg 134

QY 3401 ctgagagacggcacaaagatgagggcccgcagctggccactccgcatacgcgcgcatc 3460

Db 135 ctgagagacggcacaaagatgagggcccgcagctggccactccgcatacgcgcgcatc 194

QY 3461 atgctgaactgtctgtccggagaccccaaggcgagacctgcattctcggagctggtgag 3520

Db 195 atgctgaactgtctgtccggagaccccaaggcgagacctgcattctcggagctggtgag 254

QY 3521 atcctgggggacctgctccagggcgaggggctgcaagagagagaggttctgcatggcc 3580

Db 255 atcctgggggacctgctccagggcgagggcctgcagaggaagaggtctgcatggcc 314
QY 3581 ccgcgcagctctcagagctcagaagcagaagaggcagcttctcgcaggtgtccaccatggcccta 3640
Db 315 ccgcgcagctctcagagctcagaagcagaagaggcagcttctcgcaggtgtccaccatggcccta 374
QY 3641 cacatcgcccaggtcgacgtgagcagcccgcccaagcctcagcgcacagcctggcc 3700
Db 375 cacatcgcccaggtcgacgtgagcagcccgcccaagcctcagcgcacagcctggcc 434
QY 3701 gccaggtattacaactggg 3719
Db 435 gccaggtattacaactggg 453

RESULT 40

US-60-172-373-15761

; Sequence 15761, Application US/60172373

; GENERAL INFORMATION:

; APPLICANT: Morris, MacDonald

; APPLICANT: Lal, Preeti

; APPLICANT: Diep, Dinh

; TITLE OF INVENTION: Method for the Identification of Sequence Polymorphisms Using

; FILE REFERENCE: GX-0006 P

; CURRENT APPLICATION NUMBER: US/60/172,373

; CURRENT FILING DATE: 1999-12-16

; NUMBER OF SEQ ID NOS: 25,772

; SOFTWARE: PERL Program

; SEQ ID NO 15761

; LENGTH: 1575

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc_feature

; OTHER INFORMATION: Incyte ID No: 902563.1

US-60-172-373-15761

Query Match 8.3%; Score 340; DB 56; Length 1575;

Best Local Similarity 100.0%; Pred. No. 3.7e-151;

Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3772 gatgaagacatttgagggaattccccatgaccccaacgacctacaaaggtctctggacaa 3831

Db 1 gatgaagacatttgagggaattccccatgaccccaacgacctacaaaggtctctggacaa 60

QY 3832 ccagacagacagtgaggatggtgctggtccctcgaggaggtttgagcagatagagagcaggca 3891

Db 61 ccagacagacagtgaggatggtgctggtccctcgaggaggtttgagcagatagagagcaggca 120

QY 3892 tagacaagaaagcggtcttcagctgtaaaggacctggccagaaatgtggctgtgaccaggc 3951

Db 121 tagacaagaaagcggtcttcagctgtaaaggacctggccagaaatgtggctgtgaccaggc 180

QY 3952 acacctgactcccaagggaggcggtggcctgagcggggggcccgagagagccagggt 4011

Db 181 acacctgactcccaagggaggcggtggcctgagcggggggcccgagagagccagggt 240

QY 4012 gttttacaacagcgagtatggggagctgtcgagccaaagcgagagacacactgtctccc 4071

Db 241 gttttacaacagcgagtatggggagctgtcgagccaaagcgagagacacactgtctccc 300

QY 4072 gtctgcccgcgtgactttcttcacagacaacacagctactaa 4111

Db 301 gtctgcccgcgtgactttcttcacagacaacacagctactaa 340

RESULT 41

US-60-213-847-1271

; Sequence 1271, Application US/60213847

; GENERAL INFORMATION:

Result No.	Score	Match	Query %	Length	DB	ID	Description	
1	4111	100.0	4795	1	US-08-340-011-3	Sequence 3, Appli		
2	4111	100.0	4795	3	US-08-901-710-3	Sequence 3, Appli		
3	3912	95.2	4195	1	US-08-340-011-1	Sequence 1, Appli		
4	3912	95.2	4195	3	US-08-501-710-1	Sequence 1, Appli		
5	3912	95.2	4416	3	US-08-795-430-1	Sequence 1, Appli		
6	3912	95.2	4425	1	US-08-222-616-31	Sequence 31, Appli		
7	3912	95.2	4425	5	PCT-US95-04228-31	Sequence 31, Appli		
8	3912	95.2	9108	5	PCT-US95-04228-45	Sequence 45, Appli		
c 9	950	23.1	6827	1	US-08-222-616-17	Sequence 17, Appli		
c 10	950	23.1	6827	5	PCT-US95-04228-17	Sequence 17, Appli		
11	216	5.3	216	1	US-08-795-430-2	Sequence 2, Appli		
12	76	1.8	160	1	US-08-222-616-5	Sequence 5, Appli		
13	76	1.8	160	5	PCT-US95-04228-5	Sequence 5, Appli		
14	56	1.4	70	1	US-08-340-011-7	Sequence 7, Appli		
15	56	1.4	70	3	US-08-901-710-7	Sequence 7, Appli		
16	56	1.4	70	4	US-08-510-133A-2	Sequence 2, Appli		
17	56	1.4	70	4	US-08-585-895-2	Sequence 2, Appli		
18	26	0.6	1467	1	US-08-176-620A-3	Sequence 3, Appli		
19	26	0.6	1467	1	US-08-463-862-3	Sequence 3, Appli		
20	26	0.6	1467	2	US-08-461-985-3	Sequence 3, Appli		
21	26	0.6	1467	2	US-08-458-887-3	Sequence 3, Appli		
22	26	0.6	1467	4	US-08-932-787B-3	Sequence 3, Appli		
23	26	0.6	1467	4	US-08-932-012C-3	Sequence 3, Appli		
24	26	0.6	1467	4	US-08-888-818C-3	Sequence 3, Appli		
25	23	0.6	139	2	US-08-469-537A-19	Sequence 19, Appli		
26	23	0.6	1894	4	US-07-912-122-3	Sequence 3, Appli		
27	23	0.6	1894	5	PCT-US93-06404-3	Sequence 3, Appli		

[illegible]

RESULT 2
 US-08-901-710-3 Application US/08901710
 : Sequence 3, Application 6107046
 : Patent No. 6107046
 : GENERAL INFORMATION:
 : APPLICANT: Alitalo, Kari
 : APPLICANT: Aprelikova, Olga
 : APPLICANT: Pajusola, Katri
 : APPLICANT: Korhonen, Elina
 : APPLICANT: Armstrong, Jaana
 : APPLICANT: Korhonen, Arja
 : APPLICANT: Kaipainen, Marija-Terttu
 : APPLICANT: Mälikäinen, Matti
 : APPLICANT: FLT4, A RECEPTOR TYROSINE KINASE, AND USES
 : TITLE OF INVENTION: FLT4, A RECEPTOR TYROSINE KINASE, AND USES
 :

|||||
Db 841 CGGGGTAACTGGGTGCCCGAGCCAGCGTCCACAGACAGACCACACAGAACTCTCCAGCAT 900
Qy cctgaccaaccacaacgTcagccagcacgacctgggctcgtatgtgtgcaagggcraacaa 960
Db CCGTACCATTCCAAAGCTACGCCAGCACGACCTGGCGTCGTATGTGTGCAAGGCCAACAA 960
Qy rnycatccagcyaTtccgggagagcacccaggtcatgtgcatgaaatcccttcaicag 1020
Db CGGCATCCAGCGATTTCCGGGAGACACCGAGGTCAATGTGATGAAATCCCTTCATCAG 1020
Qy cttcagTqgclTcaaaagaccatTccttgaggccacqacqagagacagctTqgTyaagct 1080
Db CTTCCAGTGGCTCAANGGACCCATCTCTGAGGCCACGCGCAGGAGACGAGCTTGGTCAAGCT 1080
Qy rrrccclqaaagclTqgcagcgtTcccccccgcgcgaatTccagTlqTlacaagqalTqaaaggc 1140
Db rTCCCTGAAGCTGGCAGCGTACCGCCCGCCCGCCAGTTCCAGTGGTACAAGGATGAAAGGC 1140
Qy actatTccyggccacacagTccacalTgccttqgtTcctcaagagagTgacagagTcaaac 1200
Db ACTTCCGGGGGCCACAGATCCACATGCCCTGGTGTCTCAAGGAGGTGACAGAGGCGAGCAC 1200
Qy aygcaactTcacacctTgcctTgtgaaactTgcctTgctgagcctgagTgagTcaacatTcagcct 1260
Db AGGCACCTACACCTCGCCCTGTGAACTTCCGCTGCTGCGCTGAGGCGCAACATCACGCT 1260
Qy ggaagctggTlqaaTgtTgccccccacagatataTlqagaagagagcctTcctcccccagcat 1320
Db GGAGTGGTGGTGAATGTGCCCGCCCGCCACATATGAGAAGGAGGCGCTCTCCCGCAGCAT 1320
Qy ctactTcgcgtTcacagccgcgcagccctTcacctTgacagTcctacgggTgccccTgctct 1380
Db CTACTTCCGCTCACAGCCCGCCAGGCCCTCACCTGACAGGCCCTACGGGGTSCCGCTGCCCTCT 1380
Qy caqcaTccagTggcactTggcgccctTgacacccctTgcaagatgtttgcccaycgtagct 1440
Db CAGCATTCAGTGGCATCGCGCCCTTGACACCCCTTGCAAGATGTTTGGCCAGCGTAGTCT 1440
Qy ccggcgccggcagcagaagacctcatTccacagTlqccgtTgactTgagggcggtacccac 1500
Db CCGGCGCGCGGACAGCAGAACCTCATGCCACAGTGGCGTACTGAGGGCGGTGACCAC 1500
Qy cgaggaTgccTgaaacccatTcgagagcctTggaacacctTgaccaggtTtTggaugga 1560
Db GCAGGATGCCGTGAACCCCATCGACGCTTGACACCTTGACCCGAGTTTGTGAGGJAAA 1560
Qy gaataaactgtTgagcaagctTgtgTlccagaatTgccaacgtTgtTgccaTytacaagTg 1620
Db CAATGAAGACTGTGAGCAAGCTGGTGTATCCAGAAATGCCAAGCTGTCTGCCATGTACAAGTG 1620
Qy TgtggtTccaaagTggccagatTgagcgctcactTacttctatTlqaccacat 1680
Db TGTGTCTCCAAAGGTGGGCCAGATGAGCGGCTCATCTACTTCTATGTGACCAACCAT 1680
Qy ccccgacggctTcaacatTcgaatccaaGCCatTccgagagctTactTgagggccagccggt 1740
Db CCCCAGCGCTTCACCATCGAATCCAGCCATCCGAGGAGCTACTAGAGGCCAGCCCGGT 1740
Qy gclctgagctTgccaagccagcagTlacaagTcagagcatTctgagctTggtTaccgcctcaa 1800
Db GCTCTGAGCTGCCAAGCCGACAGCTACAAGTACCAAGTACGAGCATCTGCGTGTACCGCCCTCAA 1800
Qy cctgtTccagctTgacagTgacagcaggaacccctTctgctgactTgcaagaacgtTqca 1860
Db CCGTTCACGCTGACAGATGCGCAGGGAACCCCGCTTCTGCTCGACTGCAAGAAGCTGCA 1860
Qy tctgtTcgccacccctTctTggccgcagcctTgagagagTggcacctggggcgccacgc 1920
Db TCTGTTCGCCACCCCTCTTGGCGCCAGCCTTGAGGAGGTGGCACCTTGGGCGGCCACGC 1920
Qy cagctcagcctTgagTataTccccccgcgtTgcgcgcagTcagagcagagggccactatTgTqca 1980
Db |||||

Db 1921 CACGCTCAGCTGAGTATCCCCCGCGTCCGCCCGAGCAGAGGGCCACTATGTGTCCGA 1980
Qy agtgaagaacggcgagccatgacaagcactgccacaagaagtacctgtcggtgcaaggc 2040
Db AGTCAAGACGGCGCAGCCATGACAAGCATGCCACAAGAAGTACCTGTGTGTCGAGGC 2040
Qy cctgaagccctcgctcagcagaactTgaccgacctcctTgctgagcTlqagcagcTc 2100
Db CCTGGAAGCCCTCGGCTCAGCGAAACTTGAACCGACTCTCTGTGAACTGAGCGTACTC 2100
Qy gctgagatcagTgctTggtTggcgagcgacgcgcgccagcaTcgtTgTlqaaaga 2160
Db GCTGAGATGAGTGTCTTGTGTGGCGGAGCGCACGCCCGCCAGCATCTGTGTGTTCAAAAGA 2160
Qy cgaagagctgctgagagaaagtctgagTgcgactTggcgactTccaaaccagaagctTgag 2220
Db CGAGAGCTGCTCGAGGAAAGTCTGGAGTGCAGTTGGCGACTTCCAACCAAGAAAGCTGAG 2220
Qy catcagcggtTgcgagagagagTgcggaagcTatctTgcaagcTlqTlqcaagcTcaa 2280
Db CATCCAGCGCTGGCGAGGAGGATGCGGAGCGTATCTGTGACAGCGTGTGCAACGCCAA 2280
Qy gggctgctTcaactcctccgcagcgtTggcggtTggaaggctTccgaggaTaaaggcagcat 2340
Db GGGCTGCGTCAACTCTCCGCCAGCGTGGCGTGCAGAGGTCCGAGGATAAGGCGAGCAT 2340
Qy ggaatcgtTaatcctTgtcgTaccggcgTcaTcgtTgctTctTctTctTctTctTctTctTct 2400
Db GGAGATCTGATCTTGTTCGGTACCGCGCTATCGCTGTCTTCTTCTTCTGGGTCTCTCTCT 2400
Qy cctcatctctTaaatgagagcgccgcacgcagacatcaagcggggctacctTgct 2460
Db CCTCATCTTCTGTAAATGAGGAGCGCGGCCACCGACATCAAGACGGGCTACCTGTCT 2460
Qy catcatcatTgacccccgggaggtTgctctTctTgaggaTgcaatTgcaatTctctTctctcga 2520
Db CATCATGACGCCCGGGAGGTGCCTTGCAGGAGCAATGCGAATACCTGTCTCTACGA 2520
Qy TgcagcagTggaaatTcccccgagagcggtcTcaactgggagagctgctcggactcagg 2580
Db TGCCAGCGAGTGGAAATTTCCCCCGAGAGCGGCTGCACCTGGGGAGAGTGTCTGGGCTACGG 2580
Qy cgctTcgggaggtTgTgagcctcgcgtTctcggcTatccacaagggcgagcagctTgta 2640
Db CGCCTTCGGGAAGTGGTGGAAAGCTTCGCTTTCGGCATCCACAAGGCGACGCTGTGA 2640
Qy caccgtTggcgtTgaaatTgTgaaagggcgccacggcgagcgagcagcgcgctTgat 2700
Db CACGTTGGCGGTGAAAATGCTGAAAGAGGGCGCCACCGCCAGCGAGCACCGCGCGCTGAT 2700
Qy gtcgagctcaagatcctcatTcacatTcgcaaccactTcaacgtTgTcaacctTctcgg 2760
Db GTCGGAGCTCAAGATCTCTCATTTACATCGGCAACCACTCAACGTGTCTCAACCTCTCTCGG 2760
Qy ggcgtTgaccaagcgcgagggccccctcatTgTgtaTcgtTgagTtctTgcaagtacggcaa 2820
Db GGCCTGCACCAAGCGCGAGGGCCCCCTCATGTGTGATCTGTGAGTTCTTCAAGTACGGCAA 2820
Qy cctctcaactTcctTgcgcgaagcgggagcctTcagccccctTgcgcgagaagctctcc 2880
Db CCTCTCAACTTCTTGGCGGCCAAAGCGGAGCGCTTTCAGCCCCCTTGCGGGAGAAAGTCTCC 2880
Qy cgaagcagcgagcgtTccccgcctatTgTlqagactTccagcctgagctgagagcgagc 2940
Db CGACGACGGGAGCGCTTCCCGCGCCATGGTGGAGCTCGCCAGGCTGGATCGAGAGCGGCC 2940
Qy ggggagcagcagggTcctctTcgcgcgctTctcgaagcagcgagggcgagcgagcg 3000
Db GGGGAGCAGCAGAGGTCTCTTTCGCGCGCTTCTCGAAGACCGAGGCGGAGCGAGCGCG 3000
Qy ggcTtctccagaccagaagcTgagggacctTgtggtTgagccccctTgacctTggaagatct 3060
Db GGCTTCTCCAGCAAGAAGCTGAGGACCTGTGGCTGAGCCCCGCTGACCATGGAAGATCT 3060

QY 301 qgtgllgctgctgcacgaaggtatcatgtccaaacgacacagcagctacgtctgtactataaa 360
Db 301 GGTGTTGCTGCTGCACAGAGGTACATGCCAACGACACAGAGCAGTACGCTTGTACTACAA 360
QY 361 qtacatacaaggcacgtatcgagggcaccacgcccgcagctcctctacgtgtlcttqtagaga 420
Db 361 GTACATCAAGGCACGCATCGAUGGCACACAGCCGCCACGCTCCTAGTGTCTCGTGAGACA 420
QY 421 cltltgagcagccattcatcaacaagccttgacacgtcttggtaacaagaauagccat 480
Db 421 CTTTGTAGCAGCCATTTCATCAACAAGCCTGCACAGCTCTTGGTCAACAGGAAGCAGCTCAT 480
QY 481 gttgggtgacctctatgtgtlccalcccccggcctcaatgltcacgcttcttccaaagctc 540
Db 481 GTGGGTGCCCTGTGCTGGTGTCCATCCCGCGCTCAATGTTCACGCTCGCTCGCAAGCTC 540
QY 541 qgtlqcltlyggccaga cyggcagaggtgggtgtggggtgaccggcggaggtcgtctgtgtc 600
Db 541 GCTGCTCTGCCAGACGGGCAGAGGTGGTGTGGGATGACCGCGGGGCATGCTCGTGTTC 600
QY 601 acyccactactgcagatgcccctgtacctgcaatgcaatgcaagaccacctggggagaccaga 660
Db 601 CAGCCCACTGCTGCACGATGCCCTGTACCTGTGAGTGCAGAGACCACTGGGGAGACCAGGA 660
QY 661 ctctccttccaaacctctctgtgtcacatcacagcaacgagctctatgacatccagct 720
Db 661 CTTTCTTTCCAAACCCCTTCTGTGTGCATATCAGAGCAAGAGCTCTATGACATCCAGCT 720
QY 721 gttggccagaaatcgctggagctgctggtaggggagaagctgggtcctgaacctgcaacct 780
Db 721 GTTGGCCAGGAAGTCGTGGAGCTGTGTGTAGGGAGAAGCTGGTCTCTGAACCTGCACCGT 780
QY 781 qtgggtgagttlaactcaggtatcaaccttgaactgggactaccceaggaagcagacaga 840
Db 781 GTGGGTGAGTTTAACTCAAGTGTCACTTTTGACTTGGACTTACCCAGGGAAGCAGGACAGA 840
QY 841 qrggggtaadtgggtgcccagagcagctcccagcagaccacacagaacctctccagcat 900
Db 841 GCGGGTAACTGGTGCCCGAGCGACGCTCCGAGCAGACCCACACAGACTCTTCCAGCAT 900
QY 901 cctlaarrvalccaaacgttcagccagacagacctggagctcgtatgtgtgaaagccaaaca 960
Db 901 CTTGACCATTCACAACGCTCAGCCAGCAGCACCTTGGCTCGTATGTGTGCAAGGCCAACAA 960
QY 961 cygcatccagcagatttcgggagagcaccaggtcattgtgtcaglaaaatcccttccacag 1020
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RESULT 5
US-08-795-430-1
; Sequence 1, Application US/08795430
; Patent No. 6130071
; GENERAL INFORMATION:
; APPLICANT: Alitalo, Kari
; APPLICANT: Joukov, Vladimir
; TITLE OF INVENTION: Vascular Endothelial Growth Factor C (VEGF-C)
; TITLE OF INVENTION: Protein and Gene, Mutants Thereof, and Uses Thereof
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/795,430
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/FI96/00427
; FILING DATE: 01-AUG-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/671,573
; FILING DATE: 28-JUN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/601,132
; FILING DATE: 14-FEB-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/585,895
; FILING DATE: 12-JAN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/510,133
; FILING DATE: 01-AUG-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/340,011
; FILING DATE: 14-NOV-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Gass, David A.

. . .

REGISTRATION NUMBER: 38,153
REFERENCE/DOCKET NUMBER: 28967/33691
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4416 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cdna
US-08-795-430-1

Query Match 95.2%; Score 3912; DB 3; Length 4416;
Best local Similarity 100.0%; Pred. No. 0;
Matches 912; Conservative 0; Mismatches 0; Indels 0; Caps 0;

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RESULT 6
US-08-222-616-31
; Sequence 31, Application US/08222616
; Patent No. 5635177
; GENERAL INFORMATION:
; APPLICANT: Bennett, Brian D.
; APPLICANT: Goeddel, David

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RESULT 7

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PCT-US95-04228-31
: Sequence 31, Application PC/TUS9504228
: GENERAL INFORMATION:
: APPLICANT: Genentech, Inc.
: APPLICANT: Bennett, Brian D.
: APPLICANT: Goeddel, David
: APPLICANT: Lee, James M.
: APPLICANT: Matthews, William
: APPLICANT: Tsai, Siao Ping
: APPLICANT: Wood, William I.
: TITLE OF INVENTION: PROTEIN TYROSINE KINASE AGONIST ANTIODIES
: NUMBER OF SEQUENCES: 45
: CORRESPONDENCE ADDRESS:
: ADDRESS: Genentech, Inc.
: STREET: 460 Point San Bruno Blvd
: CITY: South San Francisco
: STATE: California
: COUNTRY: USA
: ZIP: 94080
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: patin (Genentech)
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: PCT/US95/04228
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/222616
: FILING DATE: 04-APR-1994
: ATTORNEY/AGENT INFORMATION:
: NAME: Wendy M. Lee
: REGISTRATION NUMBER: 00,000
: REFERENCE/DOCKET NUMBER: 821P3PCT
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 415/225-1994
: TELEFAX: 415/952-9881
: TELEX: 910/371-7168
: INFORMATION FOR SEQ ID NO: 31:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 4425 bases
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
PCT-US95-04228-31
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Query Match 95.2% Score 3912; DB 5; Length 4425;

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 3912; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 72 CCTGGGACTCCTGTGACGGGCTTGGTGAGTGCTACTTCAATGACCCCGCCGACTTGAACAT 131
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Db 2892 CGAGCAGCGCGGACGCTTCGCGCCCATGTGTGAGCTCGCCAGGCTGCGATCGGAGCGGCC 2951
Qy 2941 gggtgcagcagcaggttctctcgcggttctcgaagaccagagggcgagcgagggcg 3000
Db 2952 GGGGAGCAGCAGAGGTCTCTTCCGCGGCTTCTCGAAGACCGAGGGCGGAGGGCGG 3011
Qy 3001 gggttctccagaccaaagaagctgaggaacctgtggctgagccccgtgacctggaagatct 3060
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Qy 3061 ggtctctacagcttccaggtggccagagggatggaggttcttggcttccccgaagtgc 3120
Db 3072 TGTCTCTCTACGCTTCAGGTGGCCAGAGGGATGGAGTTCTCTGGCTTCCCGAAAGTGCAT 3131
Qy 3121 ccacagagacctggctgcggaacattctctcggaagacgagctggtgaagatctg 3180
Db 3132 CCACAGAGACCTTGGCTGCTCGGAACAATTCGTCTGCGAAAGCGACGTGGTGAAGATCTG 3191
Qy 3181 tgactttggccttggccgggacatctacaagaacctgactacgtlcccgcaagggcagtg 3240
Db 3192 TGACTTTGGCCTTGCCCGGGACATCTACAAAGACCCCTGACTAGCTCCGCGCAAGGGCAGTGC 3251

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Oy 3241 ccgactgccccgaagtgtgagtgccctgaaagcatctctgacaaagtggtacaccagca 3300
Db 3252 CCGCTGCCCTCGAAGTGTGATGGCCCTGGAAGCATCTTCACAAAGGTGTACACACGCA 3311
Oy 3401 gaggagagctggttcttgggtgctctctctctctctctctctctctctctctctctcc 3360
Db 3312 CAGTGACCTGTGCTGCTTGTGGGCTGCTTCTCTGGAGATCTTCTCTGGGGGCTCCCC 3371
Oy 3361 gLacccctggagtcagatcaatgagagttctgcccagcggtgagagacggcacaagat 3420
Db 3372 GTACTCTGGGTGCAGATCAATGAGGAGTCTGCCACGGCTGAGAGACGGCACAAAGAT 3431
Oy 3421 gagggtccggagctggcactcccgccalacgcgcgcacatgctgaactgctggtccgg 3480
Db 3432 CAGGCCCCGAGCTGCCACTCCCGCATACGCGCGCATGCTGAACCTGCTGCTCCGG 3491
Oy 3481 agaccccaagcgagagactgcattctcggagctgggtgagatctctggggacctgtcca 3540
Db 3492 AGACCCCAAGCGAGACTGCAATCTCGAGCTGCTGAGATCTCTGGGGACCTGCTCCA 3551
Oy 3541 ggcaggggctcgaagaggaagaggtctgcatggccccgcgcagctctcagaactc 3600
Db 3552 CGCAGGGGCTGCAAGAGAGAGAGGTCTGCATGGCCCCCGCGCAGCTCTCAGAGCTC 3611
Oy 3601 aagaggggagctctcgcaggtgtccaccatggccctacacatcgcccaaggctgacgc 3660
Db 3612 AGAAGAGGGAGCTTCTCGAGGTGTCCACCATGGCCCTACACATGCCCGCAGGCTGACGC 3671
Oy 3661 tgaagacagccgcgaagctcgaagcgaagcagcagcctgagcaggtattacaactgggt 3720
Db 3672 TGAGCAGAGCCCGCAAGCTTGACGCCACAGCTGCGCCGCGCAGGTATTTACAACCTGGT 3731
Oy 3721 gtccttccccgggtgacctgagaggggctgagaccgtggttctccaccaggtgaagac 3780
Db 3732 GTCTTTTCCCGGTGCTGCGCCAGAGGGGCTGAGACCCGTGCTTCTTCCAGAGTGAAGAC 3791
Oy 3781 alltgagaaaltcccaagaccaccaacgactacaaggctctgtgtgacaccagacaga 3840
Db 3792 ATTTGAGGAATTCCTCATGACCCCAAGCAGCTACAAAGGCTCTCTGGACAAACGACAGA 3851
Oy 3841 cagtgagatggtgctgacctcgagagagtttgagcagatagagcagcgatagacaaga 3900
Db 3852 CAGTGGGATGCTGCGCTCGAGGAGTTTGACGATAGACAGCAGGCGCATAGACAAGA 3911
Oy 3901 aagcggtctcag 3912
Db 3912 AAGCGGCTTCAG 3923
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RESULT 8
PCT-US95-04228-45
: Sequence 45, Application PC/TUS9504228
: GENERAL INFORMATION:
: APPLICANT: Genentech, Inc.
: APPLICANT: Bennett, Brian D.
: APPLICANT: Goeddel, David
: APPLICANT: Lee, James M.
: APPLICANT: Matthews, William
: APPLICANT: Tsai, Siao Ping
: APPLICANT: Wood, William I.
: TITLE OF INVENTION: PROTEIN TYROSINE KINASE AGONIST ANTIBODIES
: NUMBER OF SEQUENCES: 45
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Genentech, Inc.
: STREET: 460 Point San Bruno Blvd
: CITY: South San Francisco
: STATE: California
: COUNTRY: USA
: ZIP: 94080
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 5.25 inch, 360 kb floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
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: SOFTWARE: patin (Genentech)
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: PCT/US95/04228
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA: 08/222616
: APPLICATION NUMBER: 04-APR-1994
: FILING DATE: 04-APR-1994
: ATTORNEY/AGENT INFORMATION:
: NAME: Wendy M. Lee
: REGISTRATION NUMBER: 00,000
: REFERENCE/DOCKET NUMBER: 821P3PCT
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 415/225-1994
: TELEFAX: 415/952-9881
: TELEX: 910/371-7168
: INFORMATION FOR SEQ ID NO: 45:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 9108 bases
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: PCT-US95-04228-45
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Query Match 95.2%; Score 3912; DB 5; Length 9108;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3912; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ccacgcgcagcgccgagatgcagcggggcgccgcgcgtgctcgcgactgtggtctcg 60
Db 944 CCACGCGCAGCGCGCGAGATGCAGCGGGCGCGCGCTGTGCTCGACTGTGGCTCTG 1003
Oy 61 cctggactctggagcggcctggtgagtggtgactactccatgacccccccgaccttgaacat 120
Db 1004 CTTGGGACTCTTGGAGCGCTGTGTGAGTGGCTACTTCATGACCCCCCGACCTTGAACAT 1063
Oy 121 cagcgagaggtcacacgtcatgcacacccggtgacagcctgtccatctctcaggggaca 180
Db 1064 CACGGAGGAGTACACGCTCATGCACACCCGCTGACACCCCTGTCCATCTCTCGAGGGGACA 1123
Oy 181 gcacccccctcagtggtggttggccaggagctcagagggcggcagccacccggagagacaaga 240
Db 1124 GCACCCCTCGAGTGGCTTGGCCAGGAGCTCAGGAGGGCGCCAGCCACCGGAGACAAGGA 1183
Oy 241 cagcagagacacgggggtggtgcgagactgcaggggacagagcgcagggccctactgaca 300
Db 1184 CACGGAGGACCGGGGTTGGTGGAGACTGCCGAGGGCACAGACGCGCCCTACTTGCAA 1243
Oy 301 ggtgttgcctgctgcagaggtacatgccaaacgacacagcagctacgtctgctactaca 360
Db 1244 GGTGTGTGCTGCTGCAGAGGTACATGCCCAACACACAGCGCAGCTACGTCTGCTACTACAA 1303
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Db 1304 GTACATCAAGGACGCGATCGAGGGCACACCGCGCCAGCTCCTACGTCTTCTGTGAGAGA 1363
Oy 421 ctttgagcagccattcatcaacaagcctgacacgtcttggccaacaggaagacgacct 480
Db 1364 CTTTGAGCAGCCATTCATCAACAAGCTGTACACGCTCTTGGTCAACAGAGGAGGAGCCCAT 1423
Oy 481 gtgggtgcctgctctggtgtccatcccgggcctcaatgtcacgctgcgctgcgaagctc 540
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Oy 541 ggtgctgtggccagacggcgagagaggtggtgagatgacccggcggtgctgctgtc 600
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Oy 601 cagccactgctgcacgatgccctgtacctgagtcgagaccacacctggggagacacaga 660
Db 1544 CACGCCACTGTGTCACGATGCCCTGTACTGTGAGTGGCAGACCCACCTGGGGAGACCAAGGA 1603
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QY 661 cttcccttccaaaccccttctggtgcacatcacaggcaacgagctctatgacatccagct 720
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QY 721 gttgccagaagtgctgagctgctgtaggggagaaagctggctcctgaaactgcacagct 780
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Db 1664 GTTGGCCAGCAAGTCTGCTGAGCTGCTGTGTACGGGAGAACTTGGTCTGAACCTGACCCGT 1723

QY 781 gtaggctgagtttaactcaagtgctucctlltgactggagactcccagggaagcagaga 840
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Db 1724 GTGGGCTGAGTTTAAC'TCAGGTGTACCTTTTACCTTGGCACTACCCAGGGGAAGTAGGCAGA 1783

QY 841 gcuqggaagtggggtgccecyagcagcgtlcccgagcagjactcacacagaactl'c'c'agrat 900
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Db 1784 GCGGGGTAAAGTGGGTGCCCGACCGAGCTCCCGACAGACCCACACAGAAGCTCTCCAGGAT 1843

QY 901 rrtlgacratccacaacgctcagccagcaagcctgggctctatgtgtcgaauqcccaaaa 960
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Db 1844 CCGTACCATCCACAACGCTGAGCCAGCAGACCTGGGCTGTGTATGTGTGCAAGGCCAACAA 1903

QY 961 cyqcatccagcagattlccggagagacacagagtgcatlgtgcatgaaaaatcc'lt'culcaq 1020
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Db 1904 CCGCATCCACCGATTTCCGGAGAGCAGCAGAGCTGGGCTGTGTATGTGTGCAAGGCCAACAA 1963

QY 1021 cgtcagtggtgtcaaaagacccatccttgaaqccacgagagcagagcagclggtgaaact 1080
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Db 1964 CCGTGCAGTGGCTCAAAAGNCCCATCTCGAGGCCACGAGAGAGAGCTGGTGAAGCT 2023

QY 1081 gccgtlgaaagctggcagcgtatcccccccccagctlccagtggttacaaggatgaaagc 1140
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Db 2024 GCCCGTGAAGCTGGCAGGCTAGCCCCCCCCAGTTCCAGTGGTACAAAGGATGGAAGGCC 2083

QY 1141 actglccggggccacagctcacatgcctcctggtcctcaagagagtgacagagccagcac 1200
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Db 2084 ACTGTCCGGGGCCACAGCTGCACATGCCCCCTGTGTCTCAAGAGAGGTGACAGAGGCCAGCAC 2143

QY 1201 aggcacctlacacctlccgctgtgaaactccgcltgcctgagcctgagggcacaacatccagct 1260
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Db 2144 AGGCACCTTACACCCCTGCGCCCTGTGGAACTCCGCTGCTGGCCCTGAGGCCAACATCAGGCT 2203

QY 1261 gtagctggtlggtgaaatgcccccccccagatacatgaaagagagcctcctccccagcat 1320
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Db 2204 GGAGCTGTGTGTGAATGTGCCCCCCCCAGATACATGAGAAGAGGCTCTCTCCCCACAGCAT 2263

QY 1321 ctactccgctcacagccagcagcctcaactgcagcctcctacaggggtgccttgcctct 1380
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Db 2564 TGTGGTCTCCAACAAGGTGGCCAGGATGAGCGGCTCATCTACTTCTATGTGACCACCAT 2623

QY 1681 ccccgacgcttccacctcaatccaaagccatccgagagactactagagggccagccggt 1740
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QY 1741 gclctgagctgccaaagccgacagctlacaagtacgagcatctgcgctggtaaccgcctcaa 1800
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Db 2684 GCTCTGAGCTGCCAAGCCGACAGCTACAAGTACGAGCATCTGCCTGCTGTAACCGCTCAA 2743

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Db 2804 TCTGTTGCCACCCCTCTGTGGCCGCGAGCTGAGGAGGTGGCACTGGGGCGCCGACGC 2863

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Db 2864 CACGCTCAGACCTGAGTATTCCTCCCGCTGCGCCGCGAGCACGAGGGCCACTATGTGTGCGA 2923

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Db 2984 CCTGGAAGCCCTCGGCTCACCGCAGAACTTGACCGACCTCTCTGTGAACGTGACCGACTC 3043

QY 2101 gctggagatgcagtgcttgtggtgcccagcagcagcagcagcagcagcagcagcagc 2160
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Db 3044 GCTGGAGATGCAGTGTGTGTGGCCGAGCGCACGCCCGCCAGCATCGTGTGTTACAAAGA 3103

QY 2161 cgaagagctgctggagaaaaagctcgtgagtcgacttgagcagctccaaacagagctgag 2220
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QY 2281 gggctgctcaactcctccgcccagcgtggtggtggaaggtccgagagataaaggcagcat 2340
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QY 2341 ggaatcgtgataccttctggttaccggcgtcatcgtgcttcttcttctggtcctcctcct 2400
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|||||

